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Aay71312 Rat neuri
Abb81077 Rat neuro
Abb89192 Human pol
Aaw53947 Human NSP
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Human RTN
Human neu
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Fragment
Extended
Human NSP
Human NOG
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Human Nog
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Human MDD
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2678.292 Million cell updates/sec
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1 QASGEAGVSCLRENFAVYSV......ESEVAISEELVQKYSNSALG 141
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                                                                                 June 16, 2005, 12:31:51 ; Search time 20.3612 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
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Maximum DB seq length: 200000000
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Match Length DB
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Human Human Human	Human Nog Human pan Human neu	Human Nog Human pol Human tru	Human Human Human	Human gen Human sec Rat Nogo	Rat neuri Human gen Rat neuro	Alternati A bone ma
Aay56967 Aab82349 Aau04591	Abg30938 1 Abp68600 1 Abb81078 1	Abr59667 Ado08103 Ado26400	Adp45551 Adp67234 Adr13966	Aae03980 Aab64514 Aay71558	Aay71383 Aae03987 Abb81076	Aay71385 Aay53624
AAY56967 AAB82349 AAII04591	ABG30938 ABP68600 ABB81078	ABR59667 ADO08103 ADO26400	ADP45551 ADP67234 ADR13966	AAE03980 AAB64514 AAY71558	AAY71383 AAE03987 ABB81076	AAY71385 AAY53624
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ALIGNMENTS

Rat Nogo Mus muscu Rat neuri

Alternati Rat neuro

Aay71557 Adt89537 Aay71310 Aay71384 Abb81074 Ado26399 Ado45572

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dysproliferative disorders e.g. psoriasis and tissue hypertrophy.

Mibozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yo proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a rat Nogo C protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, menagioma, haemancoma, croustic neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign
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 Misc-difference 298
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64 GVVFGASLFLLLSLITVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; rat; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its
                                                                                                                                                                                                                                                  GVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYL 121
prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are teferred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers
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                                                                                                                 Score 680.5; DB 3; Length 522;
Pred. No. 3.8e-71;
); Mismatches 1; Indels 1;
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98US-00218277.
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                                                                                                                                Best Local Similarity 98.6
Matches 138; Conservative
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                                                                                    Sequence 522 AA;
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22-DEC-1998;
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Novel 1405 isolated polypeptides, useful for diagnosis, treatment and

prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative

disorders

invention relates to novel genes (ABL89449-ABL90853) and proteins

Claim 11; SEQ ID NO 1568; 2081pp + Sequence Listing; English

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peptics. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system of from injury/disease, where the injury is spinal condingury blunt cramma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative crocess occurring in either gray or white matter or both. The disease is disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and correspondential sease. Carpal tunnel syndrome, peripheral as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral as ansociated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute croured as creutzfeldt-Jakob disease, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-compathies, complications of various divige (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia, anyloid genese, or lipoproteinemia. The present sequence represents the rat comparing a receptor protein nousement sequence represents the rat contrantant the rate or neuropathy, diant axonal neuropathy, selecting anyloid of or organophosphates), charcot-Marie-Tooth disease, and is neuropathy, diant axonal neuropathy, Referum's disease, republicant neuropathy, disease, and resemble of NS-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
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Pred. No. 1.4e-51;
0; Mismatches 1; Indels
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neurological disease; infection; human; secreted protein.
nucleotide sequence the NS-specific antigen
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97 9

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Score 503; DB 5; Length 118; Pred. No. 4.7e-51; 1; Mismatches 1; Indels

71.3%;

Matches 102; Conservative

Query Match Best Local Similarity

Sequence 118 AA;

from WIPO at ftp.wipo.int/pub/published_pct_sequences

1 MDGQKKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVFSIVSYTAYIALALLSVTIS 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS

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(ABB89040-ABB90444) useful for preventing, treating or amaliorating medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are medical conditions of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and overation cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract. liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing cardiovascular disorders e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as wiral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

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NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy; neurodegenerative disease; amyotrophic lateral sclerosis; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                    Human neuro-endocrine-specific protein-like proteins - useful for diagnosis, monitoring and treatment of cancer and neuro-degenerative
FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
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                                                                                                                                                                                                                                                                                                                                              Hillman
                                                                              AAW53947 standard; protein; 199 AA
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                                                                                                                                                  Human NSPLP protein A.
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                                                                                                                                                                                                                                                                                                  12-AUG-1996;
                                                                                                                                                                                                                                                                            24-JUL-1997;
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                              WO9806841-A2
                                                                                                                                                                                                                                                      19-FEB-1998.
                                                                                                                                                                                                                                                                                                                                              Bandman O,
                                                                                                     AAW53947;
98
                                                                     AAW53947
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8
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18-MAY-2001; 2001WO-US016450

WO200190304-A2.

29-NOV-2001.

19-MAY-2000; 2000US-0205515P

(HUMA-) HUMAN GENOME

Rosen CA;

Birse CE,

WPI; 2002-122018/16.

N-PSDB; ABL89601

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Feng P;
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Ebner 1
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                                                                                                                                                  This sequence is a human neuroendocrine-specific protein-like protein (NSPLP) of the invention. Recombinant cells transformed with the DNA are used to express the NSPLP proteins, which are used to treat cancer and neurodegenerative diseases unto as amyotrophic lateral sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be used to inhibit activity of the NSPLP proteins. Antibodies specific for NSPLP are used for diagnosis and monitoring treatment of diseases associated with NSPLP expression, in usual immunoassays, and to isolate NSPLP from natural sources. The NSPLP proteins, or their fragments can also be used diagnostically and for monitoring treatment (in hybridisation or amplification assays); to isolate closely related sequences; in gene therapy for both sense and antisense applications (including use of ribozymes) and for mapping the natural genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 71.3%; Score 503; DB 2; Length 199; Local Similarity 98.1%; Pred. No. 9.4e-51; les 102; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragment of human secreted protein encoded by gene 69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW78313 standard; protein; 199 AA
                                                                               Claim 1; Page 38; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9705-0049548P-
9705-0049550P-
9705-0049566P-
9705-0049607P-
9705-0049608P-
9705-0049609P-
9705-0049610P-
9705-0049611P-
9705-0059611P-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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\texttt{E} \times 
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This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAXA3122) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAXA311-X04410; amino acid sequences AAWA3126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see AAX04311 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; human; cytokine; cellular proliferation; cell movement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                       Ni J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encouseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                                                                                                                                                                                                                                                                                                 Olsen HS;
, Yu G, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 503; DB 2; Length 199;
Pred. No. 9.4e-51;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM, Lafleur DW, O
, Greene JM, Perrie AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 62; 380pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Ri
, Young P,
              970S-0058665P.
970S-0058668P.
970S-0058669P.
970S-0058971P.
970S-0058971P.
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97US-0060841P.
97US-0060844P.
97US-0060865P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 98.1
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Shi Y, Ro
Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-080881/07.
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                                                                                                                                                                                                                                                                                                        02-OCT-1997;
18-AUG-1997
                   12-SEP-1997
                                              12-SEP-1997
                                                                  12-SEP-1997
                                                                                          12-SEP-1997
                                                                                                                12-SEP-1997
                                                                                                                                                                                     02-0CT-1997
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                                                                                                                                                                                                                                                          02-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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WO9931236-A2 Homo sapiens

24-JUN-1999

17-DEC-1998; 17-DEC-1997; 09-FEB-1998; 10-AUG-1998;

3-APR-1998

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The present invention relates to a new member of the human neuroendocrine specific protein family, designated NSPH. The present sequence represents the human NSPH protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLISLTVFSIVFSIVAYIALALLSVTIS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide designated NOGO-C is a splice variant of the human NOGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                     Specific protein of human neuroendocrine, coding sequence and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 199,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.3%; Score 503; DB 3; L. 98.1%; Pred. No. 9.4e-51; ive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                         preparating process and application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB82348 standard; protein; 199 AA
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                                                           98CN-00121473
                                                                                              98CN-00121473
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                                                                                                                                                                                                                                                                                                                           Claim 4; Page 14-15; 21pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOGO-C protein.
                                                                                                                                                                                                                WPI; 2000-466537/41.
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Les 102; Conserv
                                                                                                                                   (UYFU-) UNIV FUDAN.
                                                                                                                                                                                                                                    N-PSDB; AAA72981
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 199 AA;
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                                                                                                                                                                           Zhao Y,
                                                           30-OCT-1998;
                                                                                                30-OCT-1998;
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                       17-MAY-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammanory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify shaving genetic diseases resulting from abnormal expression of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases
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cellular differentiation; immune system regulator; anti-inflammatory; haematopoiesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy; genetic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 503; DB 2;
Pred. No. 9.4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NSPH protein sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 185-186; 516pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human secreted proteins.
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                                                                                                                                                                                                                                                                  98US-0074121P.
98US-0081563P.
98US-0096116P.
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98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                    Duclert
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Homo sapiens

CN1253180-A

24-NOV-2000

MX SX MX BX BX BX SX B

AAB12805;

AAB12805 RESULT

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Query Match

Matches

Disclosure; Page 64; 68pp; English.

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variant of the human NOGO gene on chromosome 221. 2 Other splice variants, NOGO-A and NOGO-B, have previously been identified. The invention provides NOGO-B, have previously been identified. The for producing such polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated
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                                                                                             encoded by a novel splice p21. 2 Other splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; kelodi formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDGQKKOWWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 9.4e-51;
1; Mismatches 1; Indels
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                                                                                             that of human NOGO-C,
                                                                                                                                                                                                                                                                                                                     with inappropriate NOGO-C activity or levels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG30939 standard; protein; 199 AA
                                                        Claim 3; Page 25; 25pp; English
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
71.3%;
Best Local Similarity 98.1%;
Matches 102; Conservative
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                                                                                               secuence 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NogoC protein.
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                                                                                                                                                                                                                                                                                                                                                            Sequence 199 AA;
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                                                                                             The
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE bytypeptides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating cute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas). Pyperproliferative or dysproliferative disorders (e.g. cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue typertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may be useful in treating to the polynucleotide according to identify agents that may be useful in treating of Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polynucleotide encoding the BACE polypeptide are useful in manufacturing a medicament for the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the special symptoms or improving the condition of a patient suffering from this city accorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polynucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy and assays, a probe, in recombinant protein synthesis, and in gene therapy and assays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present amino acid sequence represents the human Nogoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.3%; Score 503; DB 5; Length 199; 98.1%; Pred. No. 9.4e-51; tive 1; Mismatches 1; Indels
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98US-00218277.
99US-00314161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 199 AA;
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22-DEC-1998;
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to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary syndoidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin [Ig]A- and IgG gammapathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangectasia, Friedreich's ataxia, amyloid polyneuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the human neurotransmitter receptor protein Nogo-C, an example of NS-specific
                                                                                                                                                                                                                                                                 The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                        from injury/disease, where the injury is spiral cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or autoaused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Albreimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, vitamin deficiency, intervertebral disc hermistion, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral neuropathies associated with various diseases, including but not limited
                                                                                                             Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.3%; Score 503; DB 5; Length 199; 98.1%; Pred. No. 9.4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                         Example; Page 57-58; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP19211 standard; protein; 199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted polypeptide #62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102; Conservative
                                            2002-607255/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                   N-PSDB; ABN86601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP19211;
  Moalem G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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New isolated polynucleotide encoding secreted polypeptide, useful for gene therapy, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes.

Clusel C;

Dumas Milne Edwards J, Bougueleret L, Jobert S,

(GEST) GENSET SA.

WPI; 2004-440404/41.

Duclert A;

N-PSDB; ADP18806

15-OCT-2001; 2001US-00978360.

10-JUN-2004

17-DEC-1998; 98WO-IB002122. 09-FEB-1999; 99WO-IB002282. 21-UIM-2000; 2000WO-IB009551. 15-SEP-2000; 2000US-00663600.

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proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polynucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing the human tissues and cells, and for distinguishing between human tissues and cells, and for express the polynucleotides comprising the cDNAs. The polynucleotides and polypeptides are useful in forensic procedures or diagnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence represents a human secreted polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed procedure or the polymedial of the patinted in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
                                                                                                                                                                                                                                                                                                                                                                                    invention relates to human cDNA sequences that encode human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contactin associated protein-1; Caspr; neuroprotective; gene therapy; CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Pred. No. 9.4e-51;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVOKYSNSALG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; Nogo-C; neurite outgrowth inhibitor; Nogo;
                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 467; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP67236
ID ADP67236 standard; protein; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vuery match
Best Local Similarity 98.1%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Nogo-C protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 199 AA;
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X A X S X A X A X A X Y X A X A
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Human; secreted protein; genetic disease.

US2004110939-A1

Ното варіепв

us-09-830-972-32.rag

99WO-US026160 98US-0107446P

Chen MS; Σ S. E.

Xiao Z;

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Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                               Example; Page; 122pp; English
                                                                                                                                                                                                                                               WPI; 2000-400052/34
 WO200031235-A2.
                                                                                                                                                     (SCHW/) SCHWAB
(CHEN/) CHEN M
                                                                           05-NOV-1999;
                                                                                                                 06-NOV-1998;
                                     02-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel composition comprising neurite outgrowth inhibitor (Nogo) and contactin-associated protein-1 (Caspr) or its mimetics or a substance capable of promoting interaction between Nogo and Caspr, in combination with a carrier. A composition of the invention has neuroprotective activity, and may have a use in gene therapy. The composition is useful for treating injury to or disease of the CNS, e.g. spinal cord injury, multiple solerosis, epilepsy or stroke. The present sequence represents human Nogo-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat; neurite growth inhibitor; Nogo A; Nogo C; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzhaimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
                                                                                                                                                                                                                                                                     New composition comprising Nogo and Caspr or a substance capable of promoting interaction between Nogo and Caspr useful for treating injury to or disease of the CNS, e.g., spinal cord injury, multiple sclerosis, epilepsy or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Nogo C/Nogo A proteins derived fragment to construct mutant Nogo-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nuce= "Corresponds to residues 40-50 of rat Nogo C potein shown in AAY1312"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
structural plasticity; screening; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRIYKGVIOAIOKSDEGHPFRAYLESEVAISELVOKYSNSALG 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.3%; Score 503; DB 8; 98.1%; Pred. No. 9.4e-51; iive 1; Mismatches 1;
                                                                                                                                 (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
(FORR/) FORREST G R.
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 14; 202pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71559 standard; protein; 199 AA
                                     05-DEC-2003; 2003WO-GB005329
                                                                       06-DEC-2002; 2002US-0431549P
20-JUN-2003; 2003US-0480138P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                               WPI; 2004-468705/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 199 AA;
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24-JUN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches 10
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RESULT 13

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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharymgioma, coligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent typerproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments from rat Nogo c and Nogo A proteins. The fragment is used in the construction of mutant Nogo-C which is composed of His-tag/T7-tag/Nogo-C N-terminus (II aa) + Nogo-A sequence as 975-1162. Nogo protein. Major inhibitory region was identified in the Nogo sites of Nogo protein. Major inhibitory region was identified in the composition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the composition in Addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 and Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in discourse for these SEQ ID NO: 29 in discourse for these SEQ ID NO: 2000 and sequence for these SEQ ID NO: 2000 and sequence for the sequence for the secure shown in AAV71310 and sequence for the sequence for the seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141
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Matches 103; Conservative
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/note= "Corresponds to residues 975-1162 of rat Nogo A protein shown in AAY71310"

Key Region

Region

/label= Unknown

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02-JUN-2000
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                                                                                                                                                                                                                                           CHEN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening.
                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                              New polypeptide having BACE1 activity, useful in preparing a composition for treating amyloidosis or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                            The invention relates to an isolated polypeptide having BACE1 activity. The protein is RTM4 or RTM3 protein. The polypeptide is useful in preparing a composition for treating amyloidosis or Alzheimer's disease. This sequence corresponds to the RTM-4C protein.
                          neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3; amyloidosis; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                       1 MDGOKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
                                                                                                                                                                                                                                                                                                                                                                     38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
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                                                                                                                                                                                                                                                                                                                              Length 199;
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                                                                                                                                                                                                                                                                                                                                                                                                                     FRIYKGVIQAIQKSDEGHPFPAYLESEVAISEELVQKYSNSALG 104
                                                                                                                                                                                                                                                                                                                                                 2, Indels
                                                                                                                                                                                                                                                                                                                             Score 496; DB 7;
Pred. No. 6.3e-50;
1; Mismatches 2;
                                                                                                                                                                                                                                           Claim 52; SEQ ID NO 9; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human neurite growth inhibitor Nogo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY71311 standard; protein; 1178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Unknown
                                                                                                                                                     (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                08-APR-2003; 2003WO-US008829.
                                                                                                                                  17-APR-2002; 2002US-0373284P.
                                                                                                                                                                                                                                                                                                                              70.4%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.1 Matches 101; Conservative
        Human RTN-4C protein.
                                                                                                                                                                                           WPI; 2003-854033/79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 189
                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                            Sequence 199 AA;
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                                                                          WO2003088926-A2
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                                                        Homo sapiens
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                                                                                             30-OCT-2003
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AAY71311
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The present sequence is a human Nogo protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The human Nogo sequence was derived by aligning human expressed sequence tags (ESTS) e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565, AA081525 and AA081840 whith the rat Nogo sequence. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, craniopharyngioma, ependyoma, pincaloma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve disease e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. processed to inhibit.

Ribozymes or antisense Nogo nucleic acids can be used to inhibit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating neoplastic disorders regeneration of neurons.
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/note= "Region specifically described in claim 16"
                                                                                                                                                                                                                                                                                                                                                'note= "Region specifically described in claim 16"
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Pred. No. 3.2e-43;
3; Mismatches 8; Indels 2;
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                              'label= Unknown
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Misc-difference 190
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CHEN M S.
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                                                            Misc-difference
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1014 LLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAÏSEEL 1073 g

132 VQKYSNSALG 141 |||||||||| 1074 VQKYSNSALG 1083

Search completed: June 16, 2005, 13:11:07 Job time: 21.3612 secs දු පු

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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-513-999C-7861

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US-09-149-767-45132

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Gapop 10.0 , Gapext 0.5
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No.
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Sequence 9124, Application US/09949016

Sequence 9124, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 05/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/237,768

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9124

LENGTH: 201

TYPE: PRT

US-09-949-016-9124
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Sequence 8, Appli
Sequence 8450, Ap
Sequence 14833, A
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                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 ISFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          US-09-248-796A-14833
US-09-897-425-46
                                                                                                                                                                                                               US-09-949-016-8450
US-08-470-638-6
US-09-422-936-47
US-09-422-936-75
US-09-422-936-75
US-09-422-936-75
US-09-422-936-45
US-09-422-936-49
US-09-914-259-14
US-08-262-220-8
US-08-461-733-8
US-08-475-036-8
                                                                                                                                                                                              US-08-470-638-8
                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08700607; Patent No. 5858708; GENERAL INFORMATION:
                  JS-09-949-016-9124
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37 EMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.5%; Score 349; DB 2; Length 208; 63.4%; Pred. No. 1.2e-33; tive 19; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 8, Application US/08700607; Patent No. 5858708; Patent 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 SFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                       PF-0114 US
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-855-0555
TELENGTH: 208 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
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IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: GenBactions: 307311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-700-607-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 503; DB 2; Length 199;
Pred. No. 3.8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
ITILE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
IVANBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 31'4 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
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         ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
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Patent No. 5858708
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Best Local Similarity 98.1%;
Matches 102; Conservative 1
                                  3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LIBRARY:
; CLONE: Consensus
US-08-700-607-1
                                                           CITY: Palo Alto
STATE: CA
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GRGANISM: Human
US-09-949-016-9180
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                                                        ; Score 348; DB 2; Length 267;
; Pred. No. 2.2e-33;
18; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Hu-Young, Janice
APPLICANT: Hilman, Jennifer L.
THE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       98 PRIYKGVIQAIAKSDEGHPPRAYLESEVAISEELVQKYSN 137
                                                                                                                                                                                                                                            106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
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ER: PF-0114 US
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                        49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                     Query Match
Best Local Similarity 64.0%
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
; CLONE: 281046
US-08-700-607-8
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GENERAL INCORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 00/241,755
PRIOR PELLING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PEASERG for Windows Version 4.0
SEQ ID NO 9180
LENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 KQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAXLALAALSATISFRIYKSVL 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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APPLICANT: Ba-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Hilman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
47.8%; Score 337; DB 4;
Best Local Similarity 67.4%; Pred. No. 8.9e-32;
Matches 62; Conservative 16; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 QAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
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SOFTWARE: FABLSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
pplication US/09949016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-700-607-5; Sequence 5, Application US/08700607; Patent No. 5858708
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMINICATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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ORGANISM: Human
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ZIP: 94304
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                                                                                                                                                                                                                                         TYPE: PRT
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Fatent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PELICATION NUMBER: 08/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0
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Sequence 8859, Application US/09949016
Sequence 8859, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO1307
                                                                                                                                                                                                                                                                                                                                                      46 KDKVVDLLYWRDIKKTGVVPGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
                                                                                                                                                                                                                                                                                                                                                                              46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
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                                                                                                                                                                                                                                                         47.8%; Score 337; DB 2; Length 776; 67.4%; Pred. No. 2e-31; tive 16; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.8%; Score 337; DB 4; Length 77
67.4%; Pred. No. 2e-31;
tive 16; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646 QAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 677
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CURRENT FILING DATE: 2000-04-14
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 67.4°
Matches 62; Conservative
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 62, Conserva
                                                                                                                                                                    : GenBank
307307
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ORGANISM: Human
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                                                                                                                                                                                           ; CLONE: CLONE: CUS-08-700-607-5
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49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108
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                                                                                                                                                                                                                                          Length 192;
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                                                                                                                                                                                                                                        43.8%; Score 309; DB 4; L
60.9%; Pred. No. 6.4e-29;
iive 18; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                               64 QKSEEGHPFKAYLDVDITLSSEAFHNYMAAM 95
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PRILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 8859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTMATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
                                                                                                                                                                                                                                                                         56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THP1NOB01
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Best Local Similarity
Matches 56; Conserva
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STRANDEDNESS: si
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LIBRARY: Thr.
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SEQ ID NO 45132
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                                                           49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108
                                                                                 48 VHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQAV 107
                                                                                                                                                                                                                                                                                                                         APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PILE REFERENCE: 59.US.PEG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SSEQ ID NO 7861
LENGTH: 114
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
                         Gaps
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Best Local Similarity 60.9%; Pred. No. 2.7e-28;
Matches 56; Conservative 17; Mismatches 19; Indels
                                                                                                                                                          108 QKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139
                                                                                                                                      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140
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US-09-513-999C-7861
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OTHER INFORMATION: SCORE 4.6
OTHER INFORMATION: SEQ VEGSFLLLLFSLT/QF
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; GENERAL INFORMATION:
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Best Local Similarity 62.29
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: UNSURE
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52 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKS 111
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                                                                                                                                                                                      Gaps
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                                                                                                                                  Length 219;
                                                                                                                                                                                   22; Indels
                                                                                                                               Query Match 35.5%; Score 250; DB 4; Best Local Similarity 50.6%; Pred. No. 9.1e-22; Matches 45; Conservative 22; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al. TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                              112 DEGHPFRAYLESEVAISEELVQKYSNSAL 140
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CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER PILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,133
                                                                                                                                                                                                                                                                                                                                                                         R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/038,621
R FILING DATE: 1997-03-07
A PAPLICATION NUMBER: 60/040,626
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,334
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,615
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,502
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,617
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APPLICATION NUMBER: 60/047,618
APLING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/040,336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
LENGTH: 219
TYPE: PRT
CORGANISM: Drosophila melanogaster
US-09-270-767-45132
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LING DATE: 1997-05-23
PLICATION NUMBER: 60/047,598
TIME DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314 ILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 ILING DATE: 1997-04-11 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 TILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,492 PLICATION NUMBER: 60/047,613 LING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 LING DATE: 1997-04-11 PLICATION NUMBER: 60/043,315 TILING DATE: 1997-06-06
APPLICATION NUMBER: 60/056,886 TILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 G DATE: 1997-08-22 CATION NUMBER: 60/056,880 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,671 TILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,877 APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/056,879 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 APPLICATION NUMBER: 60/043,311 1997-08-22 1997-04-11 ILING DATE: 1997-08-22 1997-04-11 ILING DATE: LING DATE: EARLIER
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APPLICATION NUMBER: 60/049,610 FILING DATE: 1997-06-13 PLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631 APPLICATION NUMBER: 60/057,761 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,588 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,585 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-08-22
APPLICATION UNDHER: 60/056,909
ELING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,875 APPLICATION NUMBER: 60/056,908 FILING DATE: 1997-08-22 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/057,650 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,669 60/056,845 APPLICATION NUMBER: 60/047,595 APPLICATION NUMBER: 60/047,599 APPLICATION NUMBER: 60/047,594 APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 APPLICATION NUMBER: 60/043,670 APPLICATION NUMBER: 60/056,632 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 APPLICATION NUMBER: 60/056,862 APPLICATION NUMBER: 60/056,887 APPLICATION NUMBER: 60/048,964 APPLICATION NUMBER: 60/056,884 APPLICATION NUMBER: 60/056,892 APPLICATION NUMBER: 60/047,614 APPLICATION NUMBER: 60/056,664 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 1997-05-23 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-09-05 FILING DATE: 1997-08-22 FILING DATE: 1997-09-05 1997-08-22 FILING DATE: 1997-05-23 LING DATE: 1997-08-22 FILING DATE: 1997-04-1 FILING DATE: 1997-08-2 APPLICATION NUMBER: FILING DATE: 1997-08 FILING DATE: SARLIER EARLIER

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Search completed: June 16, 2005, 12:33:41
Job time : 6.32448 secs
                                                                                                                                                                                                                                                                               71 LLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIQAIAKSDEGHPFRAYLESEVAISEE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 KVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 KVADLLYWKDTRISGVVFIGLMVSLLCLLHFSIVSVAAHLALLLLCGTISLRVYRKVLQA 446
                                                                                                                                 0; Gaps
                                             Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.4%; Score 214; DB 4; Length 588; Best Local Similarity 46.7%; Pred. No. 7.4e-17; Matches 42; Conservative 21; Mismatches 27; Indels
                                             32.2%; Score 227; DB 4; Length 16
60.0%; Pred. No. 3.6e-19;
tive 14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5 ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 IAKSDEGHPFRAYLESEVAISEELVQKYSN 137
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 411, Application US/08905223 Patent No. 6222029 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                            Query Match
Best Local Similarity 60.0%
-hea 42; Conservative
                                                                                                                                                                               131 LVQKYSNSAL 140
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61 AFHNYMNAAM 70
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                            US-09-949-016-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-7290
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14.0%; Score 99; DB 3; Le
Best Local Similarity 58.8%; Pred. No. 0.00028;
Matches 20; Conservative 7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
                                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: IGRAELSER, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFANS: (619) 235-850
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 411:
SEQUENCE CHARACTER.STICS:
LENGTH: 80 amino acids:
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                          MOLECULE TYPE: PROTEIN ORIGINAL SOURCE:
                                                   FILING DATE:
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 16, 2005, 12:29:05 ; Search time 18.2906 Seconds Run on:

(without alignments) 2960.058 Million cell updates/sec

Perfect score:

US-09-830-972-32 705 1 QAGGRAGVSCLRENFAVYSV.......ESEVAISEELVQKYSNSALG 141 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1714042 segs, 383979560 residues Searched:

fotal number of hits satisfying chosen parameters:

1714042

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

| cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/BCT NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:* Prodata/2/pubpaa/US09C_PUBCOMB.pep:*
ptodata/2/pubpaa/US09_NEW_PUB.pep:*
ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
ptodata/2/pubpaa/US10C_PUBCOMB.pep:* ptodata/2/pubpaa/US10E_PUBCOMB.pep: prodata/2/pubpaa/US09B_PUBCOMB.pep: ptodata/2/pubpaa/US11A PUECOMB.pep: ptodata/2/pubpaa/US11 NEW PUB.pep:* ptodata/2/pubpaa/US10_NEW_PUB.pep ptodata/2/pubpaa/US60_NEW_PUB. Published Applications_AA:* / cgn2_6/1 / cgn2_6/1 / cgn2_6/1 / cgn2_6/1 / cgn2_6/1 / cgn2_6/1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:

SUMMARIES

Description	Sequence 21, Appl	Sequence 21, Appl	Sequence 1568, Ap	Sequence 25, Appl	Sequence 467, App	Sequence 1, Appli	Sequence 11, Appl	Sequence 25, Appl	Sequence 9, Appli	Sequence 10, Appl	Sequence 10, Appl
ID	9 US-09-893-348-21	US-10-810-653-21	US-10-264-237-1568	US-09-893-348-25	US-09-978-360A-467	US-10-660-946-1	US-10-466-258-11	US-10-810-653-25	US-10-408-967-9	US-10-633-423-10	US-10-427-741-10
08	6	16	15	6	11	15	16	16	15	16	16
% Query Match Length DB ID	199	199	118	199	199	199	199	199	199	1162	1162
& Query Match	72.3	72.3	71.3	71.3	71.3	71.3	71.3	71.3	70.4	63.4	63.4
Score	510	510	503	503	503	503	503	503	496	447	447
Result No.	п		6	4	2	9	7	80	σ	10	11

63, 63,	000000	0, 4, 8	24, 6, 164 7, 7,	Sequence 127, App Sequence 8, Appli Sequence 6, Appli Sequence 3, Appli Sequence 1481, Ap Sequence 1481, Ap Sequence 23, Appl Sequence 20, Appl
v	14 US-10-060-036-71 15 US-10-267-502-429 16 US-10-327-213-9 16 US-10-466-258-9 16 US-10-810-653-23 9 US-09-893-338-20	US-10-810-65 US-09-789-386 US-09-765-205 US-09-893-348 US-10-060-03	US-10-810-853-8-9 US-10-810-653-2 US-10-347-669-6 US-10-205-194-1 US-10-267-7 US-10-267-7 US-10-660-946-7	15 US-10-205-194-127 15 US-10-660-946-8 15 US-10-660-946-5 15 US-10-660-946-5 15 US-10-260-946-5 16 US-10-723-860-1481 14 US-10-205-219-93 15 US-10-205-219-93 16 US-10-205-219-93
1163 1163 1192 1192 1192	1192 1192 1192 1192 360	360 373 373 373 373	373 373 373 1192 1163	267 356 776 776 777 777 236
6 6 6 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 4 4 4 4 4 4 4 4 8 8 8 8 8 8 8 8 8
4 4 4 4 4 4 4 4 4 4 4 4 7 7 7 7 7 7	4 4 4 4 4 4 4 4 4 4 7 7 7 4 4 4 8 7 7 7 8	# # # # # # # # # # # # # # # # # # #	44444444444444444444444444444444444444	8448 8448 847 723 748 868 868 768 768 768
112 113 114 116	18 20 22 23	400000		W W W A A A A A A A A A A A A A A A A A

ALIGNMENTS

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GENERAL IN CORTAILOR.

APPLICANT: EISENBAGH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.

APPLICANT: ESERRAMA. Pierre

APPLICANT: ESESERAMA. Pierre

APPLICANT: MOSCONEGO, Alon

APPLICANT: MOSLOWEGO, Alon

APPLICANT: MOALEM, Gila

TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE:

FILE REFERENCE: EIS-SCHWARTZ-A

CURRENT APPLICATION NUMBER: US 09/314,161

PRIOR APPLICATION NUMBER: US 09/314,161

PRIOR PELING DATE: 1999-12-27

PRIOR PELING DATE: 1999-05-19

PRIOR PELING DATE: 1998-07-21

PRIOR APPLICATION NUMBER: ECT/US98/14715

PRIOR APPLICATION NUMBER: ET 124500

PRIOR APPLICATION NUMBER: IL 124500

PRIOR FILING DATE: 1998-07-19

NUMBER: OF SEQ ID NOS: 29
                   Sequence 21, Application US/09893348 Patent No. US20020072493A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin version 3.1

SEQ ID NO 21

LENGTH: 199

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-893-348-21
US-09-893-348-21
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Gaps ö Query Match 72.3%; Score 510; DB 9; Length 199; Best Local Similarity 99.0%; Pred. No. 2.4e-49; Matches 103; Conservative 0; Mismatches 1; Indels

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Sequence 25, Application US/09893348

Sequence 25, Application US/09893348

Sequence 25, Application US/09893348

Sequence 25, Application US/09893348

Setence 25, Application US/09893348

Setence 26, Application US/09893348

APPLICANT: BESERMAN, Pierre
APPLICANT: MOSUREO, Alon
APPLICANT: MOSUREO, Alon
APPLICANT: MOSUREO, Alon
STILE REFERENCE: E16-STURARTZ=2A
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
TILE REFERENCE: E16-STURARTZ=2A
TITLE OF ILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR PILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Version 3.1
SEQ ID NO 25
SEQ ID NO 25
                         ; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1187)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-264-237-1568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
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71.3%; Score 503; DB 15;
Best Local Similarity 98.1%; Pred. No. 7.5e-49;
Matches 102; Conservative 1; Mismatches 1;
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; Sequence 467, Application US/09978360A
; Publication No. US20040110939A1
; FURINGAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas
; APPLICANT: Bouguelert, Aymeric
; APPLICANT: Bouguelert, Lydie
; APPLICANT: Clusel, Catherine
; APPLICANT: Clusel, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.1:
Matches 102; Conservative
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; ORGANISM: Homo sapiens
US-09-893-348-25
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/10810653

Sequence 21, Application No. US2004025218A1

GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: MOSONEGO, Alon
APPLICANT: NUMBER: US/09/893,348
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR PELLING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
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                                   MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFILLISLTVFSIVSVTAYIALALLSVTIS 60
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Publication No. US20040009491A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA131P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR PELING DATE: 2001-05-18

PRIOR FILING DATE: 2001-05-18

PRIOR FILING DATE: 2001-05-18

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: Patentin Ver. 3.1

LENGTH: 18

TYPE: PRI
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                                                                                                                                                            FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
                                                                                                                  98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-10-264-237-1568
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TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.1%
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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US-10-810-653-25
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TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.3%; Score 503; DB 11; Length 199; 98.1%; Pred. No. 1.5e-48;
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Goli, Surya K.
Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
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STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                             CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: US 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR PELICATION NUMBER: US 60/069,957

PRIOR FILING DATE: 1997-12-17

PRIOR PLING DATE: 1998-02-09

PRIOR PLING DATE: 1998-04-13

PRIOR PLING DATE: 1998-04-13

PRIOR PLING DATE: 1998-04-13

PRIOR PLING DATE: 1998-08-10

PRIOR PLING DATE: 1998-08-10

PRIOR PLING DATE: 1998-08-10

PRIOR PLING DATE: 1998-08-10

PRIOR PLING DATE: 1998-11-13

PRIOR PLING DATE: 1998-11-13

PRIOR PLING DATE: 1998-11-13

PRIOR PLING DATE: 1998-11-17

PRIOR PLING DATE: 1998-11-17

PRIOR PLING DATE: 1998-11-17

PRIOR PLING DATE: 1998-12-17

PRIOR PLING DATE: 1999-02-09

Remaining Prior Application data removed - 5

NUMBER OF SEQ ID NOS: 810

SEQ ID NO 467

LENGRENT 199
                                        CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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Publication No. US20040063131A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
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ZIP: 94304
COMPUTER READABLE FORM:
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Matches 102; Conservative
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: -42..-1
US-09-978-360A-467
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1 MDGOKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.3%; Score 503; DB 15; Length 199; 98.1%; Pred. No. 1.5e-48; Live 1; Mismatches 1; Indels (
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US-10-466-258-11
; Sequence 11, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: PROSSG GGW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
LENGTH: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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CLONE: Consensus
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105
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                                                                                                                                                                                                                          APPLICANT: Tobyama, Masaya
APPLICANT: Tobyama, Masaya
TITLE OR INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
FILE REFERENCE: 59150-8023.US00
CURRENT APPLICATION NUMBER: US/10/633,423
CURRENT PILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: US 2003-07-11
PRIOR APPLICATION NUMBER: US 2003-092923
PRIOR PILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTING DATE: 2003-03-13-8
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 10
LENGTH: 1162
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APPLICANT: Tohyama, Masaya
APPLICANT: Yamashita, Toshihide
APPLICANT: Yamashita, Toshihide
TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
FILE REFERENCE: 59150-8023
CURRENT APPLICATION NUMBER: US/10/427,741
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: JP 2003-92923
PRIOR FILING DATE: 2003-03-28
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Pred. No. 3.3e-41;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1162;
     61 FRIYKGVIQAIQKSDEGHPFPAYLESEVAISEELVQKYSNSALG 104
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Pred. No. 3.3e-41;
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                                                                                                                                       ; Sequence 10, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
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; Sequence 10, Application US/10427741
; Publication No. US20040191291A1
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ilarity 96.9%;
Conservative 0
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Best Local Similarity 96.9%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-633-423-10
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Matches 93; Conserv
                                                                                                                     US-10-633-423-10
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                                                                                                    APPLICANT: COHEN, Irun R.
APPLICANT: COHEN, Irun R.
APPLICANT: MSONGEGO, ALON
APPLICANT: MOSUREGO, ALON
FILE REFERENCE: EIS-SCHWARTZ=2A
FILE REFERENCE: EIS-SCHWARTZ=2A
CURRENT FILING DATE: 2004-03-29
RIOR FILING DATE: 2004-03-29
RIOR FILING DATE: 1999-05-19
RIOR PLILING DATE: 1999-05-19
RRIOR APPLICATION NUMBER: US 09/314,161
RRIOR APPLICATION NUMBER: PCT/US98/14715
RRIOR PILING DATE: 1998-05-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 9.2e-48;
1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 199;
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Pred. No. 1.5e-48;
1; Mismatches 1;
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CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                     APPLICANT: EISENBACH-SCHWARTZ, Michal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10408967
Publication No. USZ0040063161A1
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
Application US/10810653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.1%;
Matches 101; Conservative
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71.3%;
Best Local Similarity 98.1%;
Matches 102; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 6, Application US/09758140

Patent No. US20020012965A1

GENERAL INFORMATION:
TITLE OF INVENTION: No. US20020012965A10

FILER REFERENCE: 44574-5073-US

CURRENT APPLICATION NUMBER: US/09/758,140

CURRENT APPLICATION NUMBER: US 60/175,707

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: US 60/207,366

PRIOR PILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                           1002 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061
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                                                                                                                              Gaps
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                                                     Score 447; DB 16; Length 1163;
Pred. No. 3.3e-41;
0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                            1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1068
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Patent No. US20020010324A1

GENERAL INFORMATION

APPLICANT: MICHALOVICH, DAVID

APPLICANT: MICHALOVICH, DAVID

APPLICANT: MICHALOVICH, DAVID

APPLICANT: PRINJHA, RABINDER KUMAR

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GP-30165-C1

CURRENT APPLICATION NUMBER: US/09/789,386

CURRENT FILING DATE: 1999-07-19

PRIOR PILING DATE: 1998-07-22

PRIOR PILING DATE: 1998-07-22

PRIOR PILING DATE: 1998-07-22

PRIOR PILING DATE: 1999-07-22

PRIOR PILING DATE: 1999-07-22

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 2

LENGTHH: 1192
                                                           63.4%;
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                                                           Query Match
Best Local Similarity 96.9
Matches 93; Conservative
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US-09-789-386-2
US-10-810-653-18
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SEQ ID NO 6
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APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
TITLE OF INVENTION: ACTIVATED T-SCHWARTZ-2A
CURRENT APPLICATION NUMBER: US/10/810,653
CURRENT FILING DATE: 2004-03-29
PRIOR PLILNG DATE: 1999-05-19
PRIOR PPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR PPLING DATE: 1998-12-22
PRIOR PPLING DATE: 1998-05-19
PRIOR FILING DATE: 1998-07-1
PRIOR PILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
PRIOR PILING DATE: 1998-05-19
PRIOR PILING DATE: 1998-05-19
PRIOR PILING DATE: 1998-05-19
PRIOR PILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTHARE: PATENTIN VETEION 3.1
                                                                                                                                                               APPLICANT: ELSEMBALT-SCHERALS, FILLIANT: APPLICANT: ELSEMBALS, PIETE
APPLICANT: BESERMAN, PIETE
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSLEN, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
FILE REFERENCE: EIS-SCHWARTZ=2A
CURRENT PELLON NUMBER: US/09/893,348
CURRENT FILING DATE: 1999-05-19
FRIOR FILING DATE: 1999-05-19
FRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-05-19
FRIOR FILING DATE: 1998-05-19
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                                                                                                                                                     APPLICANT: EISENBACH-SCHWARTZ, Michal
                                              Sequence 18, Application US/09893348
Patent No. US20020072493A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/10810653; Publication No. US20040253218A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18
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ORGANISM: Rattus norvegicus
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LENGTH: 1163
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Matches
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                                                                                    Query Match 63.4%; Score 447; DB 9; Length 1192; Best Local Similarity 96.9%; Pred. No. 3.4e-41; Matches 93; Conservative 0; Mismatches 3; Indels 0
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6
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Search completed: June 16, 2005, 13:04:05 Job time: 19.2906 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein June 16, 2005, 12:55:32; Search time 4.23986 Seconds (without alignments) 3199.767 Million cell updates/sec Run on:

US-09-830-972-32 Title: Perfect score:

141 705 1 QASGEAGVSCLRENFAVYSV......ESEVAISEELVQKYSNSALG Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		٠			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	349	49.5	208	7	I60904	neuroendocrine-spe
7	348	49.4	267	~	A60021	tropomyosin-relate
٣	337	47.8	176	7	A46583	neuroendocrine-spe
4	162	23.0	2484	~	T26216	hypothetical prote
Ŋ	159	22.6	2607	~	T26215	
9	158	22.4	222	7	T26213	
7	83.5	11.8	295	7	S59439	probable membrane
ω	81.5	11.6	464	7	C88188	protein C18H9.5 (i
0	79	11.2	618	~	T24228	hypothetical prote
10	78.5	11.1	458	~	A72258	
11	77.5	11.0	261	7	F64924	О
12	77.5	11.0	583	7	T49359	hypothetical prote
13	76.5	10.9	481	~	C95920	hypothetical membr
14	75.5	10.7	545	7	F64665	glucose-6-phosphat
15	74.5	10.6	545	7	E71851	glucose-6-phosphat
16	74	10.5	268	0	F64024	hypothetical prote
17	73	10.4	393	~	S67763	probable membrane
18	73	10.4		0	T01081	hypothetical prote
19	72.5	10.3	278	~	AD0147	probable ABC trans
20	72.5	10.3	302	7	AE2863	conserved hypothet
21	72.5	10.3	302	~	D97640	hypothetical prote
22	2	10.3	417	7	B96977	probable Mn transp
23	72.5	10.3	598	~	T14886	leukotoxin express
24	72	10.2	271	~	T13013	hypothetical prote
25	72	10.2	299	~	B69155	hypothetical prote
56	72	10.2	1783	N	T42386	unconventional myo
	72	10.2	3511	~	A59295	unconventional myo
28	71.5	10.1	255	~	E84899	hypothetical prote
29	71.5	10.1	537	N	G82873	conserved hypothet

3beta-hydroxy-Delt	bydrovxsteroid deh	2-oxoglutarate/mal	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	phosphate transpor	hypothetical prote	membrane-associate	heavy metal-transp	hypothetical prote	hypothetical prote	conserved hypothet	spore germination
MVZ1W	7430	B97096	T25068	AB3226	A90926	E85774	B69098	AC1320	S55502	AE1678	T04714	T04821	D95248	E83898
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æ 3	346 L	476 2	1065 2											
346 1 5	346 L	476 2	10.1 1065 2	10.0	10.0	10.0	10.0	6.6	6.6	6.6	6.6	6.6	6.6	6.6

ALIGNMENTS

neuroendocrine-specific protein C - human C;Species: Homo sapiens (man) C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C;Accession: I60904

Risobroek, A.13.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V J. Biol. Chem. 268, 13439-13447, 1993
A; Hill: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe A; Reference number: A46583; MUID:93293865; PMID:7685762
A; Accession: 160904
A; Status: preliminary; translated from GB/EMBL/DDBJ

A,Molecule type: mRNA A,Residues: 1-208 <RES> A,Cross-references: UNIFROT:Q16799; GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

GDB:203968; OMIM:600865

A,Gene: GDB:RTN1; NSP A,Cross-references: GDB:2035 A,Map position: 14q21-14q22

Length 208; Query Match 49.5%; Score 349; DB 2; Best Local Similarity 63.4%; Pred. No. 6.7e-28; Matches 64; Conservative 19; Mismatches 18 96 37 EMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI ð

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Gaps

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18; Indels

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SFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137 69 δ 요

tropomyosin-related protein, neuronal - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999

C;Accession: A60021
R;Wieczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A;Reference number: A60021; MUID:91278684; PMID:1647480
A;Accession: A60021

A;Molecule type: mRNA A;Residues: 1-267 <WIE> A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550 C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo

Length 267; Query Match 49.4%; Score 348; DB 2; Length 26 Best Local Similarity 64.0%; Pred. No. 1.1e-27; Matches 64; Conservative 18; Mismatches 18; Indels

Gaps ö

2

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hypothetical protein W06A7.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2615
R;Ainscough, R.
B;Ainscough, R.
B;Ainscough, R.
A;Reference number: Z20173
A;Reference number: Z20173
A;Recession: T26215
A;Recession: T26215
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2607 <WIL>
A;Residues: 1-2607 <WIL>
A;Residues: 1-2607 <WIL>
A;Residues: clone W06A7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein W06A7.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26213
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Reference number: Z20173
A;Accession: T26213
A;Accession: T26213
A;Accession: Lype: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-222 <WILL>
A;Cross-references: UNIPROT: Q22188; EMBL: Z78066; PIDN: CAB01523.1; GSPDB: GN00023; CESP: W0C
A;Experimental source: clone W06A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 5
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
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25 HNLLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVT 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
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0
                                                                                                                                                                                                   2325 TYSLLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLPQEKV 2372
                                                                                                                                      85 AYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.6%; Score 159; DB 2; Length 26
Best Local Similarity 34.5%; Pred. No. 1.8e-07;
Matches 30; Conservative 19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.4%; Score 158; DB 2; Best Local Similarity 34.1%; Pred. No. 1.6e-08; Matches 29; Conservative 19; Mismatches 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2469 AQIKKTDSEHPFSEILAQDLTLPQEKV 2495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 QAIAKSDEGHPFRAYLESEVAISEELV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 IKKTDSEHPFSEILAQDLTLPQEKV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 IAKSDEGHPFRAYLESEVAISEELV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 5
A;Introns: 27/1; 77/2; 201/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: W06A7.3a
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26216
A;Ainscough, R.
Submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26316
A;Accession: T26316
A;Accession: T26316
A;Accession: T2644 <WILb
A;Residues: 1-2484 <WILb
A;Residues: 1-2484 <WILb
A;Residues: 1-2484 <WILb
A;Residues: 1-2684 <WILb
A;Residues: 1-2684 <WILb
A;Residues: 1-2684 <WILb
A;Residues: 1-2684 <WILb
A;Accession: CESP:W06A7.3c
A;Genetics: A;Agene: CESP:W06A7.3c
A;Antrons: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
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                               97
                                                                                                   9
                                                                   1 MDCVWSNWKSQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATIS
                               MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
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Best Local Similarity 67.4%; Pred. No. 4.6e-26;
Matches 62; Conservative 16; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Indels
                                                                                                                                                                                                   FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVOKYSN 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 QAIAKSDEGHPFRAYLESEVAISEELVOKYSN 137
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A; Cross-references: UNIPROT: Q22003; EMBL: Z50795; PIDN: CAA90663.1; GSPDB: GN00020; CESP: R1:
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 399, 323-329, 1999
A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Gross-references: UNIPROT:09X1C8; GB:AE001793; GB:AE000512; NID:g4981963; PIDN:AAD3647
A.Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                  hypothetical protein R166.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 DLLYWRDIKK-TGVVFGASLF-LLLSLTVF-----SIVSVTAYIALAL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 IYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.2%; Score 79; DB 2; Best Local Similarity 29.1%; Pred. No. 4.8; Matches 32; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-618 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 2
A;Introns: 41/3; 86/3; 118/3; 164/3; 207/3; 554/3
                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, August 1995
A;Reference number: Z19859
A;Accession: T24228
156 GTISESWSPINEIGTFVAFLSSAFQIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone R166
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                                                                                                                                                                                                                             C, Accession: T24228
R; Matthews, P.
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A;Gene: TM1408
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: C8B188
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-295 «MUR»
A;Cross-references: UNIPROT:Q04947; EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004
A;Experimental source: strain AB972
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C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S59439
R;Murphy, L.; Harris, D
submitted to the EMBL Data Library, March 1995
A;Reference number: S59423
A;Accession: S59439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 VSCLRENFAVYSVSVGMHNLLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                             probable membrane protein YDR233c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.8%; Score 83.5; DB 2; Length 295; Best Local Similarity 26.3%; Pred. No. 0.76; Matches 25; Conservative 17; Mismatches 32; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 464;
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25.9%; Pred. No. 2;
Live 28; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gener MIDD:YDR233c
A;Cross-references: SGD:SO002641
A;Amap position: 4R
C;Keywords: transmembrane protein
F;40-56/Domain: transmembrane #status predicted <TM1>
F;146-162/Domain: transmembrane #status predicted <TM2>
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Best Local Similarity 25.9%
Matches 38; Conservative
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A,Gene: C18H9.5
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37; Conservative
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probable thiosulfate-dithiol sulfurtransferase (BC 2.8.1.5) - Escherichia coli (Species: Escherichia coli C;Species: Escherichia coli F64924

R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A; FB Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: F64924

A;Accession: F64924

A;Accession: F64924

A;Accession: F64924

A;Retus: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-261 - BLAT>
A;Cross-references: UMIPROT:P77409; GB:AE000262; GB:U00096; NID:g1787955; PIDN:AAC74740.

A;Experimental source: strain K-12, substrain MG1655

C;Superfamily: byac protein

C;Keywords: sulfurtransferase; transmembrane #status predicted <TM01>
F;30-46/Domain: transmembrane #status predicted <TM02>
F;112-128/Domain: transmembrane #status predicted <TM04>
F;224-240/Domain: transm
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Cipate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

Cipate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

Cipate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #tipate: 02-Jul-2004

Air Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

By Accession: T49359

Air Reference number: 225022

Air Reference number: 225022

Air Residues: 1-583 scGH-

Air Residues: 1-583 scGH-

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Matches 28; Conserv
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RESULT 13

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hypothetical membrane protein [imported] - Sinorhizobium meliloti (strain 1021) magaplas C; Species: Sinorhizobium meliloti (b. Species: Sinorhizobium C. Species: Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Coss-references: UNIPROT:092VS2; GB:AL591985; PIDN:CAC49027.1; PID:g15140512; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymB
A;Edistor, F.; Finan, T.M.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
D.; Hyman, R.W.; Jones, T.
Ccience 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Reference number: Asfoly9; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Ricobacter pylori
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A;Cross-references: UNIDSOT:025781; GB:AE000622; GB:AE000511; NID:g2314317; PIDN:AAD0821
A;Cross-references: UNIDSOT:0258-6-phosphate isomerase
C;Superfamily: glucose-6-phosphate isomerase
C;Keywords: intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 GMENILL-----LLEGRSWQEMDGQ---KKHWKDKVVDLLYWRDIKKTGVVFGASL
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Pred. No. 6.6;
8; Mismatches
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Best Local Similarity 37.7%;
Matches 23; Conservative 8
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113 -EGHPFRAYLESEVAISEELVQKYSN 137

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RESULT 15
E71851
glucose-6-phosphate isomerase - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
C.Species: Helicobacter pylori
C.Species: 12-Feb-1999 #text_change 09-Jul-2004
C.Accession: E71851
E.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ilves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 197; I76-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: E71851
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-545 <ARN>
A;Crossreferences: UNIPROT:Q92K49; GB:AE001536; GB:AE001439; NID:g4155675; PIDN:AAD0666
A;Experimental source: strain J99
C;Genetics:
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10.6%; Score 74.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 12;
Matches 37; Conservative 19; Mismatches 45; Indels 4
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A,Gene: pgi
C,Superfamily: glucose-6-phosphate isomerase
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xenopus lae

cyprinus ca homo sapien

bos taurus

Sequence:

Run on:

Searched:

Database

Result Š.

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RY MEDINES-2715887; PubMed=12832288;
RA MEDINES-2715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT MIN'NOGO gene family.";
RI FASEB J. 17:1238-1247(2003).
C. --- MISCELLANEOUS: The sequence shown here is derived from an EMBL, GenBank/DDBJ third party annotation (TPA) entry.
DR EMBL; BRO1795; DAA01967.1; --
DR GO, GO:0005783; C:endoplasmic reticulum; IEA.
DR FARE, FASEB SETICULON: 1.
DR PEAM: PROS453; Reticulon: 1.
DR PEAM: PROS4545; RETICULON: 1.
DR PEAM: PROS4545; RETICULON: 1.
DR PEAM: PROS455; RETICULON: 1.
DR PEAM: PROS455; RETICULON: 1.
DR PEAM: PROSTES FASEB FAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.3%; Score 503; DB 2; Length 199; 98.1%; Pred. No. 5.8e-41; ive 1; Mismatches 1; Indels
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Last annotation update)
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Last annotation update)
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Best Local Similarity 98.1'
Matches 102; Conservative
                                                   197
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Sus scrofa (Pig).
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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QGIFY4
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Gapop 10.0 , Gapext 0.5
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                                                                                                     Oertle T., Klinger M., Stuermer C.A., Schwab M.E.; "A reticular rhapsody: phylogenic evolution and nomenclature of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDIJE=22715887; PubMed=12832288;
OSCILE T., Klinger M., Stuermer C.A., Schwab M.E.;
"A reticular rhapsody: phylogenic evolution and nomenclature of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). Usukaryota; Metacos, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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PAREB J. 17.1238-1247(2003).

**INSCELLANBOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.

InterPro; PRO03388; Reticulon.

PROSTE: PSSO845; Reticulon; 1.

SEQUENCE: 199 AA, 22469 MW; 761ASFDB6C1DEC3C CRC64;
                                                                                                                                                                                                                                                                                                                                           Length 199;
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Pred. No. 5.8e-41;
1; Mismatches 1; Indels
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PROSITE; PS50845; RETICULON; 1.
SROUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;
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Last annotation update)
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                                                                                                                                                                                  EMBL; AV164744; AAP47319.2; -. GO:0005783; C:endoplasmic reticulum; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                   MEDLINE=22715887; PubMed=12832288;
                                                                                                                                                                                                                                   nterPro; IPR003388; Reticulon.
                                                                                                                                             RTN/Nogo gene family.";
FASEB J. 17:1238-1247(2003).
                                                                                                                                                                                                                                                                                                                                         71.3%;
98.1%;
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1-MAR-2004 (TrEMBLrel. 26,
1-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.1'
Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                         SEQUENCE FROM N.A.
                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9541;
Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2004
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=RTN4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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RESULT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEALINE-52354683; PubMed-12466851; DOI=10.1038/nature01266;
REC STRAINE-52354683; PubMed-12466851; DOI=10.1038/nature01266;
RA OKAZAKI Y. Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
A OKAZAKI Y., Puruno M., Kasukawa Y., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Parale K.W.,
Baldarelli R., Hill D.P., Bult C., Godzik A., Gariboldi M., Gaissi C., Godzik A., Gariboldi M., Gissi C., Godzik A., Gungh J.,
A Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gungh J.,
A Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
A Kamai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
A Kanaja A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
A Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescol G., Pescol D.J., Reid J., Ring B.Z., Ringwald M.,
A Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
A Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,
A Wilming L.G., Wynblaw-Boris A., Yanagisawa M., Yang I., Yang I.,
A Wilming L.G., Wynblaw-Boris A., Yanagisawa M., Sakazume N., Sato K.,
A Shiraki T., Waki K., Kawai J., Alaxawa T., Pukuda S.,
A Shiraki T., Waki K., Kawai J., Alaxawa T., Rukuda S.,
A Nilara A., Hashizume W., Imotani K., Ishia Y., Lonha A., Hashizume W., Imotani K., Ishia Y., Lankawa T., Rukuda S.,
A Yana A., Hashizume W., Imotani K., Ishia Y., Shinagawa A.,
A Yana A., Hashizawi Y., Sasaki D., Shibata K., Lonha K., Shinagawa H.,
A Yana B., Havashizaki Y., Basaki D., Shibata R., Lonha K., Shasaki D., Shibata R., Lonha S.,
A Yana S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               help
lts (By
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SUBUNIT: Binds to RIN4R. Interacts with Bcl-xl and Bcl-2 (By similarity).
SUBCELDIAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Potent neurite outgrowth inhibitor which may also hel
block the regeneration of the nervous central system in adults
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                     05-JUL-2004 (Rel. 41, Last sequence update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
Name=Rtn4; Synonyms=NOGO;
Bus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms may be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q99P72-1; Sequence=Displayed;
SIMILARITY: Contains 1 reticulon domain.
         199 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=3T3-L1; TISSUE=Adipocyte;
Coulson A.C., Craggs P.D., Morris N.J.;
"Mouse vp20/RIN4C cDNA.";
RTN4_MOUSE STANDAKU;
099P72; 09CTE3;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 170-199 FROM N.A.
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Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Nogo-A (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Name=RTN4;
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SEQUENCE
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                                                                                                                                                                                                                                                                           27T224;
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                                                                                                                                                                               RESULT 6
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                                                                                                              GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0010176; C:integral to endoplasmic reticulum membrane; ISS:
GO; GO:0005635; C:nuclear membrane; ISS.
GO; GO:0005515; F:protein binding; ISS.
GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
GO; GO:0013017; P:negative regulation of axon extension; ISS.
GO; GO:0007399; P:negracive regulation of axon extension; ISS.
InterPro; IPR003388; Reticulon.
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
"A reticular rhapsody: phylogenic evolution and nomenclature of
RTN/Nogo gene family.";
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-!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDB third party annotation (TPA) entry.
EMBL; BK003959; DAA01971.1; -.
EMBL; BK0039783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSS0845; RETICULON; 1.
Alternative splicing; Endoplasmic reticulum; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.2%; Score 495; DB 1; Length 199; llarity 97.1%; Pred. No. 3.5e-40; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 170;
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Reticulon.
07BESDS80059ED9C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG
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Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
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                                                 EMBL; AK003859; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lumenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22715887; PubMed=12832288;
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PROSITE; PS50845; RETICULON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22466 MW;
                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02453; Reticulon; 1
                                 EMBL; AF326337; AAK08076.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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199
199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 101;
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SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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Q61G20
ID 061G
AC Q61G
DT 05-J
DT 05-
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1 MDSQPSGWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
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                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22715887; PubMed=12832288;
Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
A reticular rhapsody: phylogenic evolution and nomenclature of RTN/Nogo gene family.";
FASEB J. 17:1238-1247(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 199;
  141
                           61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FRIYKGVIQAIQKSDEGHPFRAYLESDVAVSEDLIQKYSSVVLG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 460; DB 2; Length 19
Pred. No. 9.2e-37;
5; Mismatches 7; Indelg
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AY164737, AAP47312.1; -.
GO, GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon, 1.
PROSITE; PS0845; RETICULON; 1.
SEQUENCE 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63696 MW; 832670C171E4AC61 CRC64;
98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG
                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                   199 AA
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                                                                                                                                                                                   PRT;
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PROSITE; PS50845; RETICULON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.2%;
88.5%;
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                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dest Match
Best Local Similarity 88.53,
                                                                                                                                                                                   PRELIMINARY;
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TISSUE=Testis;
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                                                                                                                                                                                                              QBIUA4;
01-MAR-2003 (
01-MAR-2003 (
05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                             Name=RTN4;
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                                                                                                                                                                             Q8IUA4
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                                                                                                   RESULT 9
Q8IUA4
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RA Attachar R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,

RA Attachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Barownstein M.J., Uodin T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rakseley R.W., Touchman J.W., Green R.D., Dickson M.C.,

Rakseley R.W., Touchman J.W., Schentch A., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Maria M.A., Schein J.E.,

Rodriguez A.C., Maria M.A., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Maria M.A., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Bouterch A., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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                                                                                                                                                                             388 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
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                                                                                                                                        46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Pred. No. 5.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70312 MW; 309A19DA37603F11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                         448 QAIQKSDEGHPFRAYLESEVAISEELVOKYSNSALG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
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SEQUENCE FROM N.A.
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Pfam; PF02453; Reticulon; 1.
PROSTIE; PS50845; RETICULON; 1.
SEQUENCE 639 AA; 70312 MW; 1.
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                                 96.98;
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                                                                         93; Conservative
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Best Local Similarity
Matches 93; Conserv
                                 Best Local Similarity
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Q8K290
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                                                01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
05-ULL-2004 (TrEMBLrel. 27, Last annotation update)
RNT4 (RTM4 isoform Ab) (RTW4 isoform D) (RTW4 isoform E)
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8; Oertle T., Huber C., van der Putten H., Schwab M.E.; "Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KUKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
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Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oertle T., Schwab M.E.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102285; AAM64244.1; -.
EMBL; AY123246; AAM64250.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       986 AA; 108449 MW; 0CDE8F647036415A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 QAIAKSDEGHPFRAYLESEVAISEELVOKYSNSALG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         891
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Pred. No. 8.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG
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EMBL; AX123248; AAM64252.1; -.
EMBL; AX123249; AAM64253.1; -.
EMBL; AX123250; AAM64254.1; -.
EMBL; AX123245; AAM64254.1; -.
EMBL; AX123245; AAM64249.1; -.
EMBL; AX123245; AAM64249.1; -.
EMBL; AX123245; AAM64249.1; -.
EMBL; AX123346; AAM64249.1; -.
InterPro; IPR003388; Reticulon.
986 AA.
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                                                                                                                                                                 (RTN4 isoform G) (RTN4 isoform Aa)
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 986 AA; 108449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse nogo/rtn4.";
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01-MAR-2003 (TrEMBLrel. 23,
05-JUL-2004 (TrEMBLrel. 27,
PRELIMINARY;
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                                                                                                                                                                                                                       Homo sapiens (Human).
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les 93; Conserv
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FUNCTION
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               STRAIN=129/SvcJ7, and 129SvcJ7; MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8; OCTILE T., Huber C., van der Putten H., Schwab M.E.; Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                          Length 1046;
                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                           1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;
                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                     QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 951
                                                                                                                                                                                                                                                                                                                            QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                                                                                                                                                                                                                                                        63.4%; Score 447; DB 2; 96.9%; Pred. No. 9.3e-35; ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                  nan and mouse nogo/rtn4.";
Mol. Biol. 325:299-323(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003).
                                                                                                                                                                                                               InterPro; IPR003388; Reticulon.
                                                                                                                                                                                                                      Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
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(TrEMBLrel. 23, I
(TrEMBLrel. 27, I
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Van der Putten H., Mir A.;
                                                                                                                                                                                                                                                                         Conservative
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                                                                                 STRAIN=129/SvcJ7;
Van der Putten H.;
Submitted (MAY-2002)
                                                                                                                                                                                                                                                                 Similarity
        FROM N.A.
                                                                                                                    SEQUENCE FROM N.A.
                                                                         SEQUENCE FROM N.A.
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Van der Putten H.
                                                                                                                                                                                                                                                           Local Sim
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05-JUL-2004
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                                                 human and
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                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Q8BGM9;
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972 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1031
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STRANTE-Spraque-Dawley, TISSUR-Adipocyte;
MEDLINE-9249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
MOTTIS N.J., ROSS S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
"Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family.";
Biochim. Biophys. Acta 1450:68-76(1999).
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-!- SUBDNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
Nature 417:547-551(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETTM4 RAT STANDARD; PRT; 1163 AA.

Q9JKI1; Q9JKI0; Q9ROD9; Q9WUE9; Q9WUF0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUD-2004 (Rel. 44, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Glut4 vesicle 20 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
Spillmann A.A., Chriet F., Schwab M.E.;
"Nogo-A is a myelln-associated neurite outgrowth inhibitor and entigen for monoclonal antibody IN-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 447; DB 2; Length 1162;
Pred. No. 1e-34;
0; Mismatches 3; Indels (
                       EMBL, AT102284; AAM73506.11, -...

EMBL, AT102284; AAM73506.11, -...

EMBL; AT102286; AAM73506.11, -...

MGD; MGI: 1915835; Rtn4.

R GO; GO: 0005783; C: endoplasmic reticulum; IDA.

R GO; GO: 0005515; F: protein binding; IPI.

R GO; GO: 0007399; P: neurogenesis; IMP.

R GO; GO: 0007399; P: neurogenesis; IDA.

InterPro; IPR003388; Reticulon; I.

R PROSITE; PS50845; RETICULON; I.

S EROUENCE 1162 AA; 126612 MW; 855697FBEE11781F CRC64;
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(MAY-2002) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              minor splice variants.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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Ito T., Schwartz S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1032 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.4%;
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Best Local Similarity 96.33,
Conservative
These 93, Conservative
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Rattus norvegicus (Rat).
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(Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                Event=Alternative splicing; Named isoforms=4;
Name=1; Synonyms=Nogo-A, NI-220-250;
IsoId=095IXI1-1; Sequence=Displayed;
Name=2; Synonyms=Nogo-B, Foocen-Mi;
IsoId=095IXI1-2; Sequence=VSP_005658;
Name=3; Synonyms=Nogo-C, VP20;
IsoId=095IXI1-3; Sequence=VSP_005656, VSP_005657;
Name=4; Synonyms=Foocen-M2;
IsoId=095IXI1-4; Sequence=VSP_005659;
IsoId=095IXI1-4; Sequence=VSP_005
                       Anchored to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0030176; C:integral to endoplasmic reticulum membrane; IDA. GO:0005635; C:nuclear membrane; ISS.
         PINITIALLY,,
SUBCELLULAR,
Membrane of the endoplasmic reticulum through 2 putative
transmembrane domains (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005515; F:protein binding; ISS.
GO:0019987; P:negative regulation of anti-apoptosis; ISS.
GO:0030517; P:negative regulation of axon extension; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in Ref. 3; AAD31020)
W; 8CB894B09E94F0B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP 005657.
Missing (in isoform 2).
/FTId=VSP 005658.
Missing (in isoform 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
Cytoplasmic (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lumenal (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 447; DB 1;
Pred. No. 1e-34;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         959500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 reticulon domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endoplasmic reticulum; Transmembrane.
DOMAIN 1 989 Cytoplasm
TRANSMEM 990 1010 Potentia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                           mainly in the nervous system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF051335; AAF01564.1; -. EMBL; AJ242961; CAB71027.1; -. EMBL; AJ242962; CAB71028.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAB71029.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF132045; AAD31019.1; -. AF132046; AAD31020.1; -.
                                                                                     ALTERNATIVE PRODUCTS
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1125
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF132046;
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EMBL;
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SEQUENCE FROM N.A. (ISOFORM 4).
Jin W.-L., Ju G.;
"Developmentally-regulated alternative splicing in a novel Nogo-A.";
Submitted (NOV-2000) to the EMEL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pituitary;
Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
Luo B., Hu K., Chen J.;
"Human neuroendocrine-specific protein C (NSP) homolog gene.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
MEDLINE-21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;
Tagami S., Equchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
"A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity.";
Oncogene 19:5736-5746(2000).
                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 45, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Neuroendocrine specific protein) (NSP) (Neuroendocrine specific protein (NSP) (Neuroendocrine specific
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
MISDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
Michalovich D., Simmons D.L., Walsh F.S.;
"Inhibitor of neurite 001growth in humans.";
Nature 403:383-384(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 3).
Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
                                                                                                                                       RTN4 HUMAN STANDARD; PRT; 1192 AA.
Q9NQC3; Q94962; Q9HXG5; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20237542; PubMed=10773680;
Yang J., Yu L., Bi A.D., Zhao S.-Y.;
"Assignment of the human reprise agene (RTN4) to chromosome 2p.1+->2p.13 by radiation hybrid mapping ";
Cytogenet. Cell Genet. 88:101-102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of a member of the reticulon gene family in human."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yutsudo M.;
"Isolation of a cell death-inducing gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                     1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1068
QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                                                                                                                                                                                                                                                                                                                         Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 2 AND 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 3).
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TISSUE=Fibroblast;
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Gaps

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3; Indels

63.4%;

93; Conservative

Matches

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HANNER BERREAR BERREAR
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TISSUB-Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
TISSUB-Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
MEDLINE-2238825; PubMed-12477932; DOI-10.1073/pnas.242603899;
A Strausberg R.D., Feingold E.A., Grouse L.H., Dorge J.G.,
A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toophiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wokernan K.J., Malek J.M., Gunstane P.H.,
Rosak S.A., McEwan P.J., McKernan K.J., Malek J.M., Gunstane D.H.,
A Norley W., Moorley K.C., Hale S., Garcia A.M., Gabbs R.A.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A.,
Richards S., Worley W., Sodergren B.J., Lu K., Gibbs R.A.,
A Nahiting M., Madan A., Young A.C., Shavorchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E.,
A Mance Chan Schein J.E., Jones S.J.M., Marra M.A.;
And mouse Chan Schein J.E., Jones E.D., Marra M.A.;
And mouse Chan S. C., Grimson G. M., Schent A. Schein J.S., Once than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECURNCE FROM N.A. (ISOFORM 3).

TISSUE-Umbilical cord blood;

MEDLINE-210499357; PubMed=11042152; DOI=10.1101/gr.140200;

Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao.M., Zhao C.-J., Fu G.,

Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,

Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen Z.,

Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen Z.,

"Cloning and functional analysis of CDNAs with open reading frames for all previously undefined genes expressed in CD34+ hematopoietic
                                                                                                                                                                                                                            Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                        Yu J., Han L.H.; "Novel human cDNA clones with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20129259; PubMed-10667797; DOI=10.1038/35000226; GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.; "Identification of the Nogo inhibitor of axon regeneration as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
                                                                                                    Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Brain;
Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sha J.H., Zhou Z.M., Li J.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                         MEDLINE=99156230; PubMed=10048485;
                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stem/progenitor cells.";
Genome Res. 10:1546-1560(2000).
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Nature 403:439-444(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
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                                                                                                                                                                                                                                                              J. Neurosci. Res. 67:559-565 (2002).

-I-FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults. Isoform 2 reduces the ani-apoptotic activity of Bcl-xl and Bcl-2. This is likely consecutive to their change in subcellular location, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.

-I-SUBUNI: Binds to RTWAR. Interacts with Bcl-xl and Bcl-2.

-I-SUBUNI: Binds to RTWAR. Interacts with Bcl-xl and Bcl-2.

-I-SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in brain
"Identification of a receptor mediating Nogo-66 inhibition of axonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoid=Q9NQC3-4; Sequence=VSP_005654;
TISSUB SPECIFICITY: Isoform 1 Is specifically expressed in brain
and testis and weakly in heart and skeletal muscle. Isoform 2 is
widely expressed excepted for the liver. Isoform 3 is expressed
brain, skeletal muscle and adipocytes. Isoform 4 is testis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                            MEDLINE-21888956; PubMed=11891768; DOI=10.1002/jnr.10134;
Ng C.E.L., Tang B.L.;
"Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.4%; Score 447; DB 1; Length 1192; 96.9%; Pred. No. 1.1e-34; tive 0; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific.
SIMILARITY: Contains 1 reticulon domain.
CAUTION: Ref.11 sequence differs from that shown due to frameshifts in positions 1149 and 1156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Furthermative apilcing; Named isoforms=4;
Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
IsoId=QSNOC3-1; Sequence=Displayed;
Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
IsoId=QSNOC3-2; Sequence=VSP_005655;
Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
IsoId=QSNQC3-3; Sequence=VSP_005655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    through 2 putative transmembrane domains. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAA74909.2; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ251383; CAB99248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ251384; CAB99249.1;
AJ251385; CAB99250.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB020693; BAA74909.2;
EMBL; BC001035; AAH01035.1;
EMBL; BC007109; AAH07109.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG40878.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD31021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD31022.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAA83712.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG17976.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAB18928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAB18927.
                                                      Nature 409:341-346(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG12177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                        regeneration.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF148538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF087901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB040462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF148537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF320999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Sim:
Matches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                         REVIEW
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EMBL;
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EMBL;
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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Search completed: June 16, 2005, 13:17:44
Job time : 20.1287 secs
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Matches
    DDR REAL PRESENT OF SOLUTION O
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Nausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldow M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toodhyuki S., Carminci P., Frange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKernan K.J., Maake J.A., Gunzarne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.J.,
Jones S.J., Marra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 443; DB 2; Length 34:
Pred. No. 7.3e-35;
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Submitred (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC071848; AAH71848.1; -
GO; GO:0005783; C:endoplasmic reticulum; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEGM; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
RECHENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci. U.S.A. 99:16899-16903(2002).
                                                1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097
106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                        343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.8
Best Local Similarity 98.9
Matches 92; Conservative
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                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTN4 protein.
Name=RTN4;
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01-MAR-2003 (
01-MAR-2003 (
                                                                                                                                                                                                                                                                                               OGIPNO
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Q8BH78
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                                                                                                                                                                                                           RESULT 1
QGIPNO
ID QG1
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108
                                                                                                                                                                                                    Oertle T., Huber C., van der Putten H., Schwab M.B.;
"Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4";
J. Mol. Biol. 325:299-323 (003).
                                                                                                                                                                STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.8%; Score 443; DB 2; Length 356; 98.9%; Pred. No. 7.6e-35; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AKSDEGHPFRAYLESEVAISEELVOKYSNSALG 141
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nes 92; Conservative
                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2002)
                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=129SvcJ7;
                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                         Van der Putten H.
                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvcJ7
                                                                                                                                                 SEQUENCE
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                  Copyright
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protein search, using sw model OM protein June 16, 2005, 12:31:51; Search time 167.944 Seconds Run on:

(without alignments) 2678.292 Million cell updates/sec

US-09-830-972-2 5848 Title: Perfect score:

1 MEDIDQSSLVSSSTDSPPRP......VKDAMAKIQAKIPGLKRKAD 1163 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de				
Result No.	Score	Query Match	Length	DB	ID	Description
-	5848	100.0	1163	2	ABB81074	Abb81074 Rat neuro
7	5848	100.0	1163	œ	AD026399	Ado26399 Rat trunc
٣	5848	100.0	1163	80	ADP45572	Adp45572 Rat NogoA
4	5846	100.0	1163	m	AAY71310	0 Rat
S	5840	6.66	1162	e	AAY71557	Aay71557 Rat Nogo
9	5823	9.66	1163	٣	AAY71384	4 Alte
7	5312.5	90.8	1162	80	ADT89537	Adt89537 Mus muscu
8	5307	90.7	1163	80	AD008105	Ado08105 Mouse pol
6	4921	84.1	974	٣	AAY71560	Aay71560 Rat Nogo
10	4403.5	75.3	1192	4	AAU04591	
11	4403.5	75.3	1192	'n	ABP68600	Human
12	4403.5	75.3	1192	9	ABR59667	Abr59667 Human Nog
13	4403.5	75.3	1192	œ	ADP,45551 .	Adp45551 Human Nog
14	4398.5	75.2	1192	٣	AAY56967	Aay56967 Human MAG
15	4398.5	75.2	1192	4	AAB82349	Aab82349 Human NOG
16	4398.5	75.2	1192	ß	ABG30938	Abg30938 Human Nog
17	4398.5	75.2	1192	Ŋ	ABB81078	Abb81078 Human neu
18	4398.5	75.2		œ	AD008103	Ado08103 Human pol
19	4398.5	75.2		œ	ADP67234	Adp67234 Human Nog
20	4398.5	75.2		œ	ADR13966	Adr13966 Human NOG
21	4389.5	75.1		7	ADK67502	Adk67502 Human RTN
22	4358.5	74.5	1192	80	AD026400	Ado26400 Human tru
23	4276.5	73.1	1178	m	AAY71311	Aay71311 Human neu
24	4116	70.4	1246	4	AAU33228	Aau33228 Novel hum
25	4023	68.8	803	c	AAY71562	Aay71562 Rat Nogo

26 3834 65.6 798 8 ADOZ6414 27 3714 63.5 737 3 AAY71386 29 3651.5 62.1 736 3 AAY71391 30 3650.5 62.1 732 3 AAY71399 31 3584 61.3 732 3 AAY71399 32 3436 58.8 684 3 AAY71394 33 3385.5 57.9 983 6 ABUIL573 36 2801 47.9 983 6 ABUIL573 37 2280.5 42.8 642 2 AAW88383 38 2500.5 42.8 642 2 AAW88383 39 2500.5 42.8 642 2 AAW88383 41 2388 40.8 47.5 552 3 AAY71396 42 2291 39.2 45.7 3 AAY71399 43 1987 34.0 403 3 AAY71393 44 1868 31.9 41.7 3 AAY71393	Ado26414 Rat trunc	Aay71386 Rat Nogo	Aay71391 Rat Nogo	Aay71398 Rat Nogo	Rat	Ado26415 Rat trunc		Aay71394 Rat Nogo	Hume		Adp45553 Human NiG			Aab90682 Human BG1	Aay71396 Rat Nogo	Aay71389 Rat Nogo	Aay71392 Rat Nogo	Rat	Aay71393 Rat Nogo	Rat
6 6 5 5 6 6 5 5 6 6 5 5 6 6 6 5 5 6 6 6 5 5 6	AD026414	AAY71386	AAY71391	AAY71398	AAY71399	AD026415	AAY71387	AAY71394	ABU11573	AAY95012	ADP45553	AAY71388	AAW58383	AAB90682	AAY71396	AAY71389	AAY71392	AAY71563	AAY71393	AAY71390
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0.000000000000000000000000000000000000	3834	3714	3699.5	3651.5	3630.5	3584	3494	3436	3385.5	3280.5	2801	2779	2500.5	2500.5	2432	2388	2291	1987	1868	1801
	56	27	58	53	30	31	32	33	34	32	36	37	38	39	40	41	45	43	44	45

ALIGNMENTS

Nerve regeneration, neuroprotection, neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; opthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy; Rat neurotransmitter receptor protein Nogo-A. neurotransmitter receptor; rat; receptor ABB81074 standard; protein; 1163 AA (first entry) 05-NOV-2002 ABB81074; RESULT 1 ABB81074

Rattus norvegicus

US2002072493-A1.

13-JUN-2002

28-JUN-2001; 2001US-00893348 19-MAY-1998;

98WO-US014715. 98US-00218277. 99US-00314161. 21-JUL-1998; 22-DEC-1998; 19-MAY-1999; (YEDA) YEDA RES & DEV CO LTD

Beserman P, Mosonego A; Cohen IR, Eisenbach-Schwartz M, Hauben E, Moalem G;

WPI; 2002-607255/65.

N-PSDB; ABN86600.

the Promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.

Example 5; Page 44-47; 93pp; English.

The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering

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NS-specific activated T cells, NS-specific antigen, its analogue or peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt crauma, penetrating trauma, hemorrhagic stroke, ischemenc stroke or autoimmune disease, where the injury is spinal cord injury, blunt crauma, penetrating trauma, hemorrhagic stroke, ischemenc stroke or autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-atteritic optic neuropathy, and as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral contental, hypodlycemia, Sjorgren Larsson syndrome, acute to uremia, porphyria, hypodlycemia, Sjorgren Larsson syndrome, acute contental, non-atteritic neuropathy, malabsorption and last neuropathy, chronic ataxic neuropathy, malabsorption and last neuropathy and sensory neuropathy, chronic ataxic neuropathy, malabsorption and last sensor syndromes, polycythemia vers immunoglobulin (Ig)A- and IgG gamma-pathian committed and incomes, polycythemia vers immunoglobulin (Ig)A- and IgG gamma-pathian committed and incomes, polycythemia vers immunoglobulin (Ig)A- and IgG gamma-pathian committed and incomes, polycythemia vers immunoglobulin (Ig)A- and IgG gamma-pathian committed and incomes, polycythemia vers immunoglobulin (Ig)A- and IgG gamma-pathian committed and incomes, polycythemia vers immunoglobulin (Ig)A- and IgG gamma-pathian committed and IgG amma-pathian committed and incomes, polycythemia vers immunoglobulin (Ig)A- and IgG gamma-pathian committed and incommitted a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangectasia, Friedreich's ataxia, amyloid polyneuropathies, adrenomyloneuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-A, an example of NS-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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Best Local Similarity 100.0%; Pred. No. 3.7e-298;
Matches 1163; Conservative 0; Mismatches 0;
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1020 New isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein, useful for identifying a compound having detectable affinity to a Nogo-A protein. 780 840 960 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED VIISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP LPSAGASVVQPSVSPLEAPPPVSYDS1KLEPENPPPYEEAMNVALKALGTKEGIKEPESF IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL FLVDDLVDSLKFAVLMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLA FLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA rat; human; Nogo-A; truncated; affinity; membrane-bound protein. NKSVKDAMAKIQAKIPGLKRKAD 1163 ADO26399 standard; protein; 1163 AA. Rat truncated Nogo-A protein. 31-OCT-2002; 2002WO-EP012210. 31-OCT-2002; 2002WO-EP012210. (PIER-) PIERIS PROTEOLAB AG Fiedler M; (first WPI; 2004-376159/35. WO2004039836-A1 29-JUL-2004 13-MAY-2004. Skerra A, Rattus sp. 1021 1081 1081 1141 AD026399; 841 901 961 1021 1141 601 661 661 721 721 901 196 601 RESULT 2 ADO26399

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NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPINSL

OIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLIPDLVQEACESEL

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                            The present invention relates to an isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein from the rat and from the human. The truncated polypeptide is useful for identifying a compound having detectable affinity to a Nogo-A protein. The present sequence is a Nogo-A polypeptide of the invention.
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                                                                                                                                                  Length 1163;
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                                                                                                                                                Score 5848; DB 8;
Pred. No. 3.7e-298;
Mismatches 0;
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0
 English
                                                                                                                                             LOCAL MATCH 100.0%;
Best Local Similarity 100.0%;
Matches 1163; Conservative 0;
6A; 80pp;
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 Claim 1; Fig
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                                                                                                                                                                                                                                                                VIISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL
                                                                                                                                                                                                                                                                                                                                            nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder;
                                       DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED
                                                                                                                                                   VTISPRIYKGVIQAIQKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL
   DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED
                                                                                                            RSLSAVLSABLSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS
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and C
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 'note= "used as immunogen to generate antibody AS 472"
                                                                                                                                                                                                                                                                                                                         note= "This region is not essential for inhibitory
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/label= Transmembrane domain
/note= "C-terminal hydrophobic region specifically
described in claim 16"
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/note= "C-terminal hydrophobic region specifically
described in claim 16"
                                                                                                                                                                                                                                                                                                                                                       note= "C-terminal common region found in Nogo A,
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                                                                                                                                                                                                                                                                                                      note= "PKC and casein kinase II sites"
                   "Protein kinase C (PKC) site"
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N-PSDB; AAD01173.
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CHEN M S.
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The present sequence is a rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) wyelin material with which it is natively associated. The protein was drived from a cDNA generated by fusing RO(8037-3, R1-3121 cDNAs isolated from hexanucleotides-primed rat brain stem/spinal cord library, and oliis con A fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, and fragments displaying neurona, oligodendrocyte library. Nogo proteins and treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, neuroblastoma, craniopharyngioma, ependyoma, pinealoma, menagioblastoma, craniopharyngioma, oligodendroglioma, menagioma, cranioplastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. poriable and tissue hypertrophy.

CNIDOZYMES Or antisense Nogo nucleic acids can be used to inhibit con production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in disgnostic and screening methods for predisposition or promote as SEQ ID No: 2 is stated to be the same as the sequence designated as SEQ ID No: 2 is stated to be the same as the sequence for maintenance and screening methods for predisposition in Pig. 13 (see AAXT1384) of the specification. However, this sequence given in Fig. 13 (see AAXT1384) of the specification. However, the sequence given in Fig. 13 SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID No: 29 in disclosure of the 240 240 300 300 360 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAFSLP 120 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360 9 9 go proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons. MEDIDOSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDBEBEDDEBDLEBLEVLERK PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPALP AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRGSGSVDETLFALP GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL ö Length 1163; ; Score 5846; DB 3; Pred. No. 4.8e-298; 1; Mismatches 0; Claim 3; Fig 2A; 122pp; English. 100.0%; 99.9%; 1 Best Local Similarity 99.9 Matches 1162; Conservative Sequence 1163 AA; these SEQ ID 61 121 121 181 181 241 301 Query Match 241 셤 원 g ò 유 ď 8 ď ઢ ठ ò ઠે

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181 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540

PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCIEDSLEQKSLGKDSEGR 420 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480

PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR

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                                                       LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF
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                                         NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEBAEATPSPVLPDIVMEAPLNSL
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central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.
                                                                                                                                 Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
                                                                                                                                                                 neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
                                  Ä
                             AAY71557 standard; protein; 1162
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GNLSAVSSSEGTIEFTLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGES

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05-NOV-1999;

02-JUN-2000

WO200031235-A2

AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTWDIFNEMQMSVVA 360

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contributions activity are used in tragments displaying neutric growth cassociated. Nogo proteins and tragments displaying neutric growth contributions, activity are used in the treatment of neoplastic disease of the contributions, planealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, planealoma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.

Controposation and promote Nogo activity can be used to treat or prevent hyperpropit production of Nogo protein to induce regeneration of and tissue hypertrophy. Ribozymes or antisease Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where contributing the can be used in diagnostic and screening methods for neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for treat or prevent disorders and to screen for or test molecules which can careful treat or prevent disorders or diseases of the CNS. The present sequence of used in the construction of mutant Nogo. A nogon has inhibitory accounts of the control of the specification of the specification or control of the specification.

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1; Mismatches 0;
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                                                                     RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS
AILVENTKEEVIVRSKOKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA
                    PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR
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                                                          NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA
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hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening.
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shown in AAY71310"
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shown in AAY71310"
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/note= "Inhibits NIH 3T3 fibroblast
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/note= "Asn is N-glycosylated"
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/note= "used as immunogen
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The present sequence is an alternative version of rat Nogo A protein
which is a potent neural cell growth inhibitor and is free of all central
nervous system (CNS) myelin material with which it is natively
sesociated. Nogo proteins and fragments displaying neurite growth
inhibitory activity are used in the treatment of neoplastic disease of
the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
pendyoma, pinealoma, haemangioblastoma or retinoblastoma and
cligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
Therapeutics which promote Nogo activity can be used to treat or prevent
hyperproliferative or benign dysproliferative disorders e.g. psoriasis
and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
neurons or to promote structural plasticity of the CNS in disorders where
neurons or to promote structural plasticity of the CNS in disorders where
neurite growth, regeneration or maintenance are deficient or desired. The
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3= "This region is not essential for inhibitory
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note= "C-terminal common region found in Nogo A,
                                                                                                                                                                casein kinase II sites"
                                                                                                                                      casein kinase II sites"
                                                                                                                                                                                                                                                                                       note= "C-terminal hydrophobic region'
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|label= Transmembrane domain
|note= "C-terminal hydrophobic
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note= "Asn is N-glycosylated"
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 "Casein kinase II site'
                                                                                "Asn is N-glycosylated'
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label= Transmembrane_domain
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/note= "Ar
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animal models can be used in diagnostic and screening methods for pedisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is an alternative version of the Nogo A sequence shown in Fig. 2A (see AAY1310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID No. 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers
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                                                                                                                                                          Length 1163;
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                                                                                                                                                          Score 5823; DB 3;
Pred. No. 7.6e-297;
                                                                                                                                                                                          0; Mismatches
                                                                                                                                                         99.6%;
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DEVHVSDEFSENRSSVSKASI SPSNVSALEPQTEMGSI VKSKSLTKEAEKKLPSDTEKED
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                                                                                                                                                                                                                                       or modulating p75 signal transduction pathway by administering a transduction agent, e.g. p21 or Rho, or an agent that interacts with transduction agent.
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30-APR-2003; 2003US-00427741
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The present invention relates to a method for regenerating nerves or modulating nerve regeneration. The method involves inhibiting or modulating a p75 signal transduction pathway. The invention is useful for treating, preventing or diagnosing neurological diseases based on nerve regeneration and for identifying agents useful for nerve regeneration. The invention is also useful in gene therapy and for preparing vaccine. The present sequence is the Mus musculus Nogo protein. Note: This sequence is said to encoded by SEQ ID NO 9, however this does not appear

Sequence 1162 AA

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Example 2; SEQ ID NO 10; 209pp; English

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90.8%; Score 5312.5;
91.0%; Pred. No. 4 6
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Best Local Similarity 91.05
Matches 1064; Conservative
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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene of the agent of the gene of the agent and identifying fat cell relative to expression of the gene in an expression vector not exposed to the agent, treating a subject with the agent and identifying fat cell number or size in the subject. The agent comprises an anisense of oligonucleotide. The subject comprises a mammal, preferably a human. The collypeptide to the agent, detecting binding of the agent exposing the polypeptide or a change in an activity of the polypeptide, treating a cubject or a change in an activity of the polypeptide, treating a cubject. The agent comprises an antibody. A method of regulating fat cell subject. The agent under conditions so that fat cell number or size in the agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying a composition for treating or preventing obesity or identees. This sequence represents a composition for treating or preventing obesity or diabetes. This sequence represents a composition for treating or preventing obesity or diabetes. This sequence represents a composition for treating or preventing obesity or diabetes. This sequence represents a composition in the scope of the invention.
KELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQID 1134
                                                                                            1074 KELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQID 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; fat cell number; fat cell size; obesity; diabetes; anorectic; antidiabetic.
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Query Match 90.7%; Score 5307; DB 8; Length 11 Best Local Similarity 91.1%; Pred. No. 9e-270; Matches 1066; Conservative 34; Mismatches 56; Indels
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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, gliobiascoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, coligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alahaimer's and Parkinson's diseases.

Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in dispnetic and screening methods for predisposition to disorders and to screen for or test molecules which can the construction of mutant NiAsar. The mutant is composed of His-tag/T7-tag/VBCCC tag/Vector/Nogo-A sequence as 1-974/T7-tag. Nogo A deletion mutants were
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.
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                          IALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNST
                                                                            IKELRRIFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQI
                                                                                                 Nogo A protein fragment used in the construction of mutant NiAext
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used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-772. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from tax Nogo A sequence shown in AAY1310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID
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Pred. No. 1.3e-249;
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99.9%;
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Best Local Similarity 99.9
Matches 973; Conservative
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                                                                                                                                                                             Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein; crathal trauma; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasis demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; marchiadawa-Bignami disease; pontine myelinolysis; adrenoleukodystrophy; Pelizaeus Merzbacher disease; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; viral infection;
DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED
                        DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED
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|label= Lumenal_extracellular_domain
|note= "This sequence is specifically claimed"
                                                                                                                                                                                                                                                                                                                 /note= "Receptor binding inhibitory peptide.
sequence is specifically claimed"
1064. 1088
[label= Pep2
                                                                                                                                                                                                                                                                                                                                                                 sequence is specifically claimed"
1084. 1108
//label= pep4
                                                                                                                                                                                                                                                                                                                                                                                                                inhibitory peptide.
claimed"
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1074. 1098
[label= Pep3
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                                                                                                               AAU04591 standard; protein; 1192 AA.
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/label= Pep1
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                                                                                                                                                              Human Nogo protein.
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26-MAY-2000; 2
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The sequence is the human Nogo protein, a 250kDa myelin-associated axon or growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral trauma, spinal cord injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasis demyelinating, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiatava-Bignami disease, pontine myelinolysis, adenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease
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Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central nervous system disorders.
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                                                                                                            English.
                                                                                                                  Example 1; Page 101-104; 109pp;
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              SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEBAVMLMKESLTEVS
                     - ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKKEKISLQMEEF
                                                 NTALYSNDDLLSSKEDKIKESETFSDSSPIELIDEPPTFVSAKDDS-PKLAKEYTDLEVS
                                                                             DKSEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV
                                                                                                                            SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK
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                                                                                                                                                                                                                                                                                                                        cancer; gene therapy; vaccine; immunostimulant;
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2001US-0265682P.
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2001US-0287112P.
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12-UUL-2001; 2001US-0305484P.
20-AUG-2001; 2001US-0313999P.
27-NOV-2001; 2001US-0333626P.
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N-PSDB; ABV94680.
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28-APR-2001;
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a) Polypeptides (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer antibodies, fusion proteins, T cell populations and antigen presenting antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RG-SGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG----KED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 4403.5; DB 5; Length 1192; Pred. No. 2.3e-222;
                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 909; Conservative 104; Mismatches 145; Indels
                                                                                                              + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE
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                                                                                                              SEQ ID NO.71; 300pp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1192 AA;
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or

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The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (P1, human Nagor erceptor (NagN PHTRRCT domain), or residues 27-309 of P1 with 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive residues. The nucleic acid of the cinvention has neuroprotective acid is useful for decreasing inhibition of axonal growth by a central nervous system (CNS) neuron. The NgR polypeptide or an agent inhibits the binding of Nogo to NgR or NgR-dependent signal transduction in the central nervous system neuron may be used in traating central nervous system disease, disorder or injury, e.g. spinal cord injury. Expression of an NgR protein may be associated with thibition of axonal regeneration following cranial, cerebral or spinal trauma, stroke or a demyelinating disease, such as multiple sclerosis, monophasic demyelination, encephalomyelitis, or Krabbe's disease. The present elected in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPPERVWEVKDSKEDS-DMLAAGGKIESNL 416
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disorder
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system disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         145;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 4403.5; DB 6
Pred. No. 2.3e-222;
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                                             Disclosure; Page 131-135; 148pp; English.
 nervous
              e.g. spinal cord injury
in treating central
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75.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy; axonal growth; central nervous system; CNS; Nogo; spinal cord injury; cranial trauma; spinal trauma; stroke; Krabbe's disease; demyelinating disease; multiple sclerobis; monophasic demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.
                                                                                                                                           809
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                                                                                                                                                                                                                                                                                  SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK
                                                                                             - ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKKEKISLQMEEF
                                                                                                                                                             PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF
                                  PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDF
                                                                                                                                                                                                         NTAIYSNDDLLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS
                                                                                                                                                                                                                                                                    DKSEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV
                                                                            SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system
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                                                                                                                                                                                                                                                                          NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192
                                                                                                                                                                                                                                                                NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
                                                                                                            STAVYSNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVS
                                                                                                                                                                            SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK
                                                                                                                                                                                                                                           YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALF
        GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF
              SNYSELARPEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQBEAVMLMKESLTEVS
                                             -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKKEKISLQMEEF
                                                                             NTAIYSNDDLLSSKEDKIKESETFSDSSPIBIIDEFPTFVSAKDDS-PKLAKEYTDLEVS
                                                                                                                                    DKSEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV
                                                                                                                                                  HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV
                                                                                                                                                                  SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK
                                                                                                                                                                                                  KTGVVFGASLFLLLSLTVFSIVSVTAYIALLSVTISFRIYKGVIQAIQKSDEGHPFRA
                                                                                                                                                                                                                                                                                                                                                                                    binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder.
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(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
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The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 1000nM. Also described. (1) a polynuclectide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or dilutent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence represents human NogoA, which is used in the exemplification of the present
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|APSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPPSTPAAPKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPROPERQPSWDFSFVSTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RG-SGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS
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NogoA623-640, useful in preparing a composition for treating or neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.3%; Score 4403.5; DB 8; Length 1192; 75.9%; Pred. No. 2.3e-222; ive 104; Mismatches 145; Indels 39;
                                                                            English
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standard recombinant methodology. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, psinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleotide is also useful for chromosome localization and for tissue expression studies. The present sequence represents the human MAGI protein
                                                                                                                                                                                                                                                                                                                                                                       APSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPPSTPAAPKR 178
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                                -ETVAQHK-EERLSASPQELGKPYLESPQPNLHSTKDA-ASNDIPTLTKKEKISLQMEEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGI protein, neuroendocrine-specific protein, neuropathy, human, spinal injury, neuronal degeneration, neuromuscular disorder, cancer, psychiatric disorder, developmental disorder, inflammatory disorder;
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stroke, cytostatic, cerebroprotective, neuroprotective
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                                                                                                                                                                                                                                                                                                                                                 NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuroperotective; nootropic; neuroleptic; antiparkinsonlan; cerebroprotective; neuroleptic; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide designated NOGO-C is a splice variant of the human NOGO and may be useful in the treatment of neural disorders including
                                                                                                                                                                                        NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
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                             SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK
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                                                                                                                                                                                            agonists and agonists for use in treating conditions associated with here imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels
                                                                                                                                                                                                                                            PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P
                                                                                                                                                                                                                                                                                                                                    RG-SGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS
                                                                                                                                                                                                                                                                                                                                                                                                      LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPPERVWEVKDSKEDS-DMLAAGGKIESNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNIFPELGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVTEEVVANMPEGLIPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV
                                                                                                                                                                          MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEBDEEEDDEDLEELEVLERK
                                                                                                                                                                                                                                                                                                                APSLPPAAAVLPSKLPEDDEPPARPPPPPAGASPLAE-----PAAPPSTPAAPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG----KED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVVSPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNYSELAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - ETVAQHK-BERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKKEKISLQMEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKSEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV
                                                                                                                                          Gaps
                                                                                                                                          39;
                                                                                                       Length 1192
                                                                                                                                        Indele
                                                                                                      Score 4398.5; DB 4;
Pred. No. 4.3e-222;
4; Mismatches 146;
```

927 SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986	956 SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015	987 KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRA 1046	1016 KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRA 1075	YLBSEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALF 1106	YLESEVAISEELVQKYSNSALGHVNCTIKELRREFLVDDLVDSLKFAVLMMVFTYVGALF 1135	1107 NGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163	1136 NGLTLLILALISLESVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192
927	926	987	1016	1047	1076	1107	1136
à	qq	8	QQ	ò	qg	δ	qq

Search completed: June 16, 2005, 13:10:59 Job time : 174.944 secs

Tue

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPATING SYSTEM: DOS
SOFTWARE: Falsed Herewith
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNER: Billings, Lucy J.
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0555
TELEPHONE: A15-855-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-700-607-1
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5, Appli
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563, App
45132, A
3, Appli
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5000, Ap
32, Appl
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                                                                                                   (without alignments)
1976.818 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       5848
1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRKAD 1163
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Sequence 7
Sequence 8
Sequence 8
Sequence 5
                                                                                  June 16, 2005, 12:19:00 ; Search time 43.9175 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-08-700-607-3
5-09-949-016-7290
5-09-513-999C-5000
5-08-714-741-32
5-09-976-594-726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-149-476-563
-09-270-767-45132
                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                           513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                         Issued Patents AA:*
                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
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                                                                                                                                           US-09-830-972-2
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Match Length
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2468
2468
2522
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1786
             Copyright
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724.5
716.5
648.5
671
625.5
539.5
539.5
519
819
307.5
288
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279.5
275.5
275.5
275.5
267
267
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Maximum DB
                                                       OM protein
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                                                                                                                                                                         Sequence:
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                                                                                  Run on:
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Gaps ; 0

973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1032

Query Match 15.5%; Score 908; DB 2; Length 199; Best Local Similarity 96.3%; Pred. No. 1.5e-50; Matches 184; Conservative 3; Mismatches 4; Indels

Sequence Sequence Sequence Sequence Sequence

US-08-769-309A-5

Consensus

LIBRARY:

	174 Porter Drive Alto
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SGPARQSP--VAMETASTGVAGVSSAMDHTFSTTSKDGEG-----SCYTSLI----S 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 DICYPPQEDSTYFTGILQKENGHVTISESP---EELGTPGPSL-PDVPGIESRGLFSSDSG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFSNYSEIAKFEKSVPEHABLVEDSSPESEPVDLF-SDDSIPEV----PQTQEEAVMLMK 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESLIEVSETVAQHK----EERLSASPQELGKPYLESFQP----NLHSTKDAASND---- 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 SSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRPEVKARSGPPT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 İPSPLDHEASSAESGDSEIELVSEDPM--AAEDALPSGYVSFGHVGGPPPSPASPSIQYS 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KESETPSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEI----ANIQSG 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIV 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PPGDGALEPETPM---- 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600 -- LLPSAGASVVQPSVSPLEAPPPVSY-----DSIKLEPENPPPYEEA------M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 ISPKTSNPFLVAVQDSEADYVITDILSKVTEAAVSNMPEGLIPDLVQEACESELNEAIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVALKALGTKEGIKEPE----SFNAAVQETEAPYISIACDLIKETKLSTE-PSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    547 KIAYETKVDLVQTSEAIQ-ESLYPTAQLCPSFEEAEATPSPVLPDI---VMEAPLNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        793 IPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKI---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
13.5%; Score 789.5; DB 2;
Best Local Similarity 31.2%; Pred. No. 4.1e-42;
Matches 243; Conservative 115; Mismatches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
RESISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
                                                                                                                                                                                                                                                                                                                                                           SD
                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                       3174 Porter Drive
                                                                                                                                                        3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 776 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
  CORRESPONDENCE ADDRESS:
                                                              Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                   u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino a STRANDEDNESS:
                      ADDRESSEE:
                                                         CITY: Pal
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-700-607-5
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOTUME FAILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOTUME: FaetSEQ for Windows Version 4.0

LENGTH: 201
                                                                                                                                        1093 AVLAWVFTYVGALFNGLTLILILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ 1152
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                                                                                                                                                             69 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKF 128
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                  9 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
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Patent No. 5858708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 908; DB 4;
Pred. No. 1.5e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Sequence 9124, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.5%;
96.3%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                      RESULT 2
US-09-949-016-9124
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US-08-700-607-5
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Sequence 9180, Application US/09949016

Sequence 9180, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 9180

SEQ ID NO 9180
                                                                                                                                                                                                                                                                                                             985 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPF 1044
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195 IPSPLDHEASSAESGDSEIELVSEDPM--AAEDALPSGYVSFGHVGGPPPSPASPSIQYS 452
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                                                                                                                                ADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIV
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                                            ---KESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEI-
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%; Pred. No. 2.6e-38;
64; Mismatches 135;
                                                                                                                                                                        510 APSRRGLAEPG--SFLD-YPSTEPQPGPEL----
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Best Local Similarity 38.0<sup>3</sup>
Matches 190; Conservative
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TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-9-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASISEQ for Windows Version 4.0
                                                                                                                                                                                             | RAYLESEVAISBELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGA 1104
                                                                                                         IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPF 1044
                                                                                                                                  487 TSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGT 546
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                  KSKSLTKEAEKKLPSDTEKEDRSLSAVLSAE-
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Sequence 6998, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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; ORGANISM: Human
US-09-949-016-6998
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                                                                                                883 LPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSK 942
                                      ---PPGDGALEPETPM----- 129
                                                                         943 SLTKEAEKKLPSDTEKEDRSLSAVLSAE------LSKTSVVDLLYWRDIKK 987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
ITILE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
                                    93 RRGLAEPG--SFLD-YPSTEPQPGPEL--
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08700607
Patent No. 5858708
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Incyte P
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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MOLECULE TYPE:
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Best Local Simi
Matches 128;
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                                                                                                                               1024 SFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLV 1083
                                                                                                                                                                                                      1084 DDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKS 1143
360 QDLVDSLKFAVLMMLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTH 419
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                                                                             240 APPPLLFLNKQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATI
                                                                                                                                                  971 -----LSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALASVTI
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APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2e-38
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46.1%; Pred. No. 6.2e
ive 48; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAMME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0114 US
                                                                                                                                                                                                                                                                              1144 VKDAMAKIQAKIPGLKRKAD 1163
                                                                                                                                                                                                                                                                                                         420 INAVVAKIQAKIPGAKRHAE 439
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08700607
Patent No. 5858708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
 | ||:|| | 200 ----PPGDGALEPETPM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.13
Matches 164; Conservative
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MEDIUM TYPE: Diskett
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129 AVLMWLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQ 188
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Best Local Similarity 60.0%;
Matches 114; Conservative 46
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183 LPGIAKKKAE 192
                                   1153 AKIPGLK 1159
                                                                       189 AKIPGAR 195
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US-09-949-016-8859
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              1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKF 1092
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Gollin, Surya K.
APPLICANT: Gollin, Surya K.
APPLICANT: Gollin, Two Novel HUMAN NSP-LIKE PROTEINS
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
TORRESPONDENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.5%; Score 671; DB 2;
66.3%; Pred. No. 3.3e-35;
cive 33; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.

ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.38
Matches 124; Conservative
                                                                                                                                                         1153 AKIPGLKRKAD 1163
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198 AKIPGAKRHAE 208
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STATE: CA
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MOLECULE TYPE:
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US-08-700-607-8
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sequence 8859, Application US/09949016

patent No. 6812339

GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 8859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 FWHIMTYVGAVFNGITLILABLLIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 625.5; DB 4;
; Pred. No. 1.7e-32;
40; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPLICANT: Rosen et al.
TITLE OF INVENTION: 166 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,626
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R APPLICATION NUMBER: 60/047,617
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,618
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,503
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,592
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,581
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,500
R R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,500
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,507
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,507
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,507
R FILING DATE: 1997-05-23 R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,615

R PILING DATE: 1997-05-23

R PILING DATE: 1997-05-38

R FILING DATE: 1997-05-28

R R FILING DATE: 1997-05-28

R R FILING DATE: 1997-05-28

R R FILING DATE: 1997-05-23 R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,598

R APPLICATION NUMBER: 60/047,613

R PILING DATE: 1997-05-23

 APPLICATION NUMBER: 60/047,632 R FILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/047,601 R FILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/043,580 R FILING DATE: 1997-04-11 PLICATION NUMBER: 60/040,336 LING DATE: 1997-03-07 APPLICATION NUMBER: 60/040,163 FILING DATE: 1997-03-07 APPLICATION NUMBER: 60/047,600 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,569 APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 APPLICATION NUMBER: 60/040,334 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,583 FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 :CATION NUMBER: 60/043,313 1997-04-1 BARLIER
EARLIER
EARLIER SARLIER SARLIER SARLIER SARLIER PARLIER SARLIER

FILING DATE: 1997-08-22
APPLICATION WUMBER: 60/056,877
APPLICATION WUMBER: 60/056,889
APPLICATION WUMBER: 60/056,889 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 PILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,595 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,599 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 APPLICATION NUMBER: 60/056,888 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 APPLICATION NUMBER: 60/057,761 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,588 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 APPLICATION NUMBER: 60/047,614 APPLICATION NUMBER: 60/056,662 APPLICATION NUMBER: 60/056,636 APPLICATION NUMBER: 60/047,585 1997-08-22 LING DATE: 1997-08-22 LING DATE: 1997-08-22 1997-08-22 LING DATE: 1997-08-22 LING DATE: 1997-08-22 1997-05-23 1997-08-22 1997-05-23 LING DATE: LING DATE: LING DATE: LING DATE: EARLIER EARLIER

APPLICATION NUMBER:

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                                                                                                                                                                        1014 IALALLSVIISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNST 1073
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                                                                                                                                                                                                     SCCAVHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSV 103
                                                                                                        957 EKEDRSLSA---VLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY
                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08700607

Patent No. 5858708

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: STREET: 3174 Porter Drive
                              Indels
     7.8e-26;
thes 55;
     Best Local Similarity 47.8%; Pred. No. 7.8e-
Matches 97; Conservative 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        1134 DHYLGLANKSVKDAMAKIQAKIP 1156
                                                                                                                                                                                                                                                                                                                                                                                                                    181 DTHLDLVRSKLTEITDKIRVAIP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THP1NOB01
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3174 POI
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CLONE: 31870
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US-08-700-607-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      998 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 APHNYMNAAMVHINRALKCLIRLFLVEDLVDSLKCAVFWHLMTYVGAVFNGITLLILAEL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLESLAAFSVISVVSYLIIALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: 05/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 45132

LENGTH: 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKAE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 539.5; DB 4; Length Similarity 59.3%; Pred. No. 4.3e-27; Onservative 36; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.9%; Score 522.5;
                                                                                                                                                                                                                                                               REFLIENCE DATE: 1997-08-22
REPLICATION NUMBER: 60/056,881
RETLING DATE: 1997-08-22
RETLING DATE: 1997-08-22
REPLICATION NUMBER: 60/056,805
RETLING DATE: 1997-08-22
REPLING DATE: 1997-06-06
REPLING DATE: 1997-06-06
REPLING DATE: 1997-06-06
REPLING DATE: 1997-06-06
REPLING DATE: 1997-06-06
REPLING DATE: 1997-06-06
                       R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/047,501
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043,670
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/056,632
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-28
R PILING DATE: 1997-08-28
R PILING DATE: 1997-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-09-05
APPLICATION UNMBER: 60/056,884
ELING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/049,610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-270-767-45132
; Sequence 45132, Application US/09270767
; Patent No. 6703491
60/043,576
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-270-767-45132
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Query Match Best Local (

Best Loca Matches

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SUCH GENES
                                                                                                                                                                                          Sequence 5000, Application US/09513999C

Sequence 5000, Application US/09513999C

Retent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Parent pm
SEQ ID NO 5000

LENGTH. 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    698 IAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-ETVA 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKKEKISLQMEEFNTAIY 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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APPLICANT: Briles, David E.

APPLICANT: Swiatlo, Larry S.

APPLICANT: Swiatlo, Edwin

APPLICANT: Yother, Janet

APPLICANT: Yother, Janet

APPLICANT: Tother, Janet

APPLICANT: Tart, Rebecca

APPLICANT: Tart, Rebecca

APPLICANT: Brooks Walter, Alexis

TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF STITLE OF INVENTION: PORTIONS AND PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ë.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 387.5; DB 462.8%; Pred. No. 1.6e-17;
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                           1132 QIDHYLGLANKSVKDAMAKIQAKIPG 1157
                                                     ||| |:|| |:|| 544 QIDQYVGLVTNQLSHIKAKIRAKIPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/08714741 Patent No. 6500613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 107
; OTHER INFORMATION: Xaa=Lys or Thr
US-09-513-999C-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 106
OTHER INFORMATION: Xaa=Glu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.8*
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNDDLFISK 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNDDLLSSK 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: UNSURE
                                                                                                                                                         RESULT 14
US-09-513-999C-5000
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US-08-714-741-32
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FACENTERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PEASESE FOR WINGOWS VERSION 4.0

LENGTH: 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .012 AYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVN 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1072 STIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 1131
1032 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLK 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 KWAKSPRS-SGVPSLSLGADMGSKVADLLYWKDTRTSGVVFTGLMVSLLCLLHFSIVSVA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 IQAVQKSEEGHPFKAYLDVDITLSSEAPHNYMNAAMVHINRALKLIIRLFLVEDLVDSLK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 EAP-----STASSTPDSTEGGNDDSDFRELHTAREFSEEDEEETTSQDWGTPRELIFSY 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | : | : | : | : | : | 10 IAFDGVVGSGGRRDSTARRPRPQGRSVSEPRDQHPQPSLGDSLESI--PSLSQSPEPGRR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 -------BEEP---QEPNRLETGEAGE------EL--DLRLRLAQPSSPE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           668 EAPYISIACDLIKETKLSTEPSPDFSNYSEI---AKFEKSVPEHAELVEDSSPESEPVDL 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                725 FSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYL-ESFQPNLH 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       784 STKDAASNDIPTLTKKEKISLOMBEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIEIID 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              844 EFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEV 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.4%; Score 490; DB 4; Length 588;
Best Local Similarity 28.3%; Pred. No. 4e-23;
Matches 160; Conservative 76; Mismatches 202; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           904 HVSDEFSENRSSVSKASISP----SNVSALEPQTE-----
                                                                                                       1092 FAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 1131
                                                                                                                                     935 -----MGSIVK--SKSLTKEAEKKLP-----
                                                                                                                                                                                                                                                                                            Sequence 7290, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7997 PEG---KTQDELDKEAARAELNKKVEALPNQVSELEEELSKLEDNLKDAETNNVEDYIKE 8053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8054 GLEBAIATKQAELEKTPKELDAALN--ELGPDGDEBETPPPE------APAE 8097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8152 APAPKPEQPAPA-PKSRGLATKKKINLAEARIELLLKKIGLEPGLEKAGAGLGNLLSTLD 8210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 LLDFSSDSVPPAPRGPLPAAPPRAPERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPP 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 DLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSF-----KEHGYLGNLSAVSS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 SEGTIEETLNEASKELPERATNPFVNRDLAEFSEL--EYSEMGSSFKGSPKGESAILVEN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 TKEEVIVRSK---DKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVAPVR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 EEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLED--SLEQKSLGKDSEGRN 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 PRPPPARKYOFVTEPEDEEDEEEEDEEDEEDEEDEEDEETENEEKPAAGLSAAAVPPAAAAP 77
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                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
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530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: amino acid
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                                                                                      New York
: U.S.
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STRANDEDNESS: si
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Search completed: June 16, 2005, 12:33:36 Job time: 45.9175 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 16, 2005, 12:29:05 ; Search time 150.865 Seconds Run on:

(without alignments) 2960.058 Million cell updates/sec

US-09-830-972-2

Perfect score: Sequence:

5848' 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRKAD 1163

BLOSUM62 Gapop 10.0 , Gapext.0.5 Scoring table:

Total number of hits satisfying chosen parameters: 1714042 seqs, 383979560 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUBL.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUBL.pep:*
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/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Ouery e Match Length DB I	DB	ID	Description
-	5848	100.0	1163	16	US-09-893-348-18	Sequence 18, Appl
7	5848	100.0		16	US-10-810-653-18	Sequence 18, Appl
٣	5312.5	90.8	1162	16	US-10-633-423-10	Seguence 10, Appl
4	5312.5			16	US-10-427-741-10	Sequence 10, Appl
S	5307			15	US-10-267-502-431	Sequence 431, App
9	4403.5			6	US-09-758-140-6	Sequence 6, Appli
7	4403.5			σ	US-09-972-599A-6	Sequence 6, Appli
80	4403.5			14	US-10-060-036-71	Sequence 71, Appl
σ	4398.5			0	US-09-789-386-2	Sequence 2, Appli
10	4398.5				9 US-09-893-348-23	Sequence 23, Appl
11	4398.5				US-10-267-502-429	Sequence 429, App

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Gaps

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Length 1163; IndelB

Query Match 100.0%; Score 5848; DB 9; Best Local Similarity 100.0%; Pred. No. 1.9e-256; Matches 1163; Conservative 0; Mismatches 0;

Sequence 9, Appli Sequence 9, Appli	Sequence 23, Appl	19		Sequence 20, Appl	Sequence 6, Appli	w	Sequence 24, Appl	Sequence 72, Appl	Sequence 8, Appli	Sequence 24, Appl	ý	4	Seguence 21, Appl	21,	22,	Sequence 1, Appli	25	Ų,	4	Sequence 4, Appli	0	٠.	v.	5,	Sequence 430, App		Sequence 6, Appli	Sequence 2892, Ap	,	Sequence 127, App	Sequence 8, Appli
	16 US-10-810-653-23		9 US-09-893-348-20	16 US-10-810-653-20	9 US-09-789-386-6	9 US-09-765-205-6	9 US-09-893-348-24		15 US-10-408-967-8		17 US-10-347-669-6	16 US-10-466-258-4	9 US-09-893-348-21	16 US-10-810-653-21	9 US-09-893-348-25	15 US-10-660-946-1	16 US-10-810-653-25	15 US-10-408-967-9	11 US-09-978-360A-467	9 US-09-789-386-4	16 US-10-466-258-11	Þ		Þ	Þ	Þ	Þ		15 US-10-660-946-7		15 US-10-660-946-8
1192	1192	379	360	360	373	373	373	373	373	373	373	373	199	199	199	199	199	199	199	289	199	777	780	176	176	116	356	593	208	267	267
75.2	75.2	25.9	24.1	24.1	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.3	15.8	15.8	15.5	15.5	15.5	15.4	15.4	15.2	٠	٠	٠	•	•	٠	•	•	11.7		11.5
398.	4398.5	1513	1411.5	1411.5	1191	1191	1191	1191	1191	1191	1191	1183	925	925	806	806	806	901	899	888	898	801	792	789.5	789.5	789.5	716.5	706.5	685	671	671
12	14 7	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	. 35	36	37	38	39	40.	41	42	43	44	45

ALIGNMENTS

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US-9-893-348-14B

Sequence 18, Application US/09893348

Fatent No. US20020072493A1

GENERAL INFORMATION:

APPLICANT: BISENBACH-SCHWARTZ, Michal

APPLICANT: BISENBACH-SCHWARTZ, Michal

APPLICANT: BISENBACH-SCHWARTZ=2A

TILLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE

FILE REFERENCE: BIS-SCHWARTZ=2A

CURRENT APPLICATION NUMBER: US/09/893,348

CURRENT APPLICATION NUMBER: US 09/314,161

FILE REFERENCE: 1999-05-19

FRIOR FILING DATE: 1999-05-19

FRIOR PILING DATE: 1998-07-21

FRIOR PILING DATE: 1998-07-21

FRIOR PILING DATE: 1998-07-21

FRIOR FILING DATE: 1998-05-19

FRIOR FILING DATE: 1998-05-19

FRIOR FILING DATE: 1998-05-19

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FRIOR FILING DATE: 1998-05-19

FRIOR FILING DATE: 1998-05-19
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JS-09-893-348-18
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oy Op	1 MEDIDQSSLVSSSTDSPPRPPRAFKYQFVTEPEDEBEBEBEBEBEDDEDLEELEVLERK 60	1081 FLVDDLVDSLKFAVLMWVFTYVGZ
9 G	61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGFLPAAPPAAPERQPSWERSPAABAPSLP 120 	CY 1141 NKSVKDAMAKIQAKLYGLKKAD 1163 Db 1141 NKSVKDAMAKIQAKIYGLKRKAD 1163
රු අ	121 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPSTPAAPKRRGGGSVDETLFALP 180 	RESULT 2 US-10-810-653-18 ; Sequence 18, Application US/10810653 ; Dublication US/10810653
کن م	181 AASEPVIPSSAEKIMDLMEQPCNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240	
දු පු	241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300 	
දුරු දුරු	301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360 	
. Ag	361 PVREBYADFKRPEQAMEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEGKSLGKDSEGR 420 	FRIOR FILING DATE: 2001-06-28 FRIOR FILING DATE: 1999-05-19 FRIOR FILING DATE: 1999-05-19 FRIOR APPLICATION NUMBER: US 09/218,277
<u>ئ</u> و	421 NEDASPPSTBEPVKOSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480 	
oy Op	481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLIPDLVQEACESEL 540 	ഗ
<u>ئ</u> ۾	541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600 	S-
60 91	601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660 	Query Match 100.0%; Score 5848; DB 16; Length 1163; Best Local Similarity 100.0%; Pred. No. 1.9e-256; Matches 1163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
cy Op Op	661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720 	Qy 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEDEEDEEDEEDEELEVLEEK 60
λό qa	721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKERRLSASPQELGKPYLESFQP 780 	Qy 61 PAAGLSAAAVPPAAAAPILDFSSDSVPPARRGPLPAAPPAAPERQPSWERSPAAPSLP 120 Db 61 PAAGLSAAAVPPAAAAPILDFSSDSVPPARRGPLPAAPPAAPERQPSWERSPAAPAFSLP 120
op O	781 NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIE 840 	QY 121 PAAAVLPSKLPEDDEPPARPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP 180 . </td
9y Dp	841 IIDBEPTFVSAKDDSPKLAKBYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900 	Qy 181 AASEPVIPSSAEKIMDLMEQPCNIVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240 Db 181 AASEPVIPSSAEKIMDLMEQPGNIVSSGQEDFPSVLLETAASLPSLSFLSTVSFKEHGYL 240
	901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED 960 	Qy 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300
& 8	961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020 	Qy 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360
S G	1021 VTISPRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080 	Qy 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR 420
ò	1081 FLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140	Qy 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480

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QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL
                                     NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL
                                                                       PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKERLSASPQELGKPYLESFQP
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; Publication No. US20040191240A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD F.
FILE REFERENCE: 5915.0-8023.US00
; CURRENT APPLICATION NUMBER: US/10/633,423
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 10/427,741
; PRIOR APPLICATION NUMBER: UP 2003-92923
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHOD
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TYPE: PRT
ORGANISM: Mus musculus
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US-10-633-423-10
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                                                                                                              60 PAAGLSAAPUPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP
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                         Gaps
  Length 1162
                         13;
                         55; Indels
  16;
; Score 5312.5; DB 10; Pred. No. 3.3e-232; 37; Mismatches 55;
 90.8%;
                         Conservative
              Similarity
                         Matches 1064;
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Best Local
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Best Local Similarity 91.1%; Pred. No. 5.8e-232;
Matches 1066; Conservative 34; Mismatches 56;
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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 431
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US-10-267-502-431
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Sequence 10, Application US/10427741

Sequence 10, Application US/10427741

Sequence 10, Application US/10427741

Sequence 10, Application No. US20040191291A1

SERVERAL INFORMATION:

APPLICANT: Tohyama, Masaya

ITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION

FILE REFERENCE: 59150-8023

CURRENT APPLICATION NUMBER: US/10/427,741

CURRENT FILING DATE: 2003-03-04-30

PRIOR FILING DATE: 2003-03-04-30

PRIOR FILING DATE: 2003-03-28

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.1

LENGTH: 1162
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TITLE OF INVENTION: No. US20020012965Alo Receptor-Mediated Blockade of A.
FILE REFERENCE: 44574-5073-US
CURRENT APPLICATION NUMBER: US/09/75g,140
CURRENT FILING DATE: 2001-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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DHYLGLANKSVKDAMAKI QAKI PGLKRKAE
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US-09-758-140-6
US-09-758-140-6
Sequence 6, Application US/09758140
Patent No. US20020012965A1
GENERAL INFORMATION:
APPLICANT: Strittmatter, Stephen M
TITLE OF INVENTION: No. US20020012
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Qy 574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633 	Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF 692 	Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS 752	Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKKEKISLQMEEF 809	Oy 810 NTALYSNDDLLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868	Qy 869 DKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNV 926	Qy 927 SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986	Qy 987 KTGVVFGASLFLLLSLTVFSIVSVTAYTALALLSVTISFRIYKGVIQAIQKSDBGHPFRA 1046	Qy 1047 YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALF 1106 	QY 1107 NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163	RESULT 7 US-09-972-599A-6	; Sequence 6, Application US/09972599A ; Patent UNFORMATION: ; GENERAL INFORMATION: ; APPLICANT: STRITTMATTER, STEPHEN M.	; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH ; FILE REPELICE C077 CIP US ; CURRENT AFPELICATION NUMBER: US/09/972,599A ; CURRENT FILING DATE: 2001-10-06	; PRIOR APPLICATION NUMBER: PCT/USO1/01041 ; PRIOR FLING DATE: 2001-01-12 ; PRIOR APPLICATION NUMBER: 09/758,140 ; PRIOR FILING DATE: 2001-01-12	; PRIOR APPLICATION NUMBER: 60/236,378 ; PRIOR FLING DATE: 2000-09-29 ; PRIOR APPLICATION NUMBER: 60/207,366 ; PRIOR FILING DATE: 2000-05-26	; PRIOR APPLICATION NUMBER: 60/175,707 ; PRIOR FILING DATE: 2000-01-12 ; NUMBER OF SEQ ID NOS: 57 ; SOFTWARE: Patentin Ver. 2.1	; SEQ ID NO 6 ; LENGTH: 1192 ; TYPE: FRT ; ORGANISM: Homo sapiens	<pre>US-09-972-599A-6 Query Match</pre>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANT: PRINAHA, RABINDER KUMAR
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30165-C1
CURRENT FILING DATE: 2001-02-21
FRIOR APPLICATION NUMBER: U.K. 9916898.1
PRIOR APPLICATION NUMBER: U.K. 9916898.1
PRIOR APPLICATION NUMBER: U.K. 9916898.1
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: U.S. 9916894.5
PRIOR APPLICATION NUMBER: U.S. 991899.07
PRIOR APPLICATION NUMBER: U.S. 991899.07
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
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APPLICANT: Benson, Darin R.
APPLICANT: ABLOS, Michael D.
APPLICANT: Ablos, Michael D.
APPLICANT: Ablos, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Helpler, William T.
APPLICANT: Helpler, William T.
APPLICANT: Helpler, William T.
APPLICANT: Helpler, William T.
APPLICANT: Helpler, William T.
APPLICANT: Hongy Yugiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.566
CURRENT APPLICANTON NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 75.9%; Pred. No. 4.8e-191;
Matches 909; Conservative 104; Mismatches 145; Indels
                                                                                                                                                                                      Sequence 71, Application US/10060036
Publication No. US20030073144A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-71
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                                  KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL
                                            PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF
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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
TITLE OF INVENTION Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 429
LENGTH: 1192
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CRGANISM: Homo
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Query Match 75.2%; Score 4398.5; DB 15; Best Local Similarity 75.9%; Pred. No. 8.1e-191; Matches 908; Conservative 104; Mismatches 146;

DB 15; Length 1192

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                CPSFEEERATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN
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                                                                                                                              SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS
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Local Similarity 75.9%; Pred. No. 8.1e-191;
Les 908; Conservative 104; Mismatches 146; Indels
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 Sequence 9, Application US/10327213
Sequence 9. Application No. US20040121341A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FILBIN, MARIE T.
APPLICANT: DOMENICONI, MARCO
APPLICANT: TOO, ZIXUAN
TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
FILE REFERENCE: CINY/003
CURRENT APPLICATION NUMBER: US/10/327,213
CURRENT FILING DATE: 2002-12-20
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                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
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; ORGANISM: Homo sapiens
US-10-327-213-9
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US-10-327-213-9
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Sequence 23, Application US/10810653
Publication No. US20040253218A1
GENERAL INFORMATION:
APPLICANT: BISENBACH-SCHWARTZ, Michal
APPLICANT: BESENBACH, Pierre
APPLICANT: BESENBAN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
TILLA OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR
FILE REFERENCE: BIS-SCHWARTZ-2A
CURRENT APPLICATION NUMBER: US/10/810,653
CURRENT APPLICATION NUMBER: US/09/893,348
PRIOR FILING DATE: 1999-05-19
PRIOR PLING DATE: 1999-05-19
PRIOR PLING DATE: 1999-05-19
PRIOR PLING DATE: 1998-05-19
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larity 75.9%; Pred. No. 8.1e-191;
Conservative 104; Mismatches 146;
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US-10-810-653-23
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908; Conserv
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Best Local S
Matches 908
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                           RG-SGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS
                                          LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY
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339 115 166 178 225 237 285 297 357 340 RVVSPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANV 395 416 454 513 536 573 596 9 28 ESKVDRKCLEDSLEGKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT TNIFPLIGDPISENKIDEKKIEEKKAQIVTEKNISTKISNPFLVAAQDSEIDYVITDNLI PAAGLSAAAVP--PAAAAPLLDFSSDSVPPARGPLPAAPPAAPERQPSWERSPAA---P RG-SGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG----KED KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 1 MEDIDOSSLVSSSTDSPPRPPARKYOFVTEPEDEEDEEBEBEBEBDBDLEBLEVLERK APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE------PAAPPSTPAAPKR APSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAAPAPAPPSTPAAPKR ANTFPLLEDHTSENKTDEKKI EERKAQI I TEK-TSPKTSNPFLVAVQDSEADYVTTDTLS KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL Length 1192; 537 8 셤

RESULT 14 US-10-810-653-23

State Comparison State	116 APSILPPAAAVI.PSKI.PEDDEPPARASPIAEPAAPPSTPAAPKR 166	Oy 286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVGKED 339	358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 41 396 ESKVDRKCLEDSLEQKSLGKDSEGRNEDASPPSTPEPVKDSSRAYITCASFT-SATESTT 45		Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573	Qy 574 CPSFEEARATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLRAPPPVSYDSIKLEPEN 633	Qy 634 PPPYEBAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEBSPDF 692	Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLAKESLTEVS 752 : : :	Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKKEKISLQMEEF 809	QY 810 NTAIVSNDDLLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868	OY 869 DKSEIANIOSGADSLECLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNV 926	Qy 927 SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLVWRDIK 986	QY 987 KTGVVFGASLFLLASLTVFSIVSVTAVIALALLSVTISFRIYKGVIQAIQKSDEGHPFRA 1046 L	VOKYSNSALGHVNSTIKELRRLFLVDDLVDSLKRAVLMWVFTYVGALF 	Qy 1107 NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
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US-09-830-972-2 5848 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRKAD 1163 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues Searched:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scription	neuroendocrine-spe	neuroendocrine-spe	tropomyosin-relate	hypothetical prote		microtubule-associ	elastic titin - hu	hypothetical prote	44	hypothetical prote		hypothetical prote	· CO	hypothetical prote					ankyrin 2, neurona	hypothetical prote		hypothetical prote	RESA-H3 antigen PF	tegument protein 2			gravin - human	microtubule-associ	microtubule-associ
SUMMARIES	- Ω	A46583	160904	A60021	T26216	T26215	T13564	138346	T26213	A47283	T24583	A47282	T34513	A56577	T19431	QRMSP1	T34418	T22523	A82255	S37431	T47182	T30351	T16251	B71603	T42567	T22458	T30826	JW0057	A40115	\$13507
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d	Query Match	13.5	11.7	11.5	8.8	8.6	5.6	5.5	٠	5.2	5.2	5.1	5.0	5.0	4.9	4.9	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.5	4.5
	Ü	789.5	685	671	517	503.5	328.5	322	320	304.5	302.5	295.5	292	291.5	288.5	284	281	279.5	277	275.5	275	273.5	273.5	273	272.5	270	269.5	267	265.5	
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ALIGNMENTS

ABSULT 1 A46583 A46583 N.Contains: C.Species: A.Rebrock, A.Reference A.Reference A.Reference A.Residues:	RESULT 1 A46583 A46583 A46583 N. Contains: neuroendocrine-specific protein Cippecies: Homo sapiens (man) Cippecies: Homo sapiens (man) Ciptecies: Constant A46583; MGD 80464, H.J.; Van B J. Biol. Chem. 268, 13439-13447, 1993 A5.Title: Cloning and expression of alternat A5.Title: Cloning and expression of alternat A5.Title: Cloning and expression of alternat A5.Title: Cloning and expression of alternat A5.Title: Cloning and expression of alternat A5.Status: preliminary; translated from GB/E A5.Status: preliminary; translated from GB/E A5.Coss-references: UNIPROT:Q16799; GB:L103 A5.Molecule type: mRNA A5.Molecule type: mRNA A5.Molecule type: mRNA A5.Molecule type: mRNA A5.Molecule GDB:RTN1; NSP A5.Coss-references: GB:L10334; NID:g307308; Cigenei: GDB:RTN1; NSP A5.Coss-references: GB:L10334; MIM:600865 A5.Map position: 14421-14422	m A - human , splice for ay-1996 #tex okhoven, A.; ive transcri PMID:7685762 MBL/DDBJ MBL/DDBJ PIDN:AAAS99	re, F.C.; V docrine-spe PID:g307307
Query Match Best Local Matches 24	tch al Simi 243;	13.5%; Score 789.5; DB 2; Length 776; .larity 31.2%; Pred. No. 8.5e-25; .Conservative 115; Mismatches 252; Indels 169; Gaps 28.	8;
6 6	487 TSPKTSNPFLVAV : : 65 SGPARQSP VAM	487 TSPKTSNPFLVAVODSBADYVTTDTLSKVTBAAVSNMPEGLTPDLVQBACESELNEATGT 546 :	v 0
o da	547 KIAYETKVDLVQT : : 111 DICYPPQEDSTYF	547 KIAYETKVDLVQTSEAIQ-ESLYPTAQLCPSFERAEATPSPVLPDIWMEAPLNS 599 111 DICYPPQEDSTYFTGILQKENGHVTISESPEELGTPGPSLPDVPGIESRGLFSSDSG 167	9
ъ Вр. Ф	600LLPSAGASVVQ : : 168 IEMTPAESTEVNK	600LLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAM 641 :	1,7
& a	642 NVALKALGTKEGI ::: 228 DISIKPEGV	642 NVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTE-PSP 690 ::::	
& 8	691 DFSNYSEIAKFEK : 281 VKITLTEIE	691 DFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDLF-SDDSIPEVPQTQEEAVMLMK 745 1	10 et
ò	746 ESLTEVSETVAQH :	746 ESLTEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASND 792	8

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8.8%;
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Matches 124; Conservative
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: 160904
A;Pitle: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe A;Accession: 160904
A;Accession: 160904
A;Accession: 160904
A;Accession: 160904
A;Accession: 160904
A;Accession: 160904
A;Accession: 160904
A;Accession: 160904
A;Cross-references: UNIPROT:Q16799; GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311
A;Cross-references: GDB:RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKF 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1093 AVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ 1152
                                                                                                                                                                                                                                                                                                                                            985 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPF 1044
                                                                                                                                                                                                                                                                                                                                                                                                                    RAYLESEVAISEELVOKYSNSALGHVNSTIKELRRIFLVDDLVDSLKFAVLMWVFTYVGA 1104
                                                                                                                                                                                                                              549
                                                                                                                                                                                                                                                                                                                                                               138 AVLMWLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQ 197
                                                                                                                                                                                                                                                                   984
                                                                                                                                                                                                                                                                                        550 ------LPRKPEEDSSSNOSPAATKGPGPLGPGAPPPLLFLNKOKAIDLLYWRD 597
                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRPEVKARSGPPT 394
                                                                      395 IPSPLDHEASSAESGDSEIELVSEDPM--AAEDALPSGYVSFGHVGGPPPSPASPSIQYS 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 KSQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroendocrine-specific protein C - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I60904
                                                                                                                                                                                      880 ADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIV
                                                                                                                                                                                                                              ----PPGDGALEPETPM----
                                                                                                                                   940 KSKSLTKEAEKKLPSDTEKEDRSLSAVLSAE------LSKTSVVDLLYWRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                               ---KESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 11.7%; Score 685; DB 2; Length 208; Best Local Similarity 67.0%; Pred. No. 2.3e-21; Matches 128; Conservative 32; Mismatches 31; Indels
                                   IPTLTKKEKISLOMEEFNTAIYSNDDLLSSKEDKI-
                                                                                                                                                                                                                          510 APSRRGLAEPG--SFLD-YPSTEPQPGPEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1153 AKIPGLKRKAD 1163
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A,Accession: A60021
A,Molecule type: mRNA
A,Residues: 1-267 «MIE»
A,Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
C,Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2484 <WIL>
A;Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:WO
A;Experimental source: clone W06A7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tropomyosin-related protein, neuronal - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
C;Accession: A660021
R;Wieczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A;Teile: Developmentally regulated cDNA expressed exclusively in neural tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | || :| | :| || FGTESSEESQKADGNQENQEEDDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVGCITDV 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1555 IIADAVKEVSEMEVVTĖSEISEMAPQVSESTCPIPEPLADLKLPVEDDĖKTPEPEPVVPG 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GASPLAEPAAPPSTPAAPKRRGSGSVDETLFALPAASEPVIPS-SAEKIMDLMEQPGNTV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26216
R;Ainscough, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 -----ERKPAAGLSAAAVPPAAAAPL-LDFSSDSVPPAPRGPLPAAPPAAP--ERQPSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Matches 262; Conservative 189; Mismatches 413; Indels 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2484;
                                                                                                                                                                                                                                                                                                                                                                                         11.5%; Score 671; DB 2; Length 267; 66.3%; Pred. No. 1.2e-20; ive 33; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --DEDLEELEVL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , DB 2;
4.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, August 1996
A;Reference number: 220173
A;Accession: T26216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 517;
Pred. No. 4
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qq		Db 2429 LLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEK
රු දු	206 SSGQEDFPSVILETAASLPSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELP 265 	RESULT 5 T26215 hypothetical protein W06A7.3a - Caenorhabditis elegan
& g	266 ERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVRSKDKB 319 :	Ÿ
કે દ	320 DIVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQ-MSVVAPVREEYADFKPFEQAWEV 378	submitted to the EMBL Data Library, August 1996 A; Reference number: Z20173 A; Accession: T26215
3 &	KDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSGRNEDASFPSTPEPVKDS	A;Rodeuds: presidentify; cransraded from 50 Enby, DD50 A;Robidues: 1-2607 <wil> A;Cross-references: UNIPROT:Q23187; EMBL:Z78066; PIDN</wil>
g &	1764 KDNESLEAPEIINEPIRRVLVETKIMGPGKSLNEDNDD	A;Experimental source: clone W06A7 C;Genetics: A;Gene: CESP:W06A7.3a A;Ama.modition:
ΩÞ	1802TIQRFN 1824	A;Introne: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 22
පු දු	497 VAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKI 548 ::	Query Match 8.6%; Score 503.5; DB 2; Best Local Similarity 20.8%; Pred. No. 1.7e-12; Matches 280; Conservative 181; Mismatches 481;
ර සි	549 AYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASV 608 :::	Qy 28 FVIEPEDEEDESEBEDEED
ò	BPENPPPYEEAMNVALKALGTKEGIKEPESFNAA	58
qq	1899SPGPENTAQFLEKLQQEDRPSAEGSIDSSGFEKVDHEG 1937	: : : :
& 9	664 VQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPE 707 	Oy 109BRSPAAPAPSLPPAAAVLPS Db 1555 IIADAVKEVSEMEVVTESEISEMAPQVSESTCPIPEPLA
ò	708 HAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTE 750	Qy 147 GASPLAEPAAPPSTPAAFKRGGGSUDETLFALPAASEP
qa	1995 HNDVIEKNYFNDNAPTAALLESPIAERARKLVQDAVESASEYKKQAVDSGDEIGRELLDN 2054	Db 1615 QVQERIIPIEVEQAPTIPQRPPRAPKSBLPKVAKP
ර යි	751 VSETVAQHKE	Qy 206 SSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNLS
රු සි	781NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKIKES 830 	Qy 266 ERATNPFVNRDLAEFSELEYSEMGSSFKGSPKG Db 1696 EXPTEDIGALSPLSPNTLAEYEEVPMMDM-QSVPHSP
<i>አ</i> ස	831 BTFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCL 886 .	
è	ELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEM	376
අු	2223 EMFGHQKFETVPRPPTPPKDISDEDVKPSTVNLGPSHHSHPSSPH 2268	DDDDGSEC
රු සි	936 GSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGAS 995 : : 2269 HSILKHHGDAWIDFKTVPPCVLDVIYWRDAKKSAIVLSLA 2308	Qy 419 GRNEDASPPSTPEPVKDSSRAYITCASFTS
රු සි	996 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAIS 1055 	Cy 463DHTSENKTDEKKIEERKAQII Dh 1912 KLQQEDRPSAEGSIDSSGFEKVDHEGLDEFAAPPVHDPM
ò		QY 496 LVANQDSEADYVŢTDŢLSK
g	2369 QEKVHAQADVEVEHATCIANKLKKLVFVESPLESIKFGLVIMSLTYIASWFSGFTLAILG 2428	Db 1972 FVFIERNEANEATLKKNOKMSSHHNDVIEKNYFNDNAPT
È	1116 LISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLK 1159	Qy 534 BACESELNEATGTKIAYETKVDLVQTSEAIQESL

DN:CAB01522.2; GSPDB:GN00023; CESP:W0 2289/1; 2412/1; 2462/2; 2586/2 |||: |: | DEDVISLQSLKSLVAEVGCITDV 1496 ----KLP-EDDEPPARPPPPA 146 KGESALLVENTKEEVIVRSKDKE 319 : | | : | | :-----QEKQEEIEALSEIIE 1746 1; Indels 407; Gaps 52; |:| || || KVIHVPIPLMEPATMYLEEMVEW 1554 EPVIPS-SAEKIMDLMEOPGNTV 205 :|: | : | : KPLDDSKSRVRFAPLNIKLGRTY 1670 :: | :: | :: | :: | :: | :: | :: | : :|| |TREDSFSSISSFGDRQKFRTAIE 1854 | :: : DSPSDLSPNAPPVGFENTAQFLE 1911 :: ; : PMQKSVFGSLGSDDMKPGSQDDG 1971 : |: :: | | |: ESPIAEEARKLVQDAVE 2031 PAPRGPLPAAPPAAP--ERQPSW 108 LSAVSSSEGTIEETLNEASKELP 265 TSATESTT-----ANTFPLLE 462 MSVVAPVREEYADFK---PFEQA 375 LGKDS----E 418 -----TEKTSPKTSNPF 495 ----VTEAAVSNMPEGLTPDLVQ 533 SLYPTAQLCPSFEEAEATPSPVL 588 #text_change 09-Jul-2004 DEDLEELEVI-----2; Length 2607; EKLPFLR 2472 ans

Db 2032 SASEYKKQAVDSGDEIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVH-ETVPNAV- 2089	Qy 2 EDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEDEEDDEDLEELEVL 57 : : : :
QY 589 PDIVMEAPLINSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPYEEAMNVALKAL 648	Db 3196 DEAĎKSKEBŠRRESGAEKSPLASKEASRPASVAESIKDĒAĖKSKĒBSRRĒSVAĒKSPL 3253
Db 2090 DDFVREAE 2106	Cy 58 ERKPAAGLSAAAVPPAAAAPLLDFSSDSVPPAAPRGPLPAAPPAAP102
QY 649 GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEK 703	Db 3254 PSKEASRPTSVAKSVKDEAEKSKEESSRDSVAEKSPLASKEASRPASVAESVQDEAEK 3311
Db 2107EKIETPE2142	CY 103ERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLA-EPAA 156
QY 704 SVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKE 760	Db 3312 SKEESRRESVAEKSPLAYKEASRP-ASVAESIKDEAEKSKEESRRESVAEKSPLASKEAS 3370
Db 2143TDDVAPLSDDKPQFGNQT-PBEDETTFDRKGPLTIPBEVEKAAAAQNN 2189	Qy 157 PPSTPAAPKRRGSGSVDETLFALPAAS-EPVIPSS-AEKIMDLMEQPGNTVSSG 208
Qy 761 ERLSASPQELGKPYLBSFQPNLHSTKDAASNDIPTLTKKEKISLQMEEPNTAI 813	Db 3371 RPTSVAESVKDBAEKSKEESSRDSVAEKSPLASKEASRPASVAESVODEAEKSKEESRRE 3430
Db 2190 DLDPFDPLVTSNTGARGAAVGAAAAVESLTEEEMFGHQKFETVP 2234	Qy 209 QEDFPSVLETAASLPSLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEAS 261
QY 814 YSNDDLLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKS 871	Db 3431 SVAEKSPLASKEASRPASVAESVKDDAEKSKEESRRESVAEKSPLASKEASRPASVAESV 3490
Db 2235 RPPTPPKDISDEDVKPSTVNLGPSHHHSHPSSPHHSILKHHGDAWIDFKT 2284	CY 262 KELPERATNPFVNRDLABFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVRSKDKE 319
Qy 872 BIANIQSGADSLPCLELPCDLSFKNIYPKDEVH 904	Db 3491 KDBAEKSKEESRRESVAEKSPLPSKEASRPTSVAESVKDEAEKSKEESRRE 3541
Db 2285 VPPCAQNAFSPGEIMFLIAFFVYLSCFASFFSKSLPLLDNLLSLVVYLSISLIIH 2339	Qy 320 DLVCSAALHSPQES-PVGKEDRVV-SPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAME 377
OY 905 VSDEPSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEK 950	Db 3542 SVAEKSSLASKEASRPASVAESVKDEAEKSKEESRRESVAEKSPLASKEAS-RPASVAES 3600
Db 2340 VKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNIVLRVGLNYALVVGVAVSAHEAYK 2399	Qy 378 VKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGRNE 422
YWRDIKKTGVVFGASLFLLLSLTVF	Db 3601 VXDEAEKSKEVSRRESVAEKSPLPSKEASRPTSVAESVKDEADKSKEESRRESGAEKSPL 3660
Db 2400 LTKSSGVLRKKEVLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTV 2446	QY 423DASFP-STPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTD- 471
QY 1011 TAYIALALISVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHV 1070	Db 3661 ASMEASRPTSVAESVKDETEKSKEESRRESVTEKS-PLPSKEASRPTSVAESVKDE 3715
Db 2447 VTYSLLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLPQEKVHAQADVFVEHA 2506	Qy 472 -EKKIEERKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEG-526
Qy 1071 NSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSLFVIYERHQ 1130	Db 3716 AEKSKEBSRRESVAEKSPLASKESSRPASVAESIKDBAEGTKQESRRESMPESG 3769
: : WSLTYIASWF	Qy 527LIPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYP 569
Qy 1131 VQIDHYLGLANKSVKDAMAKIQAKIPGLK 1159	Db 3770 KAESIKGDQSSLASKETSRPDSVVESVKDETEKPEGSAIDKSQVASRPESVAVSAKD 3826
Db 2567 EAIDPHLATISGHLKNVQNIIDEKLPFLR 2595	QY 570 TAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKL 629
RESULT 6	Db 3827 EKSPLHSRPESVADKSPDASKEASRSLSVAETASSPIEEGERSIAD 3872
7.13564 microtubule-associated protein homolog - fruit fly (Drosophila melanogaster)	Qy 630 EPENPPPYEBAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPS 689
	Db 3873EVKAESSPR 3911
C.Decession. 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 C.Accession. 713564	Qy 690 PDFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEV 733
R. Spanos Papagiannakis, G.; Siden-Kiamos, I.; Louis, C. suhmitted to the EMRI. Data Library, april 1999	Db 3912 PAVLSKPAEFSQPDTGHTASTPVDEASPVLERIEVVEQHTTSGVGATGATAETDLLDL 3969
Submirced to the philip back billially, April 1999 A.Description: Squencing the distal X chromosome of Drosophila melanogaster. A.Reference number: 317689	OY 734 POTOEEAVMLMKESLTEVSETVAQHKEERLSASPOELGKPYLESFOPNLHSTKDAASNDI 793
A.Status: preliminary: translated from GR/EWRI/DDRJ	Db 3970 TETKSETVTKQSETTLFETLTSKVESKVEVLESSV-KQVEEKVQTSVKQAETTVTDSL 4026
,	
A;Cross-reterences: UNLPROT:U/6891; EMBL:ALU31128; PlDN:CAA2U0U6.1 C;Genetics:	4027 EQLIKKSSEQLIEIKSVLDINISNVINLFSIAVEIIEKKVQDVIEKTIEKAI
A;Cross-references: FlyBase:FBgn0025392 A;ntrons: 24(2; S2/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1	Qy 839 IBIIDEFPTEVSAKDDSPKLAKEYTDLEVSDKSBIANIQSGADSLPCLELPCDLSFKNIY 898 Dh
Ajwore: Ed:4924.1 C;Superfamily: Drosophila 576K microtubule-associated protein homolog	10/9 - ENVOENVIILGESSIEISQESSSELDIGIFSSELNEIHIITVGSFERIVILG
Query Match 5.6%; Score 328.5; DB 2; Length 5327; Best Local Similarity 22.7%; Pred. No. 5.5e-05;	
255; Conservat	942 KSLTKEAEKKLPSDTEKE-DRSLSAVLSAELS 972

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hypothetical protein W06A7.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26213
R;Ainscough, R.
B;Ainscough, R.
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    | :: | :: | :: | :: | :: | 1.79 PAKKPEAPPRKYPEVPTKVPEVPKAAVPEKKVPEAIPP 7237
                                                                                                                                                                                                        | :||:||| :|| 31296 VPEAPKEVVPEKKVPEVPKVAVPEKKVPEAIPPKPESPPPEVFEE 7355
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; Pred. No. 1.5e-06;
47; Mismatches 78
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Best Local Similarity 32.1%
Matches 59; Conservative
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A;Introns: 27/1; 77/2; 201/2
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 138346
R;Labeit, S.; Kolmerer, B.
Science 270, 23-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID: 96026330; PMID: 7569978
A;Recession: 138346
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-7962 RRES
A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101
C;Genetics:
A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2931-2931
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EMBL:Z49130; PIDN:CAA88964.1; GSPDB:GN00020; CESP:T0
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                                                                                                      565 VPAVEAAESTSSPIPETSLPPPNEAVA---SPEVAVAPITAPEPIPEP-EPSLATPTEPI 620
                                                                                                                                                                                                                                                                             SAKDDSPKLAKEYTDLEV-SDKSEIANIQSGAD----SLPCLELPCDLSFKNIYPKDEVH 904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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PIDVSVLSEAAIETPVAPPVEVTTEVAVADVAPPEAAEDLIIEPVEPPAPIPDLLEQTTS
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                                                    I PEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAA
                                                                                                                                                              SNDIPTLTKKEKISLOMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIEIIDEFPTFV
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Pred. No. 0.00014;
7; Mismatches 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T06D8.1 - Caenorhabditis elegans
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Best Local Similarity 21.1%; Pro
Matches 233; Conservative 157;
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A;Experimental source: clone T06D8
C;Genetics:
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VISEAPAAEVPITA 771
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                                                                                                                                                                                                             Cyperters 21-56p-1993 #s metanogater; Cyperters Droppinia metanogaters; Cyperters 21-56p-1993 #s metanogaters; Cyperters Droppinia metanogaters; Cyperters; Droppinia metanogaters; CyAccession: A47283 #salinnger, D.G.; Xue, N.; Harshman, K.D. Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993 A;Title: A Drosophila photoreceptor cell-specific protein, calphotin, binds calcium and A;Title: A Drosophila photoreceptor cells A;MulD:93165730; PMID:8434015 A;Contents: photoreceptor cells A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;Accession: A47283 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 VP-APAPIAAASVAPVASVAPVVAAPTPPAASPVSTPPVAAVAQIPVAVSAPVAPPVAAT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STPAAPKRRGSGSVDETLFALP--AASEP----VIPSSAEKIMDLMEQPGNT---VSSGQ 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIPVAPI-----PVAAPVIATPPVAASAPTPAAVTPVVSPVIATPPVVPANTTVPVAAPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 EDFPSVLLETAASL-PSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INPFVNRDLAEFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALH 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---AAEPVVVAPPATETPVVAPAAA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPQESPVGKEDRVVSPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDV 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: : | | : : | | : : | | 185 AAVPAAVAPVVAETPAPPPVAEIPVA--TIPECVAPLIPEVSVVA
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                       210
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ò	351 FNEMOMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQ 410	Nuery Best 1
qq	604 -EPPASSTSIPTELSKDDQVTEASGEETTTAAATEASEETTTSAVTEGSGEE 655	масси
ò	411 KSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKT 470	È i
qq	656 TTVVAVVESSGEBPASSSTSIPTELSKDDKVTEASGEETTTAAATDASSEETTTSAV 712	음 (
ò	471 DEKKIEERKAQIITEKTSPK-TSNPFLVAVODSEADYYTTDTLSKYTEAAVSNMPEGLTP 529	è 1
qq	713 TEGSGEETTVVAVVESSDEEPASSSTSIPTELSKDDQVTEASGEETTTAAATEASEETTT 772	9 8
ò	530 DLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSF 577	हे है
qq	773 SAVTEGSGEETTVVAVVESSGEEPASSSTSIPTELSKO-DQVTEASGEETTTAAATE 828	g (
ò	578 EEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPY 637	हे ह
qq	829 ASERTITSAVIEGSGEDTIVVAVVESSGEQPASSSTSIPTELS 871	g (
ò	638 EEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSE 697	ट्रे 1
q	872KDDQVTEASGEETTTAAATEASEETTTSAVTEGSGEETTV 911	a •
ò	698 IAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSET 754	Š 1
qq	.1 1 1 1 1 1 1 1 1 1	8 8
ò	755 VAQHKEBRLSASPQELGKPYLESFQPNLHSTKDAASN 791	Š
q	967 BGSGEETTTSAVTEGSGEETTTSAVPEGENSTTEAPAFVTGSEIEIPSSEESSSTTTHDP 1026	g ;
È	792 DIPTLIKKEKISLOMBEFNTALYSNDDLLSSKEDKIKESET-FSDSSPIELIDEPPTFVS 850	हे <i>च</i>
Db 10	1027 SIPVITPKPSVSSTIENVMSKTSSEEAAEKKIIGEHQTGKDDAGKEDEDNMPAFVT 1083	<u> </u>
ò	851 AKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCD 891	डे <i>व</i>
Db 1	1084 ANPAGISTIESAENVISIGEEDENIKMAKELGKQFAADLAKLA1126	8 8
ò	892 LSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKK 951	ठे ह
DP 11	1127AKDGVNLT-ETADAKDSGETAHVEDEQVSSTESSIGSEETTTTVNKETTEE 1176	er (
ò	952 LPSDTEKEDRSLSAVLSAELSKTS 975	ò
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calcium-binding protein calphotin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47282
R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993
A;Title: Calphotin: a Drosophila photoreceptor cell calcium-binding protein.
A;Reference number: A47282
A;Accession: A47282
A;Accession: A47282
A;Accession: A47282
A;Accession: A7282
A;Accession: A7282
A;Cross-references: UNIPROT:Q02910; GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157033'
A;Cross-references: UNIPROT:Q02910; GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157033'
A;Cross-references: Chorceceptor cells
A;Moche: sequence extracted from NCBI backbone (NCBIN:124955, NCBIP:124956)
C;Genetics:
A;Genetics:
A;Genetics:
A;Cross-references: PlyBase:PBgn0010218
C;Superfamily: collagen alpha I(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: calcium binding

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41; 390 446 619 791 62 AAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPER----OPSWERSPAAPAP 117 161 10 IAAASVTFVASVAPPVVAAPTPPAASPVSTPVAVAQIPVAVSAPVAPPVAATPTPVVQIP 129 130 VAAP-----VIATPPVAASAPTPAAVTPVISPVIASPPVVPANTTVPVAAPVAA 178 330 263 506 381 266 414 731 558 614 792 DIPTLTKKEKISLOMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIBIIDEFPTFVSA 851 651 KDDSPKLAKEYTDLEV-SDKSEIANIQSGAD----SLPCLEL-----PCDLSFKNIYP- 899 900 -KDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMG---------936 VPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVPITAGDN 766 69 ----SIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGV 990 ----SLPPAAAVLPSKLPEDDEPPARPPPPAGA-----SPLAEPAAPPSTP----| : | | | : | | | : | | EVASVAVAETTPPVVPPVAAES-----IPAPVVATTPVPATTAVTAVTDPD---EVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASN | : : : | | : | : | : | AVEAAESTSSPIPETSLPPPNEAVA---SPEVAVAPITAPEPIPEP - EPSLATPTEPIPV EAPV-----VIQEAVDAVETSTSIPETTVEFPEAVAE -AAPKRRGSGSVDETLFALP--AASEP----VIPSSAEKIMDLMEQPGNT---VSSGQED 212 FPSVLLETAASL-PSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATN 271 PFVNRDLAEFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSP 331 QESPVGKEDRVVSPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLA 264. HVS------VAP-----AVETAVVAPV--------VAP-----391 ARANVESKVDRKCLEDSLEQKSL----GKDSEGRNEDASFPSTPEPVKDSSRAYITCASF 280 -SASTEPPVAAATLTTAPETPALAPVVAESOVAANTVVATPPTPAPEPETIAPPVVAETP 447 TSATESTTANTFPLLEDHTSENKTDEKKIEERKAQIITEKTSPKTSNPFLVAVQDSEADY 507 VITDILSKVIBAAVSNMPEGLIPDLVQBACESBLNBAIGTKIAYEIKVDLVQISBAIQBS LYP-TAQLCPSF--ERAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAP----PPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACD-----LIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE--LVEDSSPESEPVDLFSD-DSIP 23.7 PLA-----AAEPVVAPPATETPVVAPAAASP -----VTASAVPELPPVIAPSPVPSA------VAETPVDLA-----PPV DVSVLSEAAIETPVAPPVEVTTEVAVADVAPPEAAADLIIEPVEPPAPIPDLLEQTTSVP 295; Length 865; Indels / Match 5.1%; Score 295.5; DB 2; Local Similarity 21.3%; Pred. No. 9.5e-05; nes 217; Conservative 127; Mismatches 379; 118 162 382 267 415 620 472 678 499 732 559 615 852 652 937

Db 2675	RESULT 13 A56577 Microtubule-associated protein MAP 1B - rat (fragment) C; Species: Rattus norregicus (Norway rat) C; Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004 C; Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004 C; Accession: A56577 R; Acuser M.; Kratz J.; Staunton, J.; Feick, P.; Wiche, G. A; Recession: A56577 A; Recession: A5677 A; R
RESULT 12 Hypotherical protein ZK783.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Ott-1999 #text_change 09-Jul-2004 C;Caccesion: T34513 R;Favello, A.; Vaudin, M. Submitted to the EMBL Data Library, August 1994 A;Roberitted to the EMB	0y 69 AVPPAAAPLIDESSDSVPPARGELBAAPPAAPEROPGNERSPAAPAPEL 119 2103 STTGGSVTGTTPFTSTSTTPFTSTTPFTYTSETRFELSASTTGDTNSTTPST 2162 120 PPAAAVLPSKLPEDDEPRARPPPPAGASP_LABPAAPSTTPAPKRAGGGS 172 2163 SSLASVKGTSAPEGTSASVAPWISSLEPPOSGOSTKTPDATESSTTGDTNSTTPST 2220. 120 PPAAAVLPSKLPEDDEPRARPPPPAGASP_LABPAAPSTTPAPKRAGGGS 172 2163 SSLASVKGTSAPEGTSASVAPWISSLEPPOSGOSTKTPDATESSTTVGAPETSGTGS 2220. 120 DET

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C;Genetics:
A;Gene: CESP:C25A1.10
A;Map position: 1
A;Introns: 38/3; 92/3; 201/3; 919/3
C;Superfamily: nucleolus-cytoplasm shuttle phosphoprotein
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T19431

hypothetical protein C25A1.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
B;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
B;Date: 119431
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B;Cacesion: 119431
B;Cacesion: 119431
B;Cacesion: 119431
B;Cacesion: 11971 cMIL>
A;Molecule type: DNA
B;Cacesion: 1971 cMIL>
A;Cacesion: 1971 cMIL>

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                                                                                                                                                                                                                                                         207 NVLQKVVAKKAASSSSDSSDDEKKPAAK-PTPAKPTPKPVVKKAESSSDSSDDEKKPVAK 265
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                                                                                                     SSLVSSSTDSPPRPPAFKYQFVTEP----EDEBDEEEEBDDEBDLEELEVLERKPAA
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                                                     Gaps
                                                  Indels 247;
  Length 971;
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Query Match
4.9%; Score 288.5; DB 2;
Best Local Similarity 20.6%; Pred. No. 0.00021;
Matches 198; Conservative 127; Mismatches 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
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	Db 1367 NERASLSPMDEPVPDSESPVEKVLSPLRSPPLLGSESPYEDFLSADSKVLGRRSESPF 1424
920 SIS -	Qy 418 EGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKT 470
Db 907 SVS 909	Db 1425 EGKNGKQGFPDRESPVSDLTSTGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETWS 1480
	Qy 471DEKKI
ated protein MAP1(X)	506 YVTDTLSKVTBAAV-SNMPEGLIPDLVQEACESELNBATGTKIAYETKVDLVQTSBAI
ייים בער_ניים מייים	Db 1539 YSHMEGVASVSTASVATSSFPEPTTDD-VSPSIHAEVGSPHSTEVDDSLSVSVVQTPTTF 1597
J. Cell Biol. 109, 3367-3376, 1989 A, Title: The microtubule binding domain of microtubule-associated protein MAPIB contains A. Reference number: A33645: MUID: 90094539: PMID: 2480963	Qy 564 QES-LYPTAQLCPSFEEREATPSPVLPDIVMEAPLNSLL 601 : : : :
	602PSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPYEEAMNVA
A;Residues: 1-2464 <nob> A;Cross-references: UNIPROT:P14873; EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g5300d D:cancher : Dadill D : Dadinod D : Tabala I C : Arila I</nob>	Db 1658 FSRQSPDHPTLGASVLHITENGPTEVDYSPCDIQDSSLSHKIPPTEEPSYTQDNDLS 1714
lin.	Oy 645 LKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKS 704
A/Accession: 544387 A/Accession: 544387 A/Status: preliminary	1/15 EDITSVERVENSFOLDSANIES
A;Molecule type: protein A;Residues: 653-663,′IC′ <san></san>	
C;Superfamily: microtubule-associated protein MAP1B C;Keywords: microtubule binding; phosphoprotein; tandem repeat F;Se9-786/Domain: microtubule binding #status experimental AMTB>	QY 761 ERLSASPQELGKPYLESFOPNILHSTKDAASNDIPTLTKKEKISLQMEEFN 810 : : : : : : : : : :
160,060-160,060-600,200-610,	1011 - QASSSELLDAAIABELIGEASSSEELDIAGEELDIAGEELSSEELDIAGEELSSEELSSEELSSEELSSEELSSEELSSEELSSEEL
F;1861-2064/Region: 17-residue repeats F;91,116,535,1888,1124,1153,31168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: ph F;147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (cc F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted	811 TAIYSNDDLLSGKEDKIKESETFSDSSPIBIIDEFFTFVSAKDDSPKLAKEYTDLE
Query Match Best Local Similarity 20.7%; Pred. No. 0.0012; Matches 233; Conservative 159; Mismatches 424; Indels 312; Gaps 51;	867 VSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVHVSDBFSENRRS
OY 31 EPEDEEDEEEEDEEEDDEDLEELEVLERKPAAGLSAAAVP 71	OY 921ISPSNYSALEPOTEMGS VVSKSLTKEAREKLPSDTEKENKS 962
QY 72 PAAAAPLLDFSSDSVPPAPRGPLPAAPPRAPERQPSWERSPAAPA 116	Search completed: June 16, 2005, 13:31:49 Job time : 42.9713 secs
QY 117 PSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPA 155	
QY 201 PGNTVSSGQEDFPSVLLETAA\$LPSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEA 260 Db 1242 SDERLSPAKSPSLSPPAKSPSLSP	
QY 261 SKELPERATNPFVNRDLABFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVR 314 Db 1266PLGERSVNFSLTPNEIKVSAEGEARSVSPGVTQAVVEEHCASPEEKTLE 1314	
QY 315 SKDKEDLVCSAALHSP-QBSPVGKEDRVVSPEKTMDIFNEMQMSVVA-PVREEYADFK 370 Db 1315 VVSPSQSVTGSAGHTPYYQSPTDEKSSHLPTEVSENAQAVPVSFEFSEAKDE 1366	
QY 371PPEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDS 417 :: : : :	

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein

; Search time 157.778 Seconds June 16, 2005, 12:33:51 Run on:

(without alignments)
3774.604 Million cell updates/sec

US-09-830-972-2

Title:

5848 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRKAD 1163 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 08 08 Minimum 1 Maximum 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot_sprot:* 2: uniprot_trembl:* UniProt 03:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMERTES	
Result		Query				
No.	Score	Match	Length	BB	Ď	Description
-	5848	100.0	1163	н	AT	Q9jk11 rattus norv
7	5312.5	90.8	1162	~		Q8bgm9 mus musculu
٣	5307	90.7	1163	~	Q8K3G8	Q8k3g8 mus musculu
4	4501.5	77.0	1046	•	Q8BGK7 Q	Q8bgk7 mus musculu
ß	4403.5	75.3	1192	-	UMAN	Ogngc3 homo sapien
φ	3627.5	62.0	986	•		homo
7	3299.5	56.4	720			mus m
σ,	2926	50.0	639	•		Q8k290 mus musculu
σ	2610	44.6	578			
10	1664	28.5	658			gallus g
11	1620	27.7	1043	~		
12	1616	27.6	1055	7		
13	1596.5	27.3	1032	7		6jrv7 xenopus lae
14	1586.5	27.1	1044	~		
15	1554.5	26.6	1024	7		
16	1539	26.3	1013	N		Q6jrv9 xenopus lae
17	1416	24.2	375	~		MUS
18	1314.5	22.5	356	~	Q8BH78 Q	mus
19	1304	22.3	357	~	Q8K3G7 Q	mus m
20	1283.5	21.9	392	~		homo
	1060	18.1	343	~	07	homo
22	917	15.7	199	-	OUSE	พนธา
23	908	15.5	199	7		Q7yrw9 bos taurus
	904	15.5	199	~		0
25	899	15.4	199	7		Q7pcj7 macaca fasc
26	896	15.3	187	N	Q6IG15 Q	'n
27	876	15.0	199	~		gall
	850	14.5	250	0		sns sci
29	844	14.4	179	7		
30	807.5	13.8	315	~	Q6IFY4 Q	
31	806	13.8	1013	~	,	06t930 homo sapien

similarity).
SUBCELUILAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).

ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=4;
Name=1; Synonyms=Nogo-A, NI-220-250;

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O61929 mus musculu (64548 rattus norv (65jrv4 xenopus lae (65jrv4 xenopus lae (65jrv4 xenopus lae (66jrv4 xenopus lae (67799 homo sapien (8799 homo sapien (8709 homo sapien (8709 kms musculu (65jrv2 xenopus lae (65jrv1 xenopus	
Q6T929 Q6JRV1 Q6JRV3 Q6JRV3 Q6JRV4 Q6RLX6 Q6RLX6 Q8KG14 RTN1 HUMAN Q6JRW2 Q6JRW2 Q6JRW1 Q6GJRW1 Q6GJRW1	
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13.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7	
803 801 797.5 796.5 792.5 792.5 792.7 777 770.5	
αααααααααααααααααααααααααααααααααα	

ALIGNMENTS

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[1] SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE. SEGUENCE. STRAIN=Spraque-Dawley, TISSUE=Adipocyte, MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6; MEDLINE=99249816; PubMed=1031557; DOI=10.1016/S0167-4889(99)00033-6; Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.; "Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family."; Biochim. Biophys. Acta 1450:68-76(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a; GrandPre T., Li S., Strittmatter S.M.; GrandPre T., Li S., Strittmatter S.M.; "Nogo-66 receptor antegonist peptide promotes axonal regeneration."; Nature 417:547-551(2002).

Nature 417:547-551(2002).

PUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
Ito T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in rat: one of two minor splice variants.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219; MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219; Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L., Spilmann A.A., Christ F., Schwab M.E.; Rank M.E., Schnell an "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an antigen for monoclonal antibody IN-1.";
                                                          Q9JKI1, Q9JK10, Q9ROD9, Q9WUB9, Q9WUF0.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2004 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity). SubUNIT: Binds to RIN4R. Interacts with Bcl-xl and Bcl-2
                                  PRT; 1163 AA
                                                                                                                                                                                                                              (Glut4 vesicle 20 kDa protein).
Name=Rtn4; Synonyms=Nogo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 403:434-439(2000).
                                  STANDARD;
                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [4]
FUNCTION.
RTN4_RAT
ID _RTN4_RAT
                                                                    DDTTTTDDDTTTDDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDT
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                   PAAAVLPSKLPBDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRKGSGSVDETLFALP
                                                                                                        GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES
                                                                                                                                                                                                                                              AILVENTKEEVIVESKOKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDI FNEMQMSVVA
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                                                                                                                                                                GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES
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               Name=2; Synonyms=Nogo-B, Foocen-M; Indee=2; Synonyms=Nogo-B, Foocen-M; Isode=Q9TX11-2; Sequence=VSP 005658; Name=3; Synonyms=Nogo-C, VP20; Name=4; Synonyms=Foocen-M2; Isode=Q9TX11-3; Sequence=VSP 005656; VSP 005657; Name=4; Synonyms=Foocen-M2; Isode=Q9TX11-4; Sequence=VSP 005659; Isode=Q9TX11-4; Sequence=VSP 005659; Isode=Q9TX11-4; Sequence=VSP 005659; Isode=Q9TX11-4; Sequence=VSP 005659; Isode=Q9TX11-4; Sequence=VSP 005659; Isode=Q9TX11-4; Sequence=VSP 005659; Isode=Q9TX11-4; Sequence=VSP 005659; Isode=Q9TX11-4; Isode=Q9TX11-4; Isode=Q9TX11-4; Isode=Q9TX11-4; Isode=Q9TX1-4; Isode=Q9T
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/FIId=VSP 005658.
Missing (in isoform 4).
/FIId=VSP 005659.
Missing (in Ref. 3; AAD31020).
MW; 8CB894B09E94F0B6 CRC64;
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EMBL, AJ242961; CAB71027.1; -.
EMBL, AJ242962; CAB71028.1; -.
EMBL, AJ242963; CAB71029.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Murinae; Mus
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A van der Putten H., Mir A.;

A van der Putten H., Mir A.;

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; AY102284; AAM73506.1; -.

R EMBL; AY102286; AAM73510.1; -.

R MGD; MGI:1915835; Rtn4.

GG; GG:0005783; C:endoplasmic reticulum; IDA.

GG; GG:0005155; P:protein binding; IPI.

GG; GG:0007395; P:neurogenesis; IMP.

GG; GG:0007395; P:neurogenesis; IDA.

InterPro; IPR003388; Reticulon.

Pfam; PR03453; Reticulon; I.

R PROSITE; PS50845; RETICULON; 1.

SEQUENCE 1162 AA; 126612 MM; 855697FBEBI1781F CRC64;
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STRAIN=129/SvcJ7;
Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                           Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                         Last sequence update)
Last annotation update)
                                                     Ź
                                                     1162
                                                                                                  Created)
                                                                                                                                                               RTN4.

Name=Rtn4;
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
(VEL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
                                                                                             (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 27,
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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QBBGM9;
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DDR REP DR us-09-830-972-2.rup

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SEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSFLSTVSFKEHGYLGN
1ALALLSVT1SFR1YKGV1QA1QKSDEGHPFRAYLESEVA1SEELVQKYSNSALGHVNST
                                                                                                          1014 IALALISVTISPRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNST
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                                      DTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAY
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STRAIN=129/SvcJ7,
MEDLINE=223/SvcJ7, Pubmed=12488097, DOI=10.1016/S0022-2836(02)01179-8;
MEDLINE=22376540; Pubmed=12488097, DOI=10.1016/S0022-2836(02)01179-8;
MEDLINE=22376540; Pubmed der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters o
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Sciurognathi, Muridae, Murinae, Mus
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Last annotation update)
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Pred. No. 5.4e-156;
0; Mismatches 68;
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                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Submitted (MAY-2002) to the
EMBL; AY102280; AAM73502.1;
EMBL; AX102286; AAM73507.1;
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hes 910; Conservative
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Van der Putten H.;
Submitted (MAY-2002)
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Van der Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                           Q8BGK7;
01-MAR-2003
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05-JUL-2004
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                                                                                                                                   Gaps
                                                                                                                                  14;
                                                                                                       Length 1163;
                                                                                                                                  Indels
                                                                              CRC64;
                                                                              6B5F362799417EA4
                                                                                                       Query Match 90.7%; Score 5307; DB 2; Best Local Similarity 91.1%; Pred. No. 2.9e-185; Matches 1066; Conservative 34; Mismatches 56;
                           reticulum; IEA
           MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic re
InterPro; IPR003188; Reticulon.
Pfam; PP02453; Reticulon; 1.
PROSITE; PS5045; RETICULON; 1.
SEQUENCE 1163 AA; 126690 MW;
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SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND MEDLINE=20237542; PubMed=10773680; Yang J., Yu L., Bi A.D., Zhao S.-Y.; "Assignment of the human reticulon 4 g
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TISSUE=Fibroblast;
                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                        Oncogene 19:5736-5746(2000).
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                        LSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGESAI
                                    ESRNENASFPRTPELVKDGSRAYITCDSFSSATESTAANIFPVLEDHTSENKTDEKKIEE
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                                                                         LVENTKEEVIVRSKDKEDLVCSAALHSPQESP----VGKEDRVVSPEKTMDIFNEMQMS
                                                                                                                           VVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDS
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                                                                                                                                                                                                                              RKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACE
                                                                                                                                                                                                                                                                              SELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPL
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Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;
Q9Y5U6;
28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUB=BRAIL;
MEDLINE=21010696; PubMed=11126360; DOI=10.1038/8j.onc.1203948;
Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
"A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity.";
                                                                                                                                                                                                                                           Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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H.N., Yu Y.,
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Pituitary;
Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu
Luo B., Hu R., Chen J.;
"Human neuroendocrine-specific protein C (NSP) homolog gen
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Gmichalovich D., Simmons D.L., Walsh F.S.;
"Inhibitor of neurite outgrowth in humans.";
Nature 403:383-384(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).

TISSUE=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in hum submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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GU J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Sqin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li Yu J., Han L.H.,

"Novel human cDNA clones with function of inhibiting of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2p14-->2p13 by radiation hybrid mapping.";
Cytogenet. Cell Genet. 88:101-102(2000).
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                      Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
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CTISSUE=Brain, Ovary, Pancreas, Placetta, and Skeletal muscle;

XX Taxusberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.;

XR Stausberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.;

XR Lausner R.D.; Collins F.S.; Wanger L.G.; Shenmen C.M.; Schuler G.D.;

XR Lausner R.D.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

XR Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

XR Diatchenko L.; Marusina K., Farmer A.A.; Rubin G.M.; Hong L.;

XR Diatchenko L.; Marusina K., Farmer A.A.; Rubin G.M.; Hong L.;

XR Stapleton M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

XR Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

XR Schards S., Worley K.C.; Hale S.; Garcia A.M.; Gabs R.A.;

XR Nilalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

XR Hallan D.K.; Muzny D.M.; Machan A.; Rodrigues S.; Sanchez A.;

XR Hiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

XR Butterfield Y.S.N.; Krzywinski M.I.; Skalska W.; Smailus D.E.;

XR Schnerch A.; Schmutz J.; Marra M.A.; Schnitz M.A.;

XR Schnerch A.; Schmutz J.; Marra M.A.;

XR Schnerch A.; Schmutz J.; Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 3).

YISSUE-Umbilical cord blood;

MEDLINE-20499367; PubMed=11042152; DOI=10.1101/gr.140200;

Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,

Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,

Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen Z., Zhong M., Zhou J., Hu G.-X., Gu J., Chen Z.,

"Cloning and functional analysis of CDNAs with open reading frames for moteviously undefined genes expressed in CD34+ hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Generation and initial analysis of more than 15,000 full-length human
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-!- FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults.
Isoform 2 reduces nati-apoptotic activity of Bol-xl and Bol-2.
This is likely consecutive to their change in subcellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
Fournier A.E., Grandpre T., Strittmatter S.M.;
"Identification of a receptor mediating Nogo-66 inhibition of axonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134; Ng C.E.L., Tang B.L.; "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226; GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.; "Identification of the Nogo inhibitor of axon regeneration as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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Sha J.H., Zhou Z.M., Li J.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4)
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                                                                      JENCE FROM N.A. (ISOFORMS 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 10:1546-1560(2000).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
                                                                                                                                                                                                                                        IsoId=Q9NQC3-4; Sequence=VSP_005654; ISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain and testis and weakly in heart and seletal muscle. Isoform 2 is widely expressed excepted for the liver. Isoform 3 is expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEDEEEDDEDLEELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 APSLPPAAAVLPSKLPEDDEPPARPPPPPAGASPLAE-----PAAPPSTPAAPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RG-SGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS
                after binding and sequestration.
SUBUNT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum. Anchored to the membrane of the endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
the mitochondria to the endoplasmic reticulum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 4403.5; DB 1; Length 1192;
                                                                                                                                                                                                                                                                                                        brain, skeletal muscle and adipocytes. Isoform 4 is testis-
                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 reticulon domain. CAUTION: Ref.11 sequence differs from that shown due to frameshifts in positions 1149 and 1156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                             through 2 putative transmembrane domains.

ALTERNATIVE PRODUCTS:

Sevent-Alternative splicing; Named isoforms=4;

Name=1; Synonyms=RTN 4A, Nogo-A, RTN-KL;

IsoId=Q9NQC3-1; Sequence=Displayed;

Name=2; Synonyms=RTN 4B, Nogo-B, RTN-KS, Foocen-M;

IsoId=Q9NQC3-2; Sequence=VSP_005655;

Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;

IsoId=Q9NQC3-3; Sequence=VSP_005655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4e-152;
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BAA74909.2; ALT_INIT.
AAH01035.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AJ251383; CAB99248.1; -. EMBL, AJ251384; CAB99249.1; -. EMBL, AJ251385; CAB99250.1; -.
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75.9%;
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BAB18928.1;
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Best Local Similarity
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MDLKEQPGNTISAGGEDFPSVLLETAASLPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNLSAVSSSEGTIE
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                                                                                                                                                     TISSUE=Testis;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                     Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1202=1202=1203=1204 | N. E.; | Carbab M. E.; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | AMM6428-11; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | Schwab M. E.; | S
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                   man and mouse nogo/rtn4.";
Mol. Biol. 325:299-323(2003)
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Best Local Similarity 75.4%;
Matches 745; Conservative 9
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Van der Putten H.;
Submitted (MAY-2002)
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                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                  EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL
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            LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY
                                                         SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG----KED
                                                                                 ESKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT
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91UA4; PRELIMINARY; PRT; 986 AA.
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
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Name=RTN4;
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SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain;

X STRAIN=C57BL/6; TISSUE=Brain;

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.B., I. Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mitching M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mitching M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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Sciurognathi; Muridae; Murinae; Mus
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Last annotation update)
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Mammalia; Eutheria; Rodentia;
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01-0CT-2003 (TrEMBLrel. 25,
01-0CT-2003 (TrEMBLrel. 25,
Hypothetical protein.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                         AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL
                                                                                                                                                                                                                                                                                                                                                                                                                          AASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSEMGSSFNGSPKGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EERKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEA
                                                                                                                                                                                 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEBEEBEEBDEEDDEDLEELEVLERK
                                                                                                                                                                                                                                                                                                                         PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKI
                                                                                                                                                 Gaps
                                                                                                                                                6
                                                                                                                 DB 2; Length 720;
                                                                                                                                                   Indels
                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                              56.4%; Score 3299.5; DB 2; 90.3%; Pred. No. 1.9e-112; iive 22; Mismatches 39;
                                                                              80AB78728F16EAB2
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                                                                Hypothetical protein.
SEQUENCE 720 AA; 77435 MW;
STRAIN=C57BL/6; TISSUE=Brain;
              Strausberg R.;
Submitted (AUG-2003) to the
EMBL; BC056373; AAH56373.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22,
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26,
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01-0CT-2002 (TrEMBLrel. 2:
01-MAR-2004 (TrEMBLrel. 2:
Rtn4 protein.
Name-Rtn4;
                                                                                                                                 Best Local Similarity 90.3
Matches 654; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Name=Nogo-A;
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                                                                    SEQUENCE FROM N.A.

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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;

MEDLINE=2318257; PubMed=12479312. DOI=10.1073/pnas.242603899;

MEDLINE=2318257; PubMed=12477932. DOI=10.1073/pnas.242603899;

MA Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zebeberg B., Buetow K.H., Schnefer C.F., Bhark N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsitch F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carrinci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakin P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 TPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMN 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 MPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309A19DA37603F11 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
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              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
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Best Local Similarity 91.6
Matches 588; Conservative
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LTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQK 1061
                                                                                                                                                              1062 YSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFS 1121
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                 477
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538 YSNSALGHVNSTIKELRRLFLVDDLVDSLKPAVLMWVFTYVGALFNGLTLLILALISLFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PSPVLPDIVWEAPLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPYXEEAMSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         584 PSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEDKIKESETFSDSSPIELIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB073672; BAC75974.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER 1 1 SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;
                                                                                                                                                                                                                                                                                       598 IPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 90.73
Matches 527; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nogo-A (Fragment).
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Tozaki H., Hirata
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649

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-VSMVSLPATGTSPSSTEKEIVSVGKPEAFEKEAERGAASAKEKE--KPTAVFSAKLNVS
                                                                                                                              470 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                                                                                                       LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK
                                                                                                                                                                                                                                                                                                                                                                               98 PPAAPERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 PSTPAAPKRRGSGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLL
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                                                                                                                                                                                                                      IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRLFLVDDLVDSLKFAV
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                                                                                              SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
Rlinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr & Ringer M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr & Cartausch B., Oertle T., Schwab M.E., Stuermer C.A.;
"Identification of two NOGO/RIN4 genes and analysis of Nogo-A expression in Xenopus laevis.";
Mol. Cell. Neurosci. 25:205-216(2004).
BMBL; AY316197; AAQ82646.1; -
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IRR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PSS0845; RETICULN; 1.
SEQUENCE 1043.AA; 113994 MW; 6AF170C14DDZCB1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea; Pipidae; Xenopodinae; Xenopus.
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Best Local Similarity
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                                   TVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKY
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caltharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
Babli, Ay44005, AAS18427-11.
GO; GO:0005783, C:endoplasmic reticulum; IEA.
InterPro, IPR003388; Reticulon.
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                                                                                                                                                                                                                                                                                    PVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
                                                                                                                                                                                                                                                                                                                           72075 MW; 14B7A000C5E8CDA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Neurite outgrowth inhibitor NOGO-A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.5%; Score 1664; DB 2; 56.7%; Pred. No. 6e-53; iive 82; Mismatches 168;
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PROSITE; PS50845; RETICULON; 1.
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Matches 379, Conservative
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                          TISSUE-Wholemount embryos;
PubMed-1501938; DOI=10.1016/j.mcn.2003.09.021;
Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Han Petrausch B., Oertle T., Schwab M.E., Stuermer C.A.;
"Identification of two NOGO/RTM4 genes and analysis of Nogo-A expression in Xenopus laevis.";
Mol. Cell. Neurosci. 25:205-216(2004).
EMBL, AY316195, AA082645.1; -.
GO: GO:0005783; C:endoplasmic reticulum; IEA.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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(TrEMBLrel. 27, Last sequence update)
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TISSUE-Wholemount embryos,
PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
Ringer M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr Petrausch B., Oertle T., Schwab M.E., Stuermer C.A.;
Identification of two NGGO/RTN4 genes and analysis of Nogo-A Margession in Xenopus laevis.";
Mol. Cell. Neurosci. 25.205-216(2004).
EMBL; AV316189; AAQ82638.1;
GO; GO:0005783; C:endoplasmic reticulum; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.1%; Score 1586.5; DB 2; Length 1044; Best Local Similarity 37.4%; Pred. No. 7.3e-50; Matches 465; Conservative 171; Mismatches 320; Indels 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1044 AA; 115088 MW; 34FB48351A6C9888 CRC64;
                                                                                                                                                                          PVIYERHOVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
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PVIYERHQTQVDHYLALINKNLKNTSDLILAKVPGLKRKSE 1032
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Last annotation update)
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Pfam; PF03453; Reticulon; I.
PROSITE; PS50845; RETICULON; I.
SEQUENCE 1044 AA; 115088 MW
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Name=RTN4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 AEFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSP--QESPV 335
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                                                                                                                                                                                                                                                                                                                              EDEBEDDEDLEELEVLERKPAAGLSAAAVPPAAAAPLLDFSSDSVPPAP----RGPLPAA 97
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EQSPDISSSHSGDERREPAQPGERKPWDDLDDVLDLTGGAGQFSQPFSGSHPARDIEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SVSRITSHLPLSDNLESKAL-DQVKEEVIFSEK-----GYVVDHPTSQQETI
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----AVVEETETPYISIACDLIKGTESVASGFTEFSKLKQ-NEFESQFMEPS---DESS
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SEQUENCE FROM N.A.

TISSUB=Wholemount embryos;
Pubmde=1501938; DOI=10.1016/j.mcn.2003.09.021;
Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr Petrausch B., Oertle T., Schwab M.E., Stuermer C.A.;
"Identification of two NOGO/RIN4 genes and analysis of Nogo-A
                                                                                                                                                                                                              Query Match 26.6%; Score 1554.5; DB 2; Length 1024; Best Local Similarity 36.4%; Pred. No. 1e-48; Matches 454; Conservative 149; Mismatches 332; Indels 311;
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                                                                                                                                                                                     1024 AA; 112016 MW; 79197ACAE7D29C5C CRC64;
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                                                                                 expression in Xenopus lacvis.";
Mol. Cell. Neurosci. 25:205-216(2004).
EMBL; AY316,195; AA082644.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
PERM: PF02453; Reticulon.
PROSITE; PS50845; RETICULON; 1.
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LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  978
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PDSE------CSEPSYKQWDSEVVQKEAFSIKTESVNAQSIIIPEQKQVFDQKSEESSP
                                                                                             ---SKSYLDSFQPEICVSKATSDLFAKGLTTLLQEK--PLQMEELDEGL-SLEKIFCTKY
                                                         QELGKPYLESFQPNL---HSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       919 IVQKYCNVALNHVNCTVKELRHLFLVEDLVDSLKFAVLMMVFTYIGALFNGLTLLIVALI
                                                                                                                                                                            DKIKESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLP
                                                                                                                                                                                                                                                                                      885 CLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIV----
                                                                                                                                                                                                                                                                                                                                                                                                            940 -KSKSLTKEAE-KKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLF
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                Copyright
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- protein search, using sw model OM protein June 16, 2005, 12:55:32 ; Search time 5.68322 Seconds Run on:

(without alignments)
3199.767 Million cell updates/sec

score:

US-09-830-972-2_COPY_975_1163 925 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189 Perfect so Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:* Database :

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	ouery Match Length	DB	ID	Description
-	679	73.4	208	. ~	I60904	neuroendocrine-spe
8	619	73.4	176	~	A46583	neuroendocrine-spe
٣	999	71.9	267	7	A60021	tropomyosin-relate
4	321	34.7	2484	~	T26216	
ហ	321	34.7	2607	N	T26215	hypothetical prote
9	320	34.6	222	7	T26213	
7	194	21.0	255	~	E84899	_
8	182	19.7	271	N	T13013	
6	163	17.6	275	~	T05595	cal
10	142	15.4	393	~	S67763	ъ
11	135.5	14.6	242	~	B85016	hypothetical prote
12	134	14.5	183	7	A84527	hypothetical prote
13	131.5	14.2	295	N	S59439	probable membrane
14	123	13.3	206	7	T01153	probable seed matu
15	109.5	11.8	264	~	T47948	hypothetical prote
16	107.5	11.6	203	~	T47571	hypothetical prote
17	94	10.2	288	~	B90043	conserved hypothet
18	93.5	10.1	457	~	H85095	hypothetical prote
19	92.5	10.0	458	~	A72258	hypothetical prote
20	92.5	10.0	677	ď	F95232	immunity protein,
21	92.5	10.0	680	7	H98096	conserved hypothet
. 55	91	9.6	160	7	C84422	hypothetical prote
23	90.5	9.6	442	0	C75057	
24		9.6	224	~	D71915	hydrogenase, cytoc
25	89	9.6	468	~	A38223	nicotinic acetylch
56	87	4.6	1065	~	E69795	acriflavin resista
27	86	9.3	589	~	F64201	transport ATP-bind
28	86	6.9	1055	7	H90023	hypothetical prote
53	85.5	9.5	296	7	S46018	probable membrane

hypothetical prote	hypothetical prote	F3F19 hypothetical	ABC-transporter ho	unknown protein, 7	glucosyltransferas	secD protein - Str	hypothetical prote	probable phosphata	hypothetical prote	conserved hypothet	conserved hypothet	conserved hypothet	SCT1 homolog SPBC1	probable peroxisom	hydrogenase (EC 1.
B69155	C64397	G86264	T09007	G96705	AD2358	\$52765	H83724	E97200	G97886	D70006	A95044	F70316	T50332	T41400	A64599
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299	299	459	689	151	445	570	823	180	252	388	410	502	675	937	224
9.5	9.5	9.5	9.	9.1	0.6	0.6	o. 0	9.0	0	0.0	6.8	8.9	6.8	9.9	8.9
85.5	85	82	82	84.5	83.5	83.5	83.5	83	83	83	82.5	82.5	82.5	82.5	82
0	31	32	33	34	35	36	37	38	39	9	41	42	13	44	2

ALIGNMENTS

neuroendocrine-specific protein C - human C; Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C;Accession: 160904
R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V
Biol. Chem. 268, 13439-13447, 1993
A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe A;Reference number: A46583; MUID:93293865; PMID:7685762
A;Accession: 160904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNĀ A;Residues: 1-208 <RES>

A; Cross-references: UNIPROT: Q16799; GB: L10335; NID: g307310; PIDN: AAA59952.1; PID: g307311 C; Genetics:

A;Gene: GDB:RTN1; NSP A;Cross-references: GDB:203968; OMIM:600865 A;Map position: 14q21-14q22

Gaps ; Query Match
73.4%; Score 679; DB 2; Length 208;
Best Local Similarity 67.9%; Pred. No. 3.6e-52;
Matches 127; Conservative 31; Mismatches 29; Indels

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62 22 IDLLYWRDIKQTGIVFGSFLILLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 81 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 셤 Š

KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122 63 g 8

142 g ઠે

183 GLKRKAD 189 | || || |: GAKRHAE 208 셤 ò

neuroendocrine-specific protein, splice form A - human N;Contains: neuroendocrine-specific protein, splice form B C;Species: Homo sapiens (man) C;Date: 24-May-1996 #text_change 09-Jul-2004 C;Accession: A46583; I60903 F;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V J. Biol. Chem. 268, 13439-13447, 1993 A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe A;Reference number: A46583; MUID:93293865; PMID:7685762

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Conservative
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   A; Gene: CESP: W06A7.3c
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            A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-776 cROE3.
A/Accession: 160903
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; AROE2.
A/Cross-references: GB:L10334; NID:g307308; PIDN:AAAS9951.1; PID:g307309
A/Cross-references: GB:L10334; NID:g307308; PIDN:AAAS9951.1; PID:g307309
A/Cross-references: GBB:Z03968; OMIM:600865
A/Map position: 14q21-14q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tropomyosin-related protein, neuronal - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 30-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
C;Accession: 460021
R;Wieczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A;Reference number: A60021
A;Reference number: A60021
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-267 <WIE>
A;Coss-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-trope
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Accession: A46583
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: LNA
A;Residues: 1-2484 <WIL>
A;Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:WO
A;Experimental source: clone W06A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein W06A7.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26215
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Reference number: Z20173
A;Accession: T26215
A;Accession: T26215
A;Accession: DAA
A;Accession: U26715
A;Accession: U26715
A;Accession: U26715
A;Coss-references: UNIPROT: Q23187; EMBL: Z78066; PIDN: CAB01522.2; GSPDB: GN00023; CESP: W0)
A;Cross-references: UNIPROT: Q23187; EMBL: Z78066; PIDN: CAB01522.2; GSPDB: GN00023; CESP: W0)
A;Cross-references: Clone W06A7
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A,Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
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hypothetical protein W06A7.3c - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2C316
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26216
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A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
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; Pred. No. 1.4e-19;
46; Mismatches 78
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32.6%;
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C;Accession: T13013

S;Bevan, W.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17587
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R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999
A;Reference number: 215419
A;Accession: T05595
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A;Experimental source: cultivar Columbia; BAC clone F8L21
                                                                                                                                                                                                                                                                                                                                                                                         127 NKTSPQIP-----EIHVPEEAFLVVASSLRNELNQAFVILKSIALGRDLKKFLMVVG 179
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                          |: ||| | :| | | :| | ::::| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | | :::|| | | :::|| | | :::|| | | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :
                                                                                                               4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
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          24; Gaps
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          IndelB
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A,Experimental source: cultivar Columbia; BAC clone F9D16
          77;
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          Mismatches
          41;
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A;Introns: 85/1; 145/2; 192/3; 216/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 AKIQAKIP--GLKRKA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 EKVLSKIPIASLKAKA 252
          Conservative
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Best Local Similarity
Matches 46; Conserv
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A; Residues: 1-275 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-271 <BEV>
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A; Introns: 89/1;
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          54;
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B84899
Cypothetical protein At2g46170 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84899
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Artle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84899
A;Status preliminary
A,Status preliminary
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A;Experimental source: clone W06A7
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A;Residues: 1-255 <STO>
A;Cross-references: UNIPROT:082352; GB:AE002093; NID:g3702332; PIDN:AAC62889.1; GSPDB:GN
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                                                          :| ||: :|:| || || || : :|:| :| || || 3532 IMSLIYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHLATISGHLKGNONIIDEKL 2591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein W06A7.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T26213
R;Ainscough, R.
Bubmitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Reference number: Z20173
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Reference: DNA
A;Residues: 1-222 <WILD
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Best Local Similarity
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A;Map position: 5
     122
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C; Genetics:

Tue Jun 21 16:29:24 2005

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A;Status: preliminary
A;Modecule type: DNA
A;Residues: 1-242 <270>
A;Cross-references: UNIPROT:Q9M145; GB:NC_001268; NID:g7267620; PIDN:CAB80932.1; GSPDB:C
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Best Local Similarity 23.8%
Matches 46; Conservative
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A;Molecule type: DNA
A;Residues: 1-183 <STC
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A, Map position: 4
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A;Map position: 2
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A.Accession: S67758
A.Accession: S67758
A.Molecule type: DNA
A.Molecule: 1-393 <SCH>
A.Foresciues: 1-393 <SCH>
A.Experimental source: strain S288C
C.Genetics
A.Genetics
A.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 09-Jul-2004
C;Accession: B85016
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Colonature 402, 769-777, 1999
A;Title: Sequence and analysis of chromcosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
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                                                                                                                                                                                                                                                                                                       62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMA----KI 177
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                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YDL204w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D1062
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 ----PAVELSTKVLFDKGVVSRFGMQESPDLVGVLKPHIDRELDRLPALEDRIRKLVPA
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R,Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S. submitted to the Protein Sequence Database, July 1996
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                                                                                                                                                      18;
                                    Ouery Match
17.6%; Score 163; DB 2; Length 275;
Best Local Similarity 25.5%; Pred. No. 7e-07;
Matches 49; Conservative 43; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.4%; Score 142; DB 2; Length 393; 26.3%; Pred. No. 7.2e-05; ive 34; Mismatches 56; Indels
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F;50-66/Domain: transmembrane #status predicted <TM1>
F;150-166/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 26.3% Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 QAKIP--GLKRK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 LSKÍPLGPĽKNK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 4L
C; Keywords: transme
F;50-66/Domain: tra
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hypothetical protein At2g15280 [imported] - Arabidopsis thaliana (Gispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: Or-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 (Cispecies: A84527 (Cispecies: A84527 (Cispecies: Arabidopsis ) (Cispecies: Arabidopsis ) (Cispecies: Arabidopsis ) (Cispecies: Arabidopsis ) (Cispecies: Arabidopsis ) (Cispecies: Arabidopsis ) (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabidopsis (Cispecies: Arabid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 --NALNKSPEN------MMDIYIPEKPILQAASAMIFELNCAFATLRSIALERDIKNFV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM-- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 KSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
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$59439
Brobable membrane protein YDR233c - yeast (Saccharomyces cerevisiae)
Brobable membranes: hypothetical protein YD9934.17c
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                   DLLYWRDIKKTGVVFGASLFLLLSLTVFSIV----SVTAYIALALLSVTISFRIYKG
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                                                                                                                                                     Gaps
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14.6%; Score 135.5; DB 2; Length 242; 23.8%; Pred. No. 0.00015; live 49; Mismatches 63; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 14.5%; Score 134; DB 2; Length 183; Best Local Similarity 24.6%; Pred. No. 0.00015; Matches 44; Conservative 38; Mismatches 79; Indels
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Search completed: June 16, 2005, 13:31:51 Job time: 7.68322 secs
             <STO>
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             A, Residues: 1-206
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C;Accession: S59439
R;Murphy, L.; Harris, D.
Bubmitted to the EMBL Data Library, March 1995
A;Reference number: S59423
A;Accession: S59439
A;Molecule type: DNA
A;Residues: 1-295 < MNR>
A;Cross-references: UNIPROT:Q04947; EMBL:248612; NID:g728671; PID:g728688; GSPDB:GN00004
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YDR233c
A;Cross-references: SGD:S0002641
A;Map position: 4R
C;Keywords: transmembrane protein
F;40-56/Domain: transmembrane #status predicted <TM1>
F;146-162/Domain: transmembrane #status predicted <TM2>
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A;Cross-references: EMBL:AC004482; NID:g3152602; PIDN:AAC17096.1; PID:g3152617
R;Cross-references: EMBL:AC004482; NID:g3152602; PIDN:AAC17096.1; PID:g3152617
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable seed maturation protein [imported] - Arabidopsis thaliana
NiAlternate names: hypothetical protein F2714.17
C;Species at Aabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01153; T02426; C84627
R;Rounsley, S.D., Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Rounsley, S.D.; Kaul, S.; Lin, X.; Kerchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence.
A;Reference number: Z14658
A;Accession: T02436
A;Status: translated from GB/EMBL/DDBJ
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A;Accession: C84627
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 VDDLVDSLKFAVLAMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQID----- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <ROU>
A;Cross-references: UNIPROT:064837; EMBL:AC003040; NID:g3242700; PID:g3242725
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLLLWRNPVQTGKYFGGSLLALLILKKVNLITFFLKVAYTILFTT-----GSIEFV-- 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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181 ISKQKTQEFSQMACEKTKPYLDKVESKL 208
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A; Molecule type: DNA
A; Residues: 1-206 <RO2>
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C;Accession: T47948
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submittee to the Protein Sequence Database, January 2000
A;Reference number: 224480
A;Accession: T47948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ILSK------VEPELSGLEVSEEFVVETVRSCRMLMEEMVRWMPRVGAESEWFVPA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAK 176
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A;Cross-references: GB:AE002093; NID:g3152617; PIDN:AAC17096.1; GSPDB:GN00139 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F2A19.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                    16 VEDIYLWRRKKLAFSTLLVSTSTWILLSFYGFTTITIVSWIGIAVVSMIF---LWGSLLR
                                                                                                                                                                                                                                                                                                                                                          2 VVDLLYWRDIKK--TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ
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                                                                                                       A,Map position: 2
A;Introns: 14/1; 76/2; 147/1
C;Superfamily: Arabidopsis thaliana hypothetical protein F27L4.17
                                                                                                                                                                                                                                  13.3%; Score 123; DB 2; Length 206;
20.9%; Pred. No. 0.0016;
tive 48; Mismatches 85; Indels
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A;Cross-references: UNIPROT:Q9M312; EMBL:AL132962
A;Experimental source: cultivar Columbia; BAC clone F2A19
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VD---PVAEKTLKELKKHYMVFDEKVLSKLPVASLKA 261
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                                                                             A; Gene: At2g23640; F26B6.29; F27L4.17
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A;Introns: 68/1; 128/2; 164/1; 210/1
A;Note: F2A19.160
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Best Local Similarity 24.9%;
Matches 54; Conservative 3
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Best Local Similarity 20.9%
Matches 40; Conservative
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June 16, 2005, 12:31:51; Search time 27.2927 Seconds (without alignments) 2678.292 Million cell updates/sec
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1 SVVDLLYWRDIKKTGVVFGA.....VKDANAKIQAKIPGLKRKAD 189
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                    2105692 seqs, 386760381 residues
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Aay71385 Alternati Aay71310 Rat neuri Abb81074 Rat neuro Ado26399 Rat trunc Adb85287 Rat NogoA Adb85287 Rat neuro Abb81077 Rat neuro Abb81077 Rat neuro Abb81077 Rat neuro Abb81076 Rat neuro Abb81076 Rat neuro Aay71359 Rat Nogo Aay71359 Rat Nogo Aay71559 Rat Nogo Aay71557 Rat Nogo Aay71557 Rat Nogo Aay71557 Rat Nogo Aay71557 Rat Nogo Aay71557 Rat Nogo Aay71557 Rat Nogo Aay71557 Human neuro Aay56057 Human neuro Aay56057 Human Nog Abb11573 Human Nog Abb11573 Human Nog Abb83349 Human Nog Abb68600 Human Nog Abb68600 Human neuron Description SUMMARIES AAY71385 AAY71310 AAY71384 ABB81074 ADO26399 ADP45572 ADB85283 ABB81077 ABB81077 AAY7183 AAY71558 AAY71558 AAY71558 AAY71558 AAY71558 AAY71557 ADB8537 ADB82349 AAY61573 AAY7157 AAY717 AAY717 AAY717 AAY717 AAY717 AAY717 AAY717 AAY717 AAY717 AAY7 В Length 361 11163 11163 11163 11163 11163 11162 11172 11172 11172 11173 11172 11173 11173 Query Match Score Result

Abr59667 Human Nog Ado08103 Human pol Ado2400 Human tru Adp45551 Human Nog Adp67234 Human Nog Adr13966 Human Nog Adr13966 Human Nop Aab53947 Human Sec Aab53947 Human NSP Aab53947 Human NSP Aab12805 Human NSP Aab12805 Human Nog Abb12806 Human Nog Abb12806 Human Nog Abb12806 Human Nog Abb12806 Human Nog Abb12806 Human Nog Abb23659 Human Nog Aab24242 Human Nog Aab24242 Human Nog Aab24242 Human Nog Aab24242 Human Nog Aab24242 Human Nog Aab62350 Human Nog Aab62350 Human Nog Aab62350 Human Nog Aab62350 Human Nog Aab62350 Human Nog	MENTS .		growth inhibitor Nogo B.	Nogo B; neural cell; myelin; CNS; stic disease; antiproliferative; glioma; lastoma; menagioma; retinoblastoma; theimer's disease; Parkinson's disease; anign dysproliferative disorder; diagnosis; neuronal regeneration; treatment;		co amino acids 1-172 of Nogo A 71310"	3T3 fibroblast spreading"	II site"		is common to Nogo A, B and C	ne domain hydrophobic region"	se C (PKC) site"	osylated"	ບ ຄ	se C (PKC) site"
ABKS 9667 AD008103 AD008103 AD05521 AD067551 AD067551 AD075510 AD0	ALIGNMENTS 361 AA.		neurite g			n/Qualifiers "Corresponds to shown in AAY713	"Inhibits NIH	g :	c regio sponds		ransmembrane -terminal hy	ein kinas	2	ein kinas	= "Protein kinas .323
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 181 IPGLKRKAD 189
                         353 IPGLKRKAD 361
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                                                                   RESULT 2
AAY71310
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which is a potent neural cell growth inhibitor and is free of all central
cc which is a potent neural cell growth inhibitor and is free of all central
cc nervous system (CNS) myelin material with which it is natively
associated. The Nogo B transcript arises as a result of alternative
splicing of Nogo gene. Nogo proteins and fragments displaying neurite
cc growth inhibitory activity are used in the treatment of neoplastic
cdisease of the CNS e.g. glioma, pinealoma, medulloblastoma, acoustic
disease of the CNS e.g. glioma, pinealoma, neuroblastoma, acoustic
craniopharyngioma, pendyoma, pinealoma, haemangioblastoma, acoustic
cc neuroma, oligodendrogliona, menagioma, neuroblastoma, acoustic
cc craniopharyngioma, menagioma, neuroblastoma, acoustic
cc craniopharyngioma, menagioma, neuroblastoma,
and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
cc or prevent hyperproliferative or benign dysproliferative disorders e.g.
cc protein and tissue hypertrophy. Nibozywes or antisense Nogo nucleic
cc cregeneration of neurons or to promote structural plasticity of the CNS in
cc disorders where neurite growth, respensation or maintenance are deficient
cc disorders where neurite growth, respensation or maintenance are deficient
cc disorders which can treat or prevent disorders or diseases of the CNS in
cc methods for predisposition to disorders and to screen for or test
cmolecules which can treat or prevent disorders or diseases of the CNS in
cc reaidues 1-172 fused to 975-1163 of Nogo A. This sequence is an
credibues 1-172 fused to 975-1163 of Nogo A. This sequence is an
catida (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in
claim 32 and SEQ ID NO; 29 in discloure of the specification. However
cc the specification does not include sequences for these sEQ ID numbers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                 Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1QKSDEGHPFRAYLESEVA1SEELVQKYSNSALGHVNST1KELRRLFLVDDLVDSLKFAV
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/label= Transmembrane_domain
/note= "C-terminal hydrophobic region"
                                                                   /note= "Protein kinase C (PKC) site"
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100.0%; Pred. No. 9.6e-90;
ive 0; Mismatches 0;
                          339. .341
/note= "Asn is N-glycosylated"
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                                                                                                                                                 99WO-US026160
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Best Local Similarity 100.
Matches 189; Conservative
                                                                                                                                                                                                                                             Chen MS;
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                            Modified-site
                                                     Modified-site
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Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiptoliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; pyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening.
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/note= "This region is not essential for inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Region specifically described in claim 16"
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note= "Inhibits NIH 3T3 fibroblast spreading"
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/note= "Asn is N-glycosylated"
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/note= "Acidic region"
31. .57
AAY71310 standard; protein; 1163 AA.
                                                                                                                                                             Rat neurite growth inhibitor Nogo A.
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/note= "nr
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neurite growth inhibitory activity
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Matches 189; Conservative
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1155 IPGLKRKAD 1163
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                                                                                                                                                                                                   these SEQ ID numbers
                                                                                                                                                                                                                       Sequence 1163 AA;
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                                                                                                                                                                                                                                note= "C-terminal common region found in Nogo A, B and C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yo proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                  note= "This region is not essential for inhibitory
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/note= "C-terminal hydrophobic region specifically
described in claim 16"
                                                                                                                                                                                                                                                   988. .1023
/label= Transmembrane domain
/note= "C-terminal hydrophobic region specifically
described in claim 16"
                                                                                                                                                           note= "PKC and casein kinase II sites"
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note= "Protein kinase C (PKC) site"
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                   "Protein kinase C (PKC)
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note= "Asn is N-glycosylated"
                                       note= "Protein kinase C (PKC)
                                                                                                           12. .914
note= "Asn is N-glycosylated"
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note= "Asn is N-glycosylated"
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                    glioblastoma
the treatment of neoplastic disease of the CNS e.g. glions, glioblastic medulloblastoms, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, accustic neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapoutics which promote Nogo activity can be used to treat or prevent hyperpoliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         975 SVVDLLÝWRDIKKTGVVFGASLFLLLSLTVFSIVSVTÁÝIALALLSVTISFRIÝKGVIQA
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    .171
/note= "Inhibits NIH 3T3 fibroblast spreading"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 4.4e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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/note= "Acidic region"
172. .259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY71384 standard; protein; 1163 AA.
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The present sequence is an alternative version of rat Nogo A protein
which is a potent neural cell growth inhibitor and is free of all central
cc which is a potent neural cell growth inhibitors associated (CNS) myelin material with which it is natively
associated. Nogo proteins and fragments displaying neurite growth
inhibitory activity are used in the treatment of neoplastic disease of
the CNS e.g. glioma, paemangioblastoma, acoustic neuroma,
celudodendroglioma, menagioma, neuroblastoma or retinoblastoma and
coligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
coligodendroglioma, menagiona, neuroblastoma or retinoblastoma and
coligodendroglioma, menagional or neurolatic neuroma,
coligodendroglioma, menagional production of seases e.g. Alzheimer's and Parkinson's diseases.
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC neurons or to promote structural plasticity of the CNS in disorders where
cc neurite growth, regeneration or maintenance are deficient or desired. The
contract or prevent disorders and to screen for or test molecules which can prevent disorders and to screen for or test molecules which creat or prevent disorders and to screen for or test molecules which creat or prevent disorders and to screen for or test molecules which creat or prevent disorders and to screen for or test molecules which creat or prevent disorders or diseases of the Nogo A sequence shown in Fig.
C 2A (see AAX71310). SBO ID numbers 35-42 are referred in claim 32 and $EQ
C does not include sequences for these SBO ID numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     go proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
                                             'note= "C-terminal common region found in Nogo A, B and
"This region is not essential for inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1163;
                                                                                                      note= "C-terminal hydrophobic region"
                                                                                                                                                                                                                                                                       region"
                                                                                                                                                                                                                                                                                                                                site"
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100.0%; Pred. No. 4.4e-89;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                       090. .1125
|abel= Transmembrane domain
note= "C-terminal hydrophobic
                                                                                                                                                                                                                                                                                                                               /note= "Protein kinase C (PKC)
                                                                                                                                                                                             "Protein kinase C (PKC)
                                                                                                                                                                                                                         "Protein kinase C (PKC)
                                                                                                                                  "Protein kinase C (PKC)
                                                                                                                                                   071. .1073
note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                   "Asn is N-glycosylated"
                                                                          88. .1023
label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 13; 122pp; English.
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Matches 189; Conservative
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                               Region
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   note= "used as immunogen to generate antibody AS Bruna"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523. .640
'note= "used as immunogen to generate antibody AS 472"
                                                                                                                                                                                                                                                                                                                               /label= Unknown
/note= "There is Lys at this position in the sequence
shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thote= "There is Asn at this position in the sequence shown in AAY71310" 594. .696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "There is Leu at this position in the sequence
shown in AAY71310"
                                          /label= Unknown
/note= "There is Leu at this position in the sequence
shown in AAY71310"
                                                                                                                                                                                                                        note= "There is Ile at this position in the sequence shown in AAY71310"
 'note= "This region is not essential for inhibitory
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956
976: "PKC and casein kinase II sites"
975. .1162
                                                                                                                                                                note= "Protein kinase C (PKC) site"
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                                                                                                                                                                                                                                                                                      468. .470
/note= "Asn is N-glycosylated"
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542. .722
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                                                                                                                                    note= "Asn is N-glycosylated'
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                  activity"
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                               Misc-difference
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Modified-site
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                             1034
                                                                                                                                    The invention relates to promoting nerve regeneration or conferring neuroportection, and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen or its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative
                                                                                                                     LMWVFTYVGALFNGLTLLILALISLFSIPVIYBRHQVQIDHYLGLANKSVKDAMAKIQAK 180
                                                                                                                                                                                                                                                                                                                                                                                                   Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; rat; receptor.
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                SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                           IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV
SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                          IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cohen IR, Beserman P, Mosonego A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.
                                                                                                                                                                                                                                                                                                                                                                          Rat neurotransmitter receptor protein Nogo-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 44-47; 93pp; English.
                                                                                                                                                                                                                                                                                  ABB81074 standard; protein; 1163 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (YEDA ) YEDA RES & DEV CO LTD
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                                                                                                                                                                              181 IPGLKRKAD 189
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N-PSDB; ABN86600.
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22-DEC-1998;
19-MAY-1999;
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process occurring in either gray or white matter or both. The disease is diabetic neuropathy, semile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and carpotrophic lateral sclerosis, non-arteritic optic neuropathy, and officiency, intervertebral disc herniation, prion diseases such car Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral interpathies associated with various diseases, including but not limited courselia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute consorty neuropathy, bilary cirrhosis, primary amyloidosis, obstructive lung diseases, accomegaly, malabsorption amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma- pathies, complications of various drugs (e.g., alcohol or organophosphates), charcot-Marie-Tooth disease, ataxia telangectasia Friedreich's ataxia, amyloid polyneuropathies, care adrenomyelomeuropathy, disea axonal neuropathy, Refemus e disease, Pabry's disease, or lipoproteinemia. The present sequence represents the rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1095 IAMVETYVGALFNGLILLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SVVDLLYWRDIKKTGVVFCASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 5; Length 1163; 4.4e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO26399 standard; protein; 1163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat truncated Nogo-A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2002; 2002WO-EP012210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2002; 2002WO-EP012210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PIER-) PIERIS PROTEOLAB AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1155 iPGLKRKAD 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-376159/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004039836-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rat; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
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Gaps

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Length 1163; Indels

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The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 633-640 with a dissociation constant of less than 1000nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the binding molecule and a carrier or composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence represents rat NogoA, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
                                                                                                                                                                                                                                                                                                                                            975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of gene sequence that is down-regulated in response to streptozocin-induced diabetes, vector, host cell, animal, polypeptide and antibody, in screening of compounds for treating or diagnosing pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat; streptozocin; kinase; phosphatase; ion channel protein; receptor; transporter; G-protein coupled receptor; GPCR; DNA-binding proteins; protease; enzyme; analgesic; gene therapy; pain; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                           1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                            LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK
                                                                                                                                                                                                                                                                                                                                                                              61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                                                                                                1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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                                                                                                                                                                                                                                              100.0%; Score 925; DB 8;
100.0%; Pred. No. 4.4e-89;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 239-240; 256pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    foocen-m2 reticulon SEQ ID NO:164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2002; 2002EP-00255228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2001; 2001GB-00018354.
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                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1155 iPGLKRKAD 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 IPGLKRKAD 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                Sequence 1163 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 LMWVFTYVGALFNGLTLILIALISLFSIPVIYERHOVOIDHYLGLANKSVKDAMAKIQAK 1154
                                                The present invention relates to an isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein from the rat and from the human. The truncated polypeptide is useful for identifying a compound having detectable affinity to a Nogo-A protein. The present sequence is a Nogo-A polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                180
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CNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder;
                                                                                                                                                                                                                                                                    975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                                                                                                                                                                                                                                LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New binding molecule that binds to the human NogoA polypeptide, NiG, D20 or NogoA623-640, useful in preparing a composition for treating Cinjury or neurodegenerative disorders.
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                                                                                                                                                                                Length 1163;
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                                                                                                                                                                              100.0%; Score 925; DB 8;
100.0%; Pred. No. 4.4e-89;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP45572 standard; protein; 1163 AA.
                    Claim 1; Fig 6A; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat NogoA protein SEQ ID NO:26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPGLKRKAD 1163
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N-PSDB; ADP45571.
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                                                                                                                                                                                               Local Similarity
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                                                                                                                                                  Sequence 1163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004052932-A2.
                                                                                                                                                                                                              189;
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                                                                                                                                                                                  Query Match
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Zurini P
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The interior fractice to a invert response to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence identity to a sequence whose expression products are kinases, phosphatases, ion channel proteins, receptors, transporters, G-protein coupled receptor proteins, DNA-binding proteins, proteases or enzymes, given in the specification. A gene of the invention has analgesic activity, and may have a use in gene therapy. The gene sequences, vector, host cell, animal, polypeptide and antibody are useful for screening of compounds for diagnosing or treating pain. The kits are useful for sequential detecting and/or quantifying downequalition of a gene sequence in the spinal cord of a mammal in response to streptozocin-induced diabetes. The compound or pharmaccutical composition is useful as a medicament for treating or diagnosing pain.

The present sequence represents a protein encoded by a gene of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                     250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV
                  invention relates to a novel isolated gene sequence that is down-
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                    Length 379;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                 Score 922; DB 7;
Pred. No. 2.1e-89;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotransmitter receptor protein Nogo-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotransmitter receptor; rat; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB81077 standard; protein; 199 AA
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98WO-US014715.
98US-00218277.
99US-00314161.
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                                                                                                                                                                                                                                                                                                                                                                  188; Conservative
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|IPGLKRKAD.379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPGLKRKAD 189
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 188; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus.
                                                                                                                                                                                                                                                                                                   Sequence 379 AA;
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21-JUL-1998;
22-DEC-1998;
19-MAY-1999;
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                                                                                                                                                                                                                                                                    invention.
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The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system (Trauma, penetrating trauma, hemorrhagic stroke, ischemenic stroke or damages caused by surgery such as tumour excision. The disease is not autoimmune disease or neoplasm. The disease results in a degenerative contourning in either gray or white matter or both. The disease is disease, facial nerve (Ball's) palsy, glaucoma, Huntington's chorea, campotrophic lateral sclerosis, non-arteritic optic neuropathy, and cultamin deficiency, intervertebral diseases. Parkinson's cultamin deficiency, intervertebral diseases, including but not limited the neuropathies associated with various diseases, including but not innervented with various diseases, including but not limited the neuropathies associated with various diseases, including but not innervented with various diseases, including but not limited the neuropathies associated with various diseases, including but not limited the neuropathies associated with various diseases, including but not innervented with various diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin [Ig]A- and IgG gammapathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia atengectasia, Friedreich's atexia, amyloid polyneuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-C, an example of NS-specific
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                                                                                                                                          Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL
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     Beserman P, Mosonego A;
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Pred. No. 1.2e-89;
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Cohen IR,
                                                                                                                                                                                                                                                                        Example 5; Page 48-49; 93pp; English.
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  Hauben E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-2000 (first entry)
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  Eisenbach-Schwartz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGLKRKAD 189
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                                                                                                    N-PSDB; ABN86600
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                         Moalem G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
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  SAXE
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central nervous system, neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a rat Nogo B protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The Nogo B transcript arises as a result of alternative splicing of Nogo gene. Nogo protesns and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating neoplastic disorders regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                /note= "Corresponds to C-terminal 188 amino acids (residues 976-1163) of Nogo A protein (AAY71310). This region is common to Nogo A, B and C isoforms" 1185. 220 /label= Transmembrane domain
                                                                                                                                                                                                     1. .172
/note= "Corresponds to amino acids 1-172 of Nogo
                                          neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;
                                                                                                                                                                                                                                                              note= "Inhibits NIH 3T3 fibroblast spreading"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         887. .322
|Jabel= Transmembrane domain
|note= "C-terminal hydrophobic region"
                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "C-terminal hydrophobic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Protein kinase C (PKC) site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Protein kinase C (PKC) site"
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                                                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                  protein shown in AAY71310
                                                                                                                                                                                                                                                                                         'note= "Casein kinase II
                                                                                                                                                                                                                                                                                           neurite growth inhibitor Nogo B.
                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                               Domain
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             Rat
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dysproliferative disorders e.g. psoriasis and tissue hypertrophy.

Ribozymes or antisense Nogo mucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is not given in the specification but is derived from Nogo A protein sequence (AAY71310) and corresponds to residues 1-172 fused to 976-1163 of Nogo A. The specification claims an alternative version of this sequence (see AAY71385) which corresponds to residues 1-172 fused to 975-1163 of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nerve regeneration, neuroprotection, neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nociropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
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              neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
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haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma
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100.0%; Pred. No. 2.6e-89;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              not include sequences for these SEQ ID numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat neurotransmitter receptor protein Nogo-B.
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98WO-US014715.
98US-00218277.
99US-00314161.
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Best Local Similarity 100.
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 360 AA;
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22-DEC-1998;
19-MAY-1999;
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Rat neurite growth inhibitor Nogo C.

02-NOV-2000 (first entry)

COLTD

(YEDA) YEDA RES & DEV

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The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is disease, facial neither gray or white matter or both. The disease is disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral selecosis, non-arteritic optic neuropathy, and call call call call call call call disc hernialation, prion disease such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral concurred with various diseases, including but not limited neuropathies associated with various diseases, including but not limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangectasia, Friedreich's ataxia, amyloid polyneuropathies, addrenomyeloneuropathy, Giant axonal neuropathy, Refeum's disease, Fabry's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (1g)A- and 1g6 gamma-
                                                                                                                                                                                                                Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or
                                                      Mosonego A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-B, an example of NS-specific
                                                      Веветтап Р,
                                                   Cohen IR,
                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 47-48; 93pp; English.
                                                   Hauben E,
                                                Eisenbach-Schwartz M,
                                                                                                                                WPI; 2002-607255/65.
N-PSDB; ABN86600.
                                                                                                                                                                                                                                                                                                      analogs/peptides.
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                                                                                                                                 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
                                                                           WUDLLYWRDIKKTGWVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
                                                                                           VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
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                                                  Gaps
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                        Length 360;
                                                  0; Indels
                       99.6%; Score 921; DB 5; I
100.0%; Pred. No. 2.6e-89;
ive 0; Mismatches 0;
                                     Best Local Similarity 100.
Matches 188; Conservative
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Sequence 360 AA;
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                        Query Match
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antigen

/note= "Encoded by TAG"

AAY71312 standard; protein; 522 AA.

RESULT 11 AAY713'12 ID AAY7 XX AC AAY7

AAY71312

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51. .238 - - - ... /note= "C-terminal common region found in Nogo A, B and C
                                                                                          Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; Apperpoliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening.
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/note= "Sequence downstream to the C-terminus of Nogo
protein"
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                                                                                                                                                                                                                                                                                                                   1. .39 ^{\prime} Note= "Sequence upstream to the N-terminus of Nogo
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AAY71559 standard; protein; 199 AA.

02-NOV-2000 (first entry)

AAY71559;

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growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for
                                                                                                                                                                                                                                                                                                                                                                                                                       go proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a rat Nogo C protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
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                     note= "Encoded by TAG"
                                                          /note= "Encoded by TAA"
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Misc-difference 482
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 Length 522;
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99.6%; Score 921; DB 3; 100.0%; Pred. No. 4.2e-89;
Query Match 99.6%; Score 921; DB Best Local Similarity 100.0%; Pred. No. 4.2 Matches 188; Conservative 0; Mismatches
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RESULT 12 AAY71559

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively central netwous associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the inhibitory activity are used in the treatment of neoplastic disease of the construction, heammagiona, neuroblastoma, acoustic neuroma, coligodendrogliona, menagiona, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.

CC Therappeutics which promote Nogo activity can be used to treat or prevent the propertion or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of for neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for creat or prevent disorders and to screen for or test molecules which can treat or prevent disorders and to screen for or test molecules which creat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments from rat Nogo C and Nogo A proteins. The fragment is used in the construction of mutant Nogo-C which is composed of His-tag/77-tag/Nogo-C N-terminal (11 aa) + Nogo-A which is composed of His-tag/77-tag/Nogo-C N-terminal (11 aa) + Nogo-A which is dedition, N-terminal region 1-12-174, particularly amino acids 542-722. In distribution, N-terminal region 1-171 was found to be inhibitory to NHH 1313 the specification but is derived from a Rogo C sequence is not given in the specification but is derived from a Nogo C sequence shown in AAY71312 and Nogo C was dequence shown in the region 1-171 was found to be inhibitory effectived by the present Rat, neurite growth inhibitor; Nogo A; Nogo C; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; Apperpoliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutent: go proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons. Rat Nogo C/Nogo A proteins derived fragment to construct mutant Nogo-C. ď, /note= "Corresponds to residues 975-1162 of rat Nogo protein shown in AAY71310" 1. .11 Note= "Corresponds to residues 40-50 of rat Nogo protein shown in AAY71312" Location/Qualifiers Example; Page; 122pp; English. 99WO-US026160 98US-0107446P. .199 (SCHW/) SCHWAB M E. (CHEN/) CHEN M S. Chen MS; WPI; 2000-400052/34 WO200031235-A2 05-NOV-1999; 06-NOV-1998; 02-JUN-2000. Schwab ME, ВĎ Rattus Region Region

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Example; Page; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                  Nogo A protein fragment used in the construction of mutant Nogo-B.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172. .359
/note= "Corresponds to residues 975-1162 of rat Nogo
protein shown in AAY71310"
32 and SEQ ID NO: 29 in disclosure of the specification. the specification does not include sequences for these SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rat Nogo
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                                                        Length 199;
                                                                         0; Indels
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                                                      DB 3; L
1.9e-89;
                                                 99.4%; Scor.
100.0%; Pred. No. 1...
0, Mismatches
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                                                                                                                                                                                                                                                                          AAY71558 standard; protein; 359 AA
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                                                                        188; Conservative
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|IPGLKRKA 199
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                                                                Similarity
                                      Sequence 199 AA;
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in claim 32
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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV
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100.0%; Pred. No. 4.2e-
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Matches 188; Conservative
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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively cassociated Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the constitution, menagioma, neonoplastoma, acoustic neuroma, cligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.

CC Therapeutics which promote Nogo activity can be used to treat or prevent hyperprophy. Albozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where constite growth, regeneration or maintenance are deficient or desired. The neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAY71310, which is used in the nogo A sequence from main acids 172974, particularly cannocatine in the Nogo A sequence from main acids 172974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 373 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence from animo acids 12974, particularly canno acids not given in the specification but is derived from rat Nogo A sequence from protein canno cannocated from a Nogo A sequence from the present sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and 580 con to include sequences for these SEQ ID numbers include sequences for these SEQ ID numbers of the sequence from sequence and sequence from the present sequence cannocate 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      go proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
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Rattus sp.
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99WO-US026160. 98US-0107446P.

05-NOV-1999; 06-NOV-1998;

02-JUN-2000.

WO200031235-A2

Rattus sp.

Chen MS;

Schwab ME,

(SCHW/) SCHWAB M E. (CHEN/) CHEN M S.

Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system, neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.

Rat Nogo A truncated protein used in the construction of mutant Nogo-A.

(first entry)

02-NOV-2000

AAY71557;

AAY71557 standard; protein; 1162 AA.

AAY71557

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the pattent relates to neutrice growth intinity. Any which it is natively associated. Nogo proteins and fragments displaying neurite growth associated. Nogo proteins and fragments displaying neurite growth associated. Nogo proteins and fragments displaying neurite growth associated. Nogo proteins and fragments displastic disease of the CNS e.g. glioma, glioma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, coligodendroglioma, menagioma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.

CC chigodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nor benign dysproliferative disorders e.g. psoriasis can disposition of Nogo protein to induce regeneration of used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where continue to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence for used in the construction of mutant Nogo-A scomposed of Hissocrafers and to screen for or test molecules which is a truncated form of rat Nogo A protein shown in AAY1310, which is cused in the construction of mutant Nogo-A is composed of Hissocrafers and to screen for or test molecules which cused for mapping the inhibitory sites of Nogo protein. Major inhibitory cregion at a 1-1162. Nogo A deletion mutants were used for mapping the inhibitory to NIH 373 fibroblast spreading. Note: The was found to be inhibitory to NIH 373 fibroblast spreading. Note: The was found to be inhibitory to NIH 373 fibroblast spreading. Note: The was found to be inhibitory sieps of the Specification in ABAY1110. SEO ID numbers 35-42 are referred in claim 32 and SEO ID NO: 29 in disclosure of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patent relates to neurite growth inhibitor Nogo which is free of all
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Indels

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Best Local Similarity 100. Matches 188; Conservative

275 120

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1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA

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IPGLKRKA 188 IPGLKRKA 403

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Sequence 1162 AA;

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                                 0; Gaps
Query Match 99.4%; Score 919; DB 3; Length 1162; Best Local Similarity 100.0%; Pred. No. 1.9e-88; Matches 188; Conservative 0; Mismatches 0; Indels
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Appli

Sequence Seq

14833,

Sequence

8, Appli 19, Appl

Sequence 1 Sequence 1 Sequence 5

Sequence Sequence

Searched:

Run on:

Database

Result

Sequence

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2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS; NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 10TYTE Palo Alto
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
ZIP.
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                  US-09-583-110-3963
US-09-107-433-5202
US-09-543-681A-6175
US-09-248-796A-14833
US-09-785-381-1
US-09-785-381-1
US-09-785-381-1
US-09-783-110-4880
US-09-583-110-4880
US-09-593-110-4880
US-09-583-110-4880
US-09-583-110-4880
US-09-583-110-4880
US-09-583-110-4880
US-09-583-110-4880
US-09-583-658A-53-8
US-09-540-536-2019
US-09-540-653-8
US-09-724-653-8
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US-09-134-001C-3805
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0114 US
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NAME: BILLINGS, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-01

TELECOMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEPAK: 415-85-0555

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 199 amino acids
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
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Sequence 411, App
Sequence 7861, Ap
Sequence 16008, A
Sequence 411, App
Sequence 8, Appli
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10152, A
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Sequence 7, Appli
Sequence 6, Appli
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1976.818 Million cell updates/sec
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(cgn2_6/ptodata//iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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                    GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-700-607-5
US-09-949-016-698
US-09-949-016-8859
US-09-149-476-563
US-09-149-476-563
US-09-149-476-5132
US-09-949-016-7290
US-09-949-016-7290
US-09-949-016-7290
US-09-949-016-7290
US-09-513-999C-7861
US-09-513-996-8
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US-09-949-016-11596
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                           E: Diskette
IBM Compatible
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
  CORRESPONDENCE ADDRESS
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; CLONE: 307311
US-08-700-607-7
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                                                                              STATE: C. COUNTRY:
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 9124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 133
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                                                                                      72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131
                                                                                                                                         122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
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12 VVDLLYMRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYAYTALALLSVTISFRIYKGVIQAI 71
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Pred. No. 8e-89;
3; Mismatches 2; Indels
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Patent No. 5858708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                   5.09-949-016-9124
Sequence 9124, Application US/09949016
Patent No. 6812339
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97.38;
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Best Local Similarity
Matches 183; Conserv
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US-08-700-607-7
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63 KSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNSTIKELRRIFLVDDLVDSLKFAVLM 122
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Patent No. 5858708

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: AU-YOUNG.
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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMINICATION INFORMATION:
TELEPHONE: 415-855-0555
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63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
                                                                                                                                                                                       123 WVFTYVGALFNGLTLILLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
                                                                                                                                                                                                                                                                     S90 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 649
                                                                                  3 VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ
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73.4%; Score 679; DB 4; Length 439; 67.9%; Pred. No. 2.9e-64; ive 31; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incvte on Suppersor
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SOPTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 415-845-055
TELEFAX: 415-845-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08700607; Patent No. 5858708; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
Query Match
Best Local Similarity 67.9%
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.4% Best Local Similarity 67.9% Matches 127; Conservative
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                           183 GLKRKAD 189
                                                                                                                                                                                                                                                                                                                                                                   433 GAKRHAE 439
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STATE: CA
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERBNCE: CL001307
CURRENT APPLICATION NUMBER: 05/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELICATION NUMBER: 60/241,768
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PLIING DATE: 2000-10-03
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PLIING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FEBLES 2000-09-08
SEQ ID NO 9180
LENGTH: 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
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73.4%; Score 679; DB 2; Length 356
Best Local Similarity 67.9%; Pred. No. 2.2e-64;
Matches 127; Conservative 31; Mismatches 29; Indels
                                            SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: FILE HELWITH
ATTORNEY/AGENT INFORMATION:
NAME: Billings Information:
                                                                                                                                                                TORNEY AGENTA
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
FF-0114 US
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                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-865-0556
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                     3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide IMMEDIATE SOURCE:
  COMPUTER READABLE FORM:
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350 GAKRHAE 356
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CLONE: 307309
US-08-700-607-6
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US-09-949-016-9180
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Sequence 8859, Application US/09949016

Sequence 8859, Application US/09949016

Berent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE FEASTER FASTER FEASTER FOR WINDOWS VERSION 4.0

SEQ ID NO 8859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 IDLLYWRDIKQTGIVFGSFLLLLFRILQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 72
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                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/TOCKET NUMB
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Matches 123; Conservative
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS: si
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                                    Palo Alto
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                                                                                            COUNTRY:
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STREET:
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Sequence 6998, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: FOLYMOREPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMOREPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMOREPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FeatSEQ for Windows Version 4.0

LENGTH: 776
                                                                                                                                                       123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
                                    KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
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APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya Ke.
APPLICANT: Goli, Surya Ke.
APPLICANT: Hilman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 6.5e-64; 31; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.4%; Score 679; 67.9%; Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 67.9%
Matches 127; Conservative
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US-09-949-016-6998
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                                                                                                                                                                                                                                                                                                                        1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
                                                                                                                                                                                                                                                                                                                                                              3 SVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVSYLILALLSVTISFRIYKSVIQA 62
                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                         67.6%; Score 625.5; DB 4; Length 192; 60.0%; Pred. No. 5e-59; Indels 1: ive 40; Mismatches 35; Indels 1
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
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R APPLICATION NUMBER: 60/040,163
R FILING DATE: 1997-03-07
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,600
R PILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,618
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/040,162
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,333
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APPLICATION NUMBER: 60/047,502
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
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APPLICATION NUMBER: 60/040,334
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APPLICATION NUMBER: 60/047,597
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APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23
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Patent No. 6420526
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                                                                                                                                                                     Query Match
Best Local Similarity 60.0°
Matches 114; Conservative
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                              ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859
LENGTH: 192
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APPLICATION NUMBER: 60/056,886
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,877
APPLICATION NUMBER: 60/056,877
APPLICATION NUMBER: 60/056,889
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
FILING DATE: 1997-05-23
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APPLICATION WUMBER: 60/647,598
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/647,613
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FILING DATE: 1997-06-23
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
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APPLICATION WUMBER: 60/043,315
ELING DATE: 1997-04-11
APPLICATION WUMBER: 60/048,974
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,630
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,662
                                         APPLICATION NUMBER: 60/047,500
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,674
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APPLICATION WUMBER: 60/043,313
ELING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
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APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/047,584
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,637
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APPLICATION NUMBER: 60/056,903
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R APPLICATION NUMBER: 60/047,593
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,614
R FILING DATE: 1997-06-23
R APPLICATION NUMBER: 60/043,578
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,576
R FILING DATE: 1997-04-11
R FILING DATE: 1997-08-22

R APPLICATION WUMBER: 60/056,880

RR FILING DATE: 1997-08-22

R APPLICATION WUMBER: 60/056,894

R FILING DATE: 1997-08-22

R APPLICATION WUMBER: 60/056,911

R RILING DATE: 1997-08-22

R APPLICATION WUMBER: 60/056,636

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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,881
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,909
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APPLICATION NUMBER: 60/047,585
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,586
FILING DATE: 1997-05-23
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,864
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APPLICATION NUMBER: 60/056,631
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,845
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APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,594
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APPLICATION NUMBER: 60/047,589
FILING DATE: 1997-05-23
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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FILING DATE: 1997-08-22
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                                                       EARLIER PARLIER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER
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65 DEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMW 124
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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Mucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILLING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45132
LENGTH: 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 LIYWRDVKKSGIVFGAGLITLAAISSFSVISVFAYLSLLTLFGTVAFRIYKSVTQAVQKT
                                                                                                                                                                                                                                                                                                                                 24 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKS
                                                                                                                                                                                                                    DB 4; Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 SLFSIPVIYERHOVQIDHYLGLANKSVKDAMAKIQAKIPGL-KRKAD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.0%; Score 518; DB 4; Length 219; 52.2%; Pred. No. 1.9e-47;
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APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                             36; Mismatches 31;
                                                                                                                                                                                                                                        7e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Mismatches
                                                                                                                                                                                                                 58.3%; Score 539.5; 59.3%; Pred. No. 6.7e
             EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
FILING DATE: 1997-09-05
                                                                                                                                                                                                                 Query Match
Best Local Similarity 59.3%
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Conservative
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Matches 93; Conserv
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US-09-270-767-45132
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US-08-700-607-3
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Length 588;

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62 OKSDEGHPFRAYLESEVAISELVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
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448 HRGDGANPFQAYLDVDLTLTREQTERLSHQITSRVVSAATQLRHFFLVEDLVDSLKLALL 507
                                                                                                                                                                                                                                                                                                                                                                     122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
                                                                                                                                                                                                                                                                                                                                                                                                   2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
                                                                                                                          54; Indels
                                                                         51.4%; Score 475; DB 4;
50.5%; Pred. No. 3.1e-42;
iive 36; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ020P1
CURRENT APPLICATION UNMER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORKELL FILING DATE: 1998-09-08

EARLIER PELLICATION NUMBER: PCT/US98/04493

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER APPLICATION NUMBER: 60/040, 162

EARLIER APPLICATION NUMBER: 60/040, 333

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,618
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Patent No. 6420526
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                                                                       Query Match
Best Local Similarity 50.5
Matches 92; Conservative
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  ; ORGANISM: Human
US-09-949-016-7290
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FACENTEAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/29146

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRALESEQ for Windows Version 4.0

LENGTH: 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQV 157
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                         ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTONNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-955-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0114 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7290, Application US/09949016
Patent No. 6812339
                                                               CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INPORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 241 amino acids TYPE: amino acids STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: THP1NOB01
CLONE: 31870
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US-09-949-016-7290
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US-08-700-607-3
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R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,613

R APPLICATION NUMBER: 60/047,582

R APPLICATION NUMBER: 60/047,582

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,596

R R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,612 R APPLICATION NUMBER: 60/047,601
R FILING DATE: 1997-05-23
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,588
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,314
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/047,500
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,587
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,492
R FILING DATE: 1997-05-23 FILING DATE: 1997-04-11
A PELLING DATE: 1997-04-11
PILING DATE: 1997-04-11
A APPLICATION NUMBER: 60/043,674
A APPLICATION NUMBER: 60/043,669
A APPLICATION NUMBER: 60/043,669
A FILING DATE: 1997-04-11 A APPLICATION NUMBER: 60/056,872
R FILING DATE: 1997-08-22
A APPLICATION NUMBER: 60/056,882
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,637
R FILING DATE: 1997-08-22 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,315
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 LICATION NUMBER: 60/056,888 FILING DATE: 1997-05-23 EARLIER BARLIER EARLIER SARLIER

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,910

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,845

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,845

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,845

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,892

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/057,761

R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

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R APPLICATION NUMBER: 60/047,586

R R PLING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,586

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599 R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,576

R FLING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R FILING DATE: 1997-05-23

R RAPLICATION NUMBER: 60/043,670

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/056,632

R R PILING DATE: 1997-08-22

R R PILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,649

R APPLICATION NUMBER: 60/056,649

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R APPLICATION NUMBER: 60/056,649

R APPLICATION NUMBER: 60/056,649

R APPLICATION DATE: 1997-08-22 R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,593
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,614
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043,578 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,875 APPLICATION NUMBER: 60/056,875 APPLICATION NUMBER: 60/056,862 LLING DATE: 1997-08-22 PPLICATION NUMBER: 60/056,894 LLING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 APPLICATION NUMBER: 60/056,908 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-08-22 CATION NUMBER: 60/048,964 G DATE: 1997-06-06 APPLICATION NUMBER: 60/057,650 FILING DATE: 1997-09-05 APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 EARLIER
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Sequence 7861, Application US/09513999C
; Sequence 7861, Application US/09513999C
; Reinstan Information:
; APPLICANT: Dumas Mille Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PLE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1999-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 7861
; ERGTH: II4
; ERGTH: II4
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                                                                                                                                                                                                                            DB 4; Length 92;
                                                                                                                                                                                                                      Query Match 30.9%; Score 286; DB 4; Length 92
Best Local Similarity 56.0%; Pred. No. 4e-23;
Matches 51; Conservative 21; Mismatches 19; Indels
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62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92
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; OTHER INFORMATION: Xaa= * or Gly or Arg
US-09-513-999C-7861
                       EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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FILING DATE: 1997-08-22
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ORGANISM: Homo sapiens
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LOCATION: -48...1
OTHER INFORMATION: 8
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Search completed: June 16, 2005, 12:33:38 Job time : 9.13706 secs

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| Cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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6 US-10-810-653-18
4 US-10-205-194-164
US-09-893-349-21
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US-09-893-346-20
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 18, Appl Sequence 21, Appl Sequence 21, Appl Sequence 20, Appl Sequence 20, Appl

Sequence 20, Appl Sequence 10, Appl Sequence 10, Appl Sequence 2, Appli Sequence 6, Appli

US-10-810-653-20 US-10-633-423-10 US-10-427-741-10

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US-09-789-386-2 US-09-758-140-6

908 98.2 1192 9 US-09-893-348-23 908 98.2 1192 9 US-09-802-594-6 908 98.2 1192 19 US-09-976-594-6 908 98.2 1192 19 US-09-976-594-6 908 98.2 1192 19 US-10-976-594-6 908 98.2 1192 19 US-10-976-593-9 908 98.2 1192 16 US-10-277-602-429 908 98.2 1192 16 US-10-277-602-43-9 904 97.7 199 15 US-10-80-46-158-9 904 97.7 199 15 US-10-80-948-15 904 97.2 190 16 US-10-80-948-15 904 97.2 190 16 US-10-80-948-15 904 97.2 190 16 US-10-80-948-15 904 97.2 190 16 US-10-80-948-15 904 97.2 190 16 US-10-80-948-15 904 97.2 190 16 US-10-80-948-15 904 97.2 190 16
Query match Best Local Similarity 100.0%; Pred. No. 4e-81; Dess Local Similarity 100.0%; Pred. No. 4e-81; Matches 189: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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Sequence 21, Application US/09893348

patent No. US20020072493A1

general Information

general Information

APPLICANT: EISENBACTON:

APPLICANT: EISENBACH:

APPLICANT: GOHEN, Irun R.

APPLICANT: BESERMAN, Pierre

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US

FILE REFERENCE: EIS-SCHWARTZ=2A

CURRENT APPLICATION NUMBER: US/09/893,348

CURRENT FILING DATE: 2001-06-28

PRIOR PILING DATE: 1999-05-19

PRIOR FILING DATE: 1998-12-22

PRIOR FILING DATE: 1998-12-22

PRIOR FILING DATE: 1998-12-22

PRIOR FILING DATE: 1998-07-21

PRIOR FILING DATE: 1998-12-22

PRIOR FILING DATE: 1998-07-21

PRIOR FILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-05-19
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                                                                                                                APPLICANT: Dixon, Alistair
APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 2000-07-24
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 177
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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Pred. No. 1.9e-81;
1; Mismatches 0; Indels
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                          GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.5%;
Matches 188; Conservative
Publication No. US20030134301A1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Rattus norvegicus
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GURRENT APPLICATION NUMBER:
GURRENT APPLICATION NUMBER:
GO/9913,34
FRIOR FILING DATE:
1999-05-19
FRIOR FILING DATE:
1999-05-19
FRIOR PELLOR APPLICANTON NUMBER:
GO/90121
FRIOR FILING DATE:
1998-07-12
FRIOR APPLICANTON NUMBER:
FRIOR FILING DATE:
1998-07-12
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Pred. No. 4e-81;
; Mismatches 0;
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; Sequence 164, Application US/10205194
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Publication No. US20040253218A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 189; Conservative 0
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Sequence 20. Application US/09893348

Sequence 20. Application US/09893348

Patent No. US2002007249341

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APPLICANT: EISENBACH-SCHWARTZ, Michal

APPLICANT: COHEN, Irun R.

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

SAPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

SAPLICANT: MOSONEGO, Alon

SAPLICANT: MOSONEGO, Alon

CURRENT APPLICATION NUMBER: US/09/893,348

CURRENT FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: US 09/314,161

PRIOR FILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-07-21

PRIOR FILING DATE: 1998-07-21

PRIOR FILING DATE: 1998-05-19

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APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: ESERBANA: Irun R.
APPLICANT: COHEN, Irun R.
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOALEM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
TITLE REFERENCE: EIS-SCHWARTZ=2A
CURRENT APPLICATION NUMBER: US/10/819,653
CURRENT APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/318,277
PRIOR APPLICATION NUMBER: US 09/218,277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20
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APPLICANT: COHEN, ITURE
APPLICANT: COHEN, ITURE
APPLICANT: MOSALEM, Pierre
APPLICANT: MOSALEM, Pierre
APPLICANT: MOSALEM, Gila
APPLICANT: MOSALEM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
FILE REFERENCE: EIS-SCHWARTZ=2A
CURRENT APPLICATION NUMBER: US/09/893,348
PRIOR FILING DATE: 2001-06-28
PRIOR FILING DATE: 1099-05-19
PRIOR FILING DATE: 1999-05-19
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       Length 199;
                                                                       0; Indels
Query Match 99.6%; Score 921; DB 9;
Best Local Similarity 100.0%; Pred. No. 1e-81;
Matches 188; Conservative 0; Mismatches 0
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APPLICANT: BISENBACH-SCHWARTZ, Michal
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Publication No. US20040253218A1
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Matches 188; Conservative
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1154 IPGLKRKAE 1162
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US-09-789-386-2
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Best Local Similarity
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| Publication No. US20040191240A1
| GENERAL INFORMATION:
| APPLICANT: Tohyama, Masaya
| APPLICANT: Tohyama, Masaya
| TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
| FILE REFERENCE: 59150-8033.US00
| CURRENT APPLICATION NUMBER: US/10/633,423
| CURRENT APPLICATION NUMBER: US/10/633,423
| PRIOR APPLICATION NUMBER: US 10/427,741
| PRIOR APPLICATION NUMBER: US 10/427,741
| PRIOR APPLICATION NUMBER: US 203-092923
| PRIOR APPLICATION NUMBER: US 203-092923
| PRIOR PRILING DATE: 2003-03-28
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 10
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Pred. No. 2.4e-80;
1; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                       Length 360;
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                                                                                                                                                                                                                                                                     Score 921; DB 16;
Pred. No. 2.2e-81;
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99.6%; Score 921; DB
Best Local Similarity 100.0%; Pred. No. 2.2
Matches 188; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US98/14715
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: IL 124500
PRIOR PILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 360
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98.9%;
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US-10-810-653-20
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CORGANISM: Mus musculus
US-10-633-423-10
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US-10-633-423-10
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; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR PILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-12
; PRIOR FILING DATE: 1998-12-2
; PRIOR FILING DATE: 1998-12-1
; PRIOR FILING DATE: 1998-07-21
; PRIOR FILING DATE: 1998-07-21
; PRIOR FILING DATE: 1998-07-21
; PRIOR FILING DATE: 1998-07-21
; PRIOR FILING DATE: 1998-05-19
; SOFTWARE: PALENTION NOWHER: PLOST DATE: 1998-05-19
; SOFTWARE: PALENTION NOS: 29
; SOFTWARE: PALENTIN VERSION 3.1
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TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REFERENCE: C077 C1P US
CURRENT APPLICATION NUMBER: US/09/972,599A
CURRENT FILING DATE: 2001-10-06
PRIOR PILING DATE: 2001-10-12
PRIOR PLICATION NUMBER: PCT/US01/01041
PRIOR PLILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/758,140
PRIOR PLILING DATE: 2000-09-29
PRIOR PLILING DATE: 2000-09-29
PRIOR PLILING DATE: 2000-09-26
PRIOR PLILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
SOFTWARE: PALENTIN VONSER: 60/175,707
PRIOR PLILING DATE: 2000-01-12
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Pred. No. 1.9e-79;
3; Mismatches 2; Indels (
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Pred. No. 1.9e-79;
3; Mismatches 2; Indele
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Best Local Similarity 97.4%;
Matches 184; Conservative
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97.4%;
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Best Local Similarity 97.4
Matches 184; Conservative
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CORGANISM: Homo sapiens
US-09-893-348-23
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Parent No. US20020012965A1

GENERAL INFORMATION:

APPLICANT: Strittmatter, Stephen M.

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/758,140

CURRENT FILING DATE: 2001-01-12

PRIOR PILING DATE: 2001-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 6

LENGTHA: 1192
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                                                 3; Mismatches
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Patent No. US20020072493A1
GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.
APPLICANT: BESERWAN, Pierre
APPLICANT: MOSOWEGO, Alon
                                                 Matches 184; Conservative
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1184 IPGLKRKAE 1192
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US-09-758-140-6
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US-09-893-348-23
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TYPE: PRT
ORGANISM: Homo sapiens
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## Sequence 71, Application US/10060036

## Publication No. US20030073144A1

## Sequence 71, Application US/10060036

## APPLICANT: Benson, Darin R.

## APPLICANT: Ralos, Michael D.

## APPLICANT: Hepler, Milliam T.

## APPLICANT: Hepler, William T.

## APPLICANT: Jiang, Yuqiu

## TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

## TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

## TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

## TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

## TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REPERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
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US-10-060-036-71
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GenCore version 5.1.6
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Q61G15
Q7PCJ7
Q6RSS8
Q7T224
Q9GM33
Q61FY5
Q6JRV0
Q6JRV0
Q6JRV1
Q6JRV1
Q6JRV1
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Q6JRV3
Q6JRV9
                                                                                                                                                  Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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187
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1024
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193
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Q6jrv7	Q6jrv8	Q6jrw4	Q6jrw1	Q6jrw3	Q6jrw0	Q6 j rw2	Q71222	Q6iei6	Q6iej4	Q66hz3	Q6iej1	Q6iax4	Q9bq59
Q6JRV7	Q6JRV8	Q6JRW4	Q6JRW1	Q6JRW3	QGJRWO	Q6JRW2	Q7T222	QGIEIG	Q6IEJ4	Q66HZ3	QGIEJ1	Q61AX4	Q9BQ59
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1032 2	1044 2	193	323	199	304	316	214	196	193	197	209	208	199
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80.8	_	80.4	80.4	80.3	80.3	80.3	79.2	7.77	6.9	76.2	75.4	73.8	73.4

ALIGNMENTS

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Nature 417:547-551(2002).
-!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
block the regeneration of the nervous central system in adults (By
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
STRANT-Spraque-Dawley, TISSUE-Addipcovte;
MEDLINE-9249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
MORTIS N.J., ROSS S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
"Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family.";
Biochim. Biophys. Acta 1450:68-76(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
STRAIN=Wistar Kyoto, TISSUE=Vascular smooth muscle;
Ito T., Schwartz S.M.,
"Cloning of a membar of the reticulon gene family in rat: one of two minor splice variants.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GrandPre T., Li S., Strittmatter S.M.;
"Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).
                                 Q9JKĪ1; Q9JK10; Q9ROD9; Q9WUB9; Q9WUF0; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last aquence update) 65-JUL-2004 (Rel. 44, Last annotation update) Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDILINE=20129281, PubMed=10667796; DOI=10.1038/35000219;
Chen M.S., Huber A.B., Wander Haar M.E., Frank M., Schnell L.,
Spillmann A.A., Christ F., Schwab M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nogo-A is a myelin-associated neurite outgrowth inhibitor and antigen for monoclonal antibody IN-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;
                     PRT; 1163 AA.
                                                                                                                                         (Glut4 vesicle 20 kDa protein)
                                                                                                                                                              Name=Rtn4; Synonyms=Nogo;
Rattus norvegicus (Rat).
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 403:434-439(2000)
                                                                                                                                                                                                                                                 !CBI_TaxID=10116;
RTN4 RAT
ID RTN4 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUNCTION
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ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=4; Name=1; Synonyms=Nogo-A, NI-220-250;

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1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
    LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LMWVFTYVGALFNGLTLILLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NOBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRANBEYNB/N, TISSUE-Mammary tumor. C3;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.1%; Score 917; DB 2; Length 578; 98.9%; Pred. No. 7e-68; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.

Tozaki H., Hirata T.;

Tozaki H., Hirata T.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AB073672; BAC75974.1; -.

GO; GO:0005783; C:endoplasmic reticulum; IEA.

InterPro; IPR03388; Reticulon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;
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Last annotation update)
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Last annotation update)
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PROSITE; PS50845; RETICULON; 1.
                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25, Nogo-A (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 187; Conservative
                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                   1155 IPGLKRKAD 1163
                                                                                      181 IPGLKRKAD 189
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Best Local Similarity
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Q80W95;
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Q8K290;
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                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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               Name=2; Synonyms=Nogo-B, Poocen-M; I sold=Q9TK11-2; Sequence=VSP 005658; Name=3; Synonyms=Nogo-C, VP20; Name=3; Synonyms=Nogo-C, VP20; Name=4; Synonyms=Poocen-M2; Name=4; Synonyms=Foocen-M2; Name=4; Synonyms=Foocen-M2; Name=4; Synonyms=Foocen-M2; I sold=Q9TK11-4; Sequence=VSP 005659; Name=4; Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Foocen-M2; Order Synonyms=Fo
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Missing (in isoform 2).
/FIId=VSP 005658.
Missing (in isoform 4).
/FIId=VSP 005659.
Missing (in Ref. 3; AAD31020).
Missing (in Ref. 3; AAD31020).
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Best Local Similarity 100.
Matches 189; Conservative
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J. Mol. Biol. 325:299-323(2003)
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              A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Jatchenko L., Marusina K.A., Rubin G.M., Hong L., A Stapleton M. Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Proshlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., A Fachy J., Helton B., Ketteman M., Madan A.M., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C., A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Touchman J.W., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Touchman J.W., Chen E.D., Dickson M.C., Generation and initial analysis of more than 15,000 full-length human mann mouse cDNA sequences.";
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STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=223/6540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032192; AAH32192.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70312 MW; 309A19DA37603F11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
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PROSITE; PS50845; RETICULON; 1.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 23, (TrEMBLrel. 23, I
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Matches 187; Conservative
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MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
OGertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                              STRAIN-1295vcJ7;

Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102286; AAM73502.1;
EMBL; AY102286; AAM73507.1;
MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:000515; F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0001399; P:neurogenesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;
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Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                         to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.1%; Score 917; DB 2; 98.9%; Pred. No. 1.3e-67; iive 1; Mismatches 1;
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J. Mol. Biol. 325:299-323(2003)
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PROSITE; PS50845; RETICULON; 1.
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01-MAR-2003 (TrEMBLrel. 23,
05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity
Matches 187; Conserv
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SEQUENCE FROM N.A.
                       STRAIN=129/SvcJ7;
Van der Putten H.;
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SEQUENCE FROM N.A.
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InterPro; IPR003388; Reticulon.
                                                                                                                                                 61
                                                                                                                                                                                             121
                                                         Query Match
Best Local 9
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RTN4 MOUSE
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8888
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                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                 121 LMWVFTYVGALFNGLTLILIALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
MCDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
MCDCTLB T., Huber C., van dr Dort Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                     61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                                                   1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                  ö
                                                                                                                                                            Length 1162;
                                                                                                                                                   Score 917; DB 2; Decessor Pred. No. 1.4e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129/SvcJ7;
Van der Putten H.,
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102284
EMBL; AY102286; AAM73511.1; -.
                                                                                                                                     1162 AA; 126612 MW; 855697FBEE11781F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van der Putten H., Mir A., Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AXI02288, AAM73504.1; -. EMBL, AXI02286, AAM73509.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                         MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
InterPro; IPR003388; Reticulon.
PROSITE; PSSO845; RETICULON; 1.
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GO:0005783, C:endoplasmic reticulum; IDA.
GO:0005515, F:procein binding; IPI.
GO:0001525, P:angiogenesis; IMP.
GO:0007399; P:neurogenesis; IDA.
                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323 (2003).
                                                                                                                                                            99.1%;
98.9%;
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                                                                                                                                                                      Best Local Similarity 98.9
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    1154 iPGLKRKAE 1162
                                                                                                                                                                                                                                                                                                                                              181 IPGLKRKAD 189
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                                                                                                                                      SEQUENCE
                                                                                                                                                             Query Match
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CYCANGE OF 1/0-19 FACUR N.A..

SECURNES CYBL/64; TISSUE=Embryo;

REDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

REDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

REDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

REDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

REDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

REDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA SAID IN. Ranapin A., Ranapin A., Satoch H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,

Radsterland T., Gariboldi M., Gissi C., Godzik A., Fazer K.S.,

Rasierriand T., Gariboldi M., Gissi C., Godzik A., Rough J.,

Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Ronagaya A., Kurochin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ranajort D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Sercu M., Shimada K.,

Nulming L.G., Wynnshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Konno H., Nakamura M., Sakazume N.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T.,

RA Salaki Y., Sasaki D., Shibata K., Shinagawa I.,

Miyazaki A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RICKARA P., Parakawa T., Konno H., Nakawa T., 
                                                                                                                                                                                                                                                                                                                                                                                                           LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 LAWYFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 366
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                 Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIN4 MOUSE STANDARD; PRT; 199 AA.
Q99P72; Q9CTE3;
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
                                                                                                                                                                                                                                                                   1; Indels
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STRAIN=3T3-L1; TISSUB=Adipocyte;
COULBON A.C., Craggs P.D., Morris N.J.;
"Mouse vp20/FRV4C CDNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 375, AA; 40300 MW; 23D9EB19BE671AE6 CRC64;
                                                                                                                                                                            2;
                                                                                                                                                                        Score 914; DB 2;
Pred. No. 8e-68;
2; Mismatches
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                                                                                                                                                                            98.8%;
98.4%;
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                              Matches 186; Conservative
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                                                                                                                                                                                                                     Local Similarity
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
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Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Bliney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:553-573(2002).
-!- FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
                                                                                                                                                                                                       similarity).
SUBCELLUIAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005783; C:endoplasmic reticulum; IDA.
GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
GO:0005615; C:integral to endoplasmic reticulum membrane; ISS.
GO:0005515; F:protein binding; ISS.
GO:0019987; P:negative regulation of anti-apoptosis; ISS.
GO:0030517; P:negative regulation of axon extension; ISS.
GO:0007399; P:neurogenegis; IDA.
                                                                                                                                                         similarity).
SUBUNIT: Binds to RIN4R. Interacts with Bcl-xl and Bcl-2 (By
similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07BE5D580059ED9C CRC64;
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                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=1; Comment=A number of isoforms may be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 913; DB 1;
Pred. No. 5.1e-68;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q99P72-1; Sequence=Displayed;
SIMILARITY: Contains 1 reticulon domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF326337; AAK08076.1; -.
EMBL; AK003859; -; NOT ANNOTATED_CDS.
MGD; MGI:1915835; Rtn4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
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PGLKRKAE 199
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163
12
199 AA;
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TRANSMEM
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
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RESULT Q8BH78

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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
05-VUL-2004 (TrEMBLrel. 27, Last sequence update)
15-VUL-2004 (TrEMBLrel. 27, Last senotation update)
18NT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E)
                                                                                                                                                                                                                                                                                                                                                                     Oertle T., Huber C., van der Putten H., Schwab M.E.; "Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 QKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL
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                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 356;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102281; AAM73503.1; -.
EMBL; AX102286; AAM73508.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4366C03BA9630B56 CRC64;
                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.7%; Score 913; DB 2;
98.9%; Pred. No. 9.2e-68;
iive 1; Mismatches 1.
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GO; GO:0005783; C:endoplasmic reticulum; IDA
GO; GO:000518; F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0001525; P:neurogenesis; IMP.
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        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003).
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PROSITE, PS50845; RETICULON, 1.
SEQUENCE 356 AA; 38403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003388; Reticulon.
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 98.9
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 PGLKRKAD 189
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                              NCBI_TaxID=10090;
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TISSUE=Brain;
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                      BARARAR BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTER BERLITTE
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                                                                                                              TISSUE=restis;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTN4 HUMAN STANDARD; PRT; 1192 AA.
Q9NQC3; Q9462; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9X293; Q9X2Y7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.2%; Score 908; DB 2; Length 98 97.4%; Pred. No. 6.8e-67; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
Oertle T., Schwab M.E.;
Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY102285; AAM64244.1; -..
                                                                                                                                                                                                                                                                                           Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108449 MW; OCDE8F647036415A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO, GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IFR003388; Reticulon.
Bern; PF05453; Reticulon.
PROSITE; PS50845; RETICULON; 1.
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SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY123246; AAM64250.1; EMBL; AY123247; AAM64251.1; EMBL; AY123249; AAM64222.1; EMBL; AY123249; AAM64253.1; EMBL; AY123250; AAM64254.1; EMBL; AY122245; AAM64291.1;
                                                                                                                                                                                               man and mouse nogo/rtn4.";
Mol. Biol. 325:299-323(2003)
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 184; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      986 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                               TISSUE=Testis;
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SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).

TISSUE=Brain, Ovary, Pancreae, Placenta, and Skeletal muscle;

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M. B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jin W.-L., Ju G.; "Developmentally-regulated alternative splicing in a novel Nogo-A."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pituitary;
Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 3).
Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                            Christie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \tilde{Y}_0 J., Han L.H.; "Novel human cDNA clones with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Nuo B., Chen J., Hu R., Chen J., Hu R., Chen J., Human neuroendocrine-specific protein C (NSP) homolog gene."; submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RTN4) to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of a member of the reticulon gene family in human."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
MEDLINE=20129242; Pubmed=10667780; DOI=10.1038/35000287;
Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation of a cell death-inducing gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                       Prinjha R., Moore S.E., Vinson M., Blake S., Michalovich D., Simmons D.L., Walsh F.S., "Inhibitor of neurite outgrowth in humans."; Mature 403:383-384(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20237542; PubMed=10773680; Yang J., Yu L., Bi A.D., Zhoo S.-Y.; "Assignment of the human reticulon 4 gene Cytogenet. Cell Genet. 89:101-102(2000).
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 2 AND 3)
TISSUE=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99156230; PubMed=10048485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 19:5736-5746(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Fibroblast;
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             Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                               TISSUB-Umbilical cord blood;

MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;

Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;

"Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Puncosci. Res. 67:559-565 (2002).

Puncosci. Res. 67:559-565 (2002).

PUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults.

Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-z. This is likely consecutive to their change in subcellular location, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.

SUBUNIT: Binds to RTNAR. Interacts with Bcl-xl and Bcl-2.

SUBCELIULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
Fournier A.E., Grandpre T., Strittmatter S.M.;
"Identification of a receptor mediating Nogo-66 inhibition of axonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum. Anchored to the membrane of the endoplasmic reticulum
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134; Ng C.E.L., Tang B.L.; "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226; GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.; "Identification of the Nogo inhibitor of axon regeneration as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sha J.H., Zhou Z.M., Li J.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms=4;
Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;
IsoId=Q9NQC3-1; Sequence=Displayed;
Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foocen-M;
IsoId=Q9NQC3-2; Sequence=VSP_005655;
                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through 2 putative transmembrane domains. ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                  and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reticulon protein.";
Nature 403:439-444(2000)
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                                                                                                                                                                                                                                                                                                                                                                       stem/progenitor cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regeneration.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                      Isoid=Q9NQC3-4; Sequence=VSP 005654;
TISSUB SPECIFICTTY: Isoform 1 is specifically expressed in brain
and testis and weakly in heart and skeletal muscle. Isoform 2 is
widely expressed excepted for the liver. Isoform 3 is expressed in
brain, skeletal muscle and adipocytes. Isoform 4 is testis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                       SIMILARITY: Contains 1 reticulon domain.
CAUTION: Ref.11 sequence differs from that shown due
frameshifts in positions 1149 and 1156.
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                    IsoId=09NQC3-3; Sequence=VSP_005652, VSP_005653;
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Last annotation update)
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3; Mismatches 2;
Synonyms=RTN 4C, Nogo-C, Foocen-S;
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                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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ilarity 97.4%;
Conservative
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(TrEMBLrel. 22,
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CAB99250.1
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AAG12177.1
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01-MAR-2004 (TrEMBLrel.
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                                      Name=4;
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TISSUE=Kidney;
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUBERGR R.L., Zeberg B.L., Grouse L.H., Derge J.G.,

MISchul S.F., Zeberg B.B., Buchcucw K.H., Schaefer C.F., Bhat N.K.,

MISchul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

MISCHOL, Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

MARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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M. Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M. Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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M. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Mannara M.A.,"

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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                            Length 1163;
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                           STRAIN-BALBC;
Jin W., Long M., Li R., Ju G.;
Jun W., Long M., Li R., Ju G.;
Jun W., Long M., Li R., Ju G.;
Submirted (NAX-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX114152; AAM77068.1; -.
MOJ; MOI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IRR003388; Reticulon.
Pfam; PP02453; Reticulon.
PROSITE; PS0845; Reticulon; 1.
SEQUENCE 1163 AA; 126690 MW; 6BSF362799417EA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Reticulon 4, isoform D (RTW4 isoform B2).
                                                                                                                                                                                                            Score 906.5; DB 2;
Pred: No. 1.1e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                           98.0%;
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(TrEMBLrel. 19, I
(TrEMBLrel. 28, I
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Best Local Similarity 98.4
Matches 187; Conservative
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              SEQUENCE FROM N.A.
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25-OCT-2004 (
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SEQUENCE FROM N.A

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                                                                                       MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8; Oertle T., Huber C., van der Putten H., Schwab M.E.; "Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
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Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
A reticular rhapsody: phylogenic evolution and nomenclature of the RTN/Nogo gene family.";
FASEB J. 17:1238-1247(2003).
BMBL; AY164744; AAP47319.2;
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PR02453; Reticulon; 1.
SEQUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC016165; AAH16165.1; -.
EMBL; AX102285; AAM64247.1; -.
EMBL; AX102285; AAM64242.1; -.
GQ; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
                      Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Pred. No. 4.7e-67;
4; Mismatches 2.
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                                                                                                                                                               human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
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96.8%;
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Matches 183; Conservative
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                                                                SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Strausberg R.
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Name=Rtn4;
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Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,
Richards S., Worley K.C., Hale S., Garcia M. K., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodiquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Mones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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97.3%; Pred. No. 2.8e-67; with ematches 2; Indels
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Strauberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC071488; AAH71848.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;
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Last sequence update)
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Matches 183; Conservative
                                                                        Matches 183; Conservative
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                                Best Local Similarity
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Name=RTN4;
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DT Q6 IPN

AC Q6 IPN

AC G6 IPN

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                                                                                                                                                                                                                         122 MWVFTYVGALFNGLTLLILALISLPSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 VVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
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                                                                                                                                            216 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL
                                                                                                            62 OKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL
                             156 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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STRAIN=BALB/C;
Jin N., Li R., Long M., Shen J., Ju G.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY114153; AAM77069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon, 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;
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Last annotation update)
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98.4%; Pred. No. 6.9e-67;
ive 1; Mismatches 1.
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Job time : 26.6406 secs
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Matches 186; Conservative
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AF132045 Rattus no
AF24265 Rattus no
AJ24265 Rattus no
AJ24266 Rattus no
AJ24262 Rattus no
AJ24262 Rattus no
BC070879 Rattus no
BC070879 Rattus no
BC03212 Mus muscu
BC03212 Mus muscu
AY102280 Mus muscu
AY102284 Mus muscu
AY102281 Mus muscu
AY102281 Mus muscu
AY10228337 Mus muscu
AY102283 Mus muscu
AY102281 Mus muscu
AY102281 Mus muscu
AY102281 Mus muscu
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AY123247 Homo sapi
AY123246 Homo sapi
AX123246 Homo sapi
AX12462 Homo sapi
AX10279 Homo sapi
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Homo sapi
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Protein s
Homo sapi
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Homo sapi
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Homo sapi
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Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AF320999 H
AF333336 H
AX766050 S
BD249446 F
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CQ829486
AX195249
AB020693
AY123250
AY123249
BD270070
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Nogo and nogo receptor derived peptides for
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Patent: WO 03002602-A 1 09-JAN-2003;
YEDA RESEARCH AND DEVELOPMENT Co. LTD. (II)
Location/Qualifiers
1. 3489
/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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Sequence 1 from Patent WO03002602.
AX766046
AX766046.1 GI:32260128
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            AF132045
AF051335
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AY102281
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AB040462
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Pred. No.:
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AX766046
LOCUS
DEFINITION
ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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-MODEL=frame+ p2n.model -DEV-xlp
-Q=/Cqm2 1/USPTO spool_p/USP0830972/runat 16062005 153944 19011/app_query.fasta_1.654
-Q=/Cqm2 1/USPTO spool_p/USP0830972/runat 16062005 153944 19011/app_query.fasta_1.654
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-UNITS-bits -START=1 -END=-1 -MATRIX-bitsmand 0.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100 -MODE-LOCAL
-UNRA=sct -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRE-US0930972 @CGN 1 1 5783 @runat 16062005 153944 19011 -NCFU=6 -ICFU=3
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-NO WMAP -LARGEQÜERY -NEG SCORES=0 -WAIT -SCAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX766046 Sequence
CQ829507 Sequence
AJ242961 Rattus no
AX700396 Sequence
                                                                                                                 (without alignments)
3345.401 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                    SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                June 19, 2005, 05:38:22 ; Search time 2737.5 Seconds
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                    - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                          4708233 segs, 24227607955 residues
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925
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6 CQ829507
10 RNO242961
6 AX700396
                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BEDDEELEELEULEKFRAAGUEAAVPPAAAPLLDFSSDSVPPAPRGPLAAPPAAP
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Sciurognathi, Muridae, Murinae,
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Nogo a binding molecules and pharmaceutical use thereof Patent: WO 200452932-A 25 24-JUN-2004;
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Eukaryota, Metazoa, Chordata;
Mammalia; Eutheria; Rodentia;
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Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                      SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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/note="Foocen-m2 reticulon"
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KTSVVDLLYWRDIKKTGVVPGASLFLLLSLIVPSIVSVTAYTALALLSVTISFRIYKG
VQ AUGKSBEGHPFRAYLESEVAI SEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD
SLKRAVLAMVPTYARALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKD
AMAKIQAKIPGLKRKAD"
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PAAPKRRGSGSVDETLFALPPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLE
TAASLPSLSPLSTVSFKEHGYLGNLSAVSSSEGTI EETLNEASKELPERATNPFVNRD
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Spoilmann,A. an experimentated neurite outgrowth inhibitor and an antigen for monoclonal antibody IN-1
Nature 403 (6768), 434-439 (2000)
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Submitted (14-JUN-1999) Van der Haar M.E., Department of
Neuromorphology, Brain Research Institute, University of Zurich,
Winterthurerstrase 190, Zurich, CH-8057, SWITZERLAND
Location/Qualifiers
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/gene="nogo-A"
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Rattus norvegicus mRNA for Nogo-A protein.
AJ242961
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3463 ATCCCTGGATTGAAGCGCAAAGCAGAT 3489
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Nogo-A protein.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Van der Haar, M.E.
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REFERENCE AUTHORS TITLE JOURNAL

JOURNAL MEDLINE PUBMED

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PAT 03-APR-2003

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                                                                                                                                                                                                                       note="Rtn4-B2; alternatively spliced"
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                /organism="Rattus norvegicus"
/mol_type="mRNA"
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/gene="Rtn4"
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Rattus norvegicus RTN4-B2 (Rtn4) mRNA, complete cds; alternatively
spliced.
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Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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A reticular rhapsody: phylogenic evolution and nomenclature
KTN/Nogo gene family
FASEB J. 17 (10), 1238-1247 (2003)
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    4000
  Conservative:
Mismatches:
Indels:
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Zurich 8057, Switzerland
Location/Qualifiers
                                                                                                              US-09-830-972-2_COPY_975_1163 (1-189)
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AY164741.1 GI:32331282
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  Percent Similarity:
Best Local Similarity:
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                                           Query Match:
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ROD 19-JAN-2000 complete cds.
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YYYYLALLSVTISFRIYKGVIQAKGHQKASLFRALLSBEVAISBELVQKYSNSA
LGHYNSTIKELRRLFLYDDLVDSLKFAVLWWYFTYVGALFRGTTLLILALISLFSIPV
IYERHQVQIDHYLGELNKSYKDAMAKIQAKIPGLKRRKAD"
                          ATCCAGABAATCAGATGAAGGCCACCCATTCAGGGGCATATTTAGAATCTGAAGGTTGTATA 1510
                                                                                               TIGATETICACTETATATETICATECETTICATECATECTETACATACTACTACTICATITATA 1690
                                                                                                                                                                                                                                                                                                                                 AlaLeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAsp 160
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                         1571 AAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCTGAAGTTTGCAGTG
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Direct Submission
Submitted (26-FEB-1998) Biochemistry, Dartmouth Medical School,
Hanover, NH 03755, USA
Location/Qualifiers
                                                                            SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
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by GenBank
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       IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="adipocyte" 57. .656 /note="vp20; similar to chicken Rex encoded by GenBar Accession Number U17605, to rat Rex encoded by GenBar neuroendocrine-specific protein C encoded by GenBar Accession Number L10335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus GLUT4 vesicle 20kDa protein mRNA, AF051335.1 GI:6016998
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/product="GLUT4 vesicle 20kDa protein"
/protein_id="AAP01564.1"
/db_xref="G1:0616999"
/db_xref="G1:0616999"
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Rattus norvegicus
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AF051335
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DEFINITION
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BRQPSWERSTSAAPABSLPPAAAVLPSKLPEDDEPPRRPPPPAGASPLAEFAAPPST
PAAPKRRGSSVDETLFALPAASPVIPSSAVVDLLYWRDIKKTGVYPGASLFELLSL
TVFSIVSVTAYIALLSYN TIKTYGVIQAIQKSDEGHPFRAYLESEVAISBELVQ
KYSNSALGHVNSTIRELRELPUNDLVDSVDRYKPAVLMWYTYVGALFNGITLLILALIS
LFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGKKRAD"
                                                                                           mRNA linear ROD 18-MAY-1999 alternate splice product,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="vascular smooth muscle"
/dev stage="3 months old"
701._.1840
/note="member of reticulon gene family, alternate splice
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                                                                                                                                                                                                                                                                                                                                   the reticulon gene family in rat: One
                                                                                                                                                                                                                                                                                                        Ito, T. and Schwartz, S.M.
Cloning of a member of the reticulon gene family minor splice variants
Unpublished
(Dases 1 to 2782)
Ito, T. and Schwartz, S.M.
Direct Submission
Submitted (27-FEB-1999) Pathology, University of
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Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualifiers

1. 2782
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar-Kyoto"
/db_xrof="taxon:10116"
/sex="male"
AF132045
2782 bp
ARattus norvegicus foocen-m2 mRNA,
complete cds.
AF132045
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'db_xref="GI:4838513"
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/product="foocen-m2"
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/gene="nogo-C"
/function="unknown"
/function="unknown"
/note="The nogo gene encodes different transcripts. Nogo-A
en -C have a unique 5' end but share the same 3' end"
/codon_start=1
/product="Nogo-C protein"
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IYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGIKRRAD"
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                                                                                                           Chen, M.S., Huber, A.B., van der Haar, M.E., Frank, M., Schnell, L. Spillmann, A.A., Christ, F. and Schwab, M.E. Nogo-A is a myelin-associated neurite outgrowth inhibitor and antigen for moncolonal antibody IN-1 Nature 403 (6768), 434-439 (2000)
Nogo-C protein.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleosu
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                   Direct Submission
Submitted (14-JUN-1999) Van der Haar M.E., Department of
Neuromorphology, Brain Research Institute, University of
Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND
Related sequences: AJ242961-2.
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Mismatches:
Indels:
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/db_xref="taxon:10116"
1. .1568
/gene="nogo-C"
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Van der Haar, M.E.
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                /note="tyrosine kinase site; phosphorylation site"
evidence=not_experimental
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/evidence=not_experimental
480...542
/note="transmembrane-region site"
/evidence=not_experimental
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/note="N-linked; glycosylation site"
/evidence=not_experimental
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                                                 132. .194
/note="transmembrane-region site"
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Van der Haar, M.E.
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EEDDEDLEELEVLERKPAAGLSAAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAP
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PRAPKRRGSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSYTAYIALALLSV
TISFRIYKGYIQAIQKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR
LFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYL
                                                                                                                                                                                                                                                                                                                                             mRNA linear ROD 30-JUN-2003 mRNA, complete cd8; alternatively
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Oertle, T. and Schwab, M.E.
Direct Submission
Submitted (16-07-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr. 190,
Zurich 8057, Switzerland
Location/Qualifiers
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 2156)
Oertle, T., Klinger, M., Stuermer, C.A. and Schwab, M.E.
A reticular rhapsody: phylogenic evolution and nomenclature of RTN/Nogo gene family
FASEB J. 17 (10), 1238-1247 (2003)
                                                                                 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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Rattus norvegicus RTN4-B1 (Rtn4)
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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Hansen,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Maduro,Q.L., Masterins,E., Mastrian,S.D.,McCloskey,J.C.,
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Submitted (17-MRZ-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Email: cgapbb.r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequenching by: National Institutes of Health Intramural
Sequenching Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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                     Submitted (14-JUN-1999) Van der Haar M.E., Department of Neuromorphology, Brain Research Institute, University of Zurich, Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND Related sequence: AJ242961.

Location/Qualifiers
1. 2156
/organism="mRNA"
/db_xref="taxon:10116"
1. 2156
/geneme="nogo-B"
1. 2171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGCGCGTGATCCAGGCTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1065 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="splice variant of nogo-A"
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                                                                                                                                                                                                                                                                                                                                                                                                          'function="unknown"
                                                                                                                                                                                                                                                                                                                                                                               /gene="nogo-B"
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99.57%
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Best Local Similari
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                                                                                                                                                                                                                                                                                              gene
                                 JOURNAL
                                                                                                                  COMMENT
FEATURES
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   TITLE
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TELEPROPPPYERAMSVALTKYSDAKERISTERESFRANAAQEABAPYISTACDLIKETKLS
TEPSPGFSNYSEIAKEEKSVPDHCELVDDSSPESEPVDLFSDDSIPEVPQTGERAWL
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OKKIDGHPTVGALFLILLILLILLILLISLFSIFVYSTYNYSTIKELRFLVDDLVVSLKFA
OKKIDGHPTVGALFRANDENGSTANANAKAKABAKTA
                                         1250 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTACTGATTTTAGCT 1309
                                                                                                                                                                                                                                                                                                                          ROD 03-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished

2 (bases 1 to 1738)

2 (bases 1 to 1738)

Direct Submission

Submitted (29-OCT-2001) Hirokazu Tozaki, Division of Brain

Function, National Institute of Genetics; Yata 1111, Mishima,

Bhizuoka 411-8540, Japan (E-mail:htozaki@lab.nig.ac.jp,

URL:http://www.nig.ac.jp/home-j.html, Tel:81-55-981-6721(ex.6721),

Fax:81-55-981-6722)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                      TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tozaki,H. and Hirata,T.
The partial sequence of mouse nogo-A cDNA clone#4109
                                                                                                                                                                                                                                                                                                                          linear
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187
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                                                                                                                                                                                                                                                                                                                        AB073672 1738 bp mRNA
Mus musculus mRNA for Nogo-A, partial cds.
AB073672
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Nogo-A"
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                            1430 CCTGGATTGAAGCGCAAAGCAGAT 1453
                                                                                                                                                                                                   ProGlyLeuLysArgLysAlaAsp 189
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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/gene="Nogo-A"
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917.00
99.47%
98.94%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                                                                                                                        162
                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
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JOURNAL
                                                                                                                                                                                                                                                                                  RESULT 12
AB073672
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BEDBEDLEELELEVLERKRPAGLSAAN PPRAAALLDFSSDSVPPARKPETLAAPPRAP
ERQDSWERSPAAPSSLPPAAAVLSKILPEDDEPPARPPPPAGASPLAEPAAPPST
PAAPKRRGSGSVVVDLLYWRDIKKTGVVFGASLPLLLSLTVFSIVSVTAYIALALLSV
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LFLVDDLVDSLKRAVLMMVPTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1070 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 1129
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Series: IRAK Plate: 175 Row: a Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929187
This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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                                                                                                                                     /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_tef="taxon:10116"
/clone="IMAGB:7096609"
/tissue_type="Lung, rat (Brown Norway)"
/clone_Tib="NIH MGC_231"
/lab_host="DH108"
/note="Vector: pExpress1"
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                      gene="ktn4"
note="synonyms: Vp20, NI-250"
db_xref="LocusID:83765"
db_xref="RGD:620989"
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Matches:
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'gene="Rtn4"
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Best Local Similarity:
Query Match:
DB:
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 56 Row: k Column: 2.
Location/Qualifiers
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Web site: http://www.nisc.nih.gov/
Rob site: http://www.nisc.nih.gov/
Achter, n., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse." /clone lib="MOI CGAP_Mam6" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSPVSY
DGIKLEPENPPPYEEAMSVALKTSDAKEEIKEPESFNAAAQEAEAPYISIACDLIKET
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KKETISLOMEBPNTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEPPTFVSAKDDS
PKEYTDLEVSNKSEIANVOSGANSLPCSELPCDLSFKNTYPKDEAHVSDEFSKSRSSV
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SVVDLLYWRDI KKTGVVFGASLFLLLSLTVFSI VSVTAYI ALALLSVTI SFRI YKGVI
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KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAM
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/gene="Rtn4"
/note="Reticulon; Region: Reticulon. Reticulon, also know
                                                                                                                                                             Direct Submission
Submitted (06-UTNN-2002) National Institutes of Health, Mammalian
Submitted (06-UTNN-2002), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="synonyms: ASY, NOGO, NSP-CL, C130026I10Rik"
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
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Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myes, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
                                   1288
                                                                                                                                                                                                                                                                                                                      1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1349 ATCCAGAAATCAGATGAAGGCCACCATTCAGGGCATATTTGGAATCTGAAGTTGCCATA 1408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1529 TTGATGTGGGTATTTACTTACGTTGGTGCCTTGTTCAATGGTTTGACACTACTGATTTA 1588
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 2958)
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                                                                                                                                                                      AGCTTATTCCTGCTGCTGTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATT
                                                                                                                                                                                                                                                           41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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      SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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as neuroendocrine-specific protein (NSP), is a protein of unknown function which associates with the endoplasmic reticulum. This family represents the C-terminal domain of the three reticulun isoforms and their homologues" /db_xref="CDD:pfam02453"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Basea I to 3812)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Mus musculus reticulon 4, mRNA (cDNA clone IMAGE:5366860), partial
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                                                                                                                                                                                                                                                                                                                                                                                                              21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaLeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValileGlnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                                                                                                         US-09-830-972-2_COPY_975_1163 (1-189) x BC032192 (1-2958)
                                                                                                                                                       Length:
Matches:
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Mismatches:
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BC032272.1 GI:22749634
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USAM

UNITADE Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs.remail.nih.gov

Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc.mgc@nhgri.nih.gov/

Contact: nisc.mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,

Blakesley,R.W., Cannite,S., Gunn,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiallo,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.E., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McBwan, P.J., McKernan, K.J., Malek, J.A., Gunardne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Retteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schain, J.B., Jones, S.J. and Marra, M.A., Green, E.D., Human and mouse cDNA sequences

N. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="Bye, retina, mouse strain C57Bl\6"
/clone lib="NIH MGC_94"
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LPSLSPLSTVSFKEHGYLGNLSAVASTEGTIEETLNEASRELPERATNPFVNRESABF
SVLEYSEGGSSFNGSFNGSSAMLVENTEBVYTKSKOKTEDLVCSAALINPQESPATLT
KVVLEYGCOWGSPENGSSAMLVENTEBVATVEBYTYTKESTOKTHOKCSAALINPQESPATLT
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TTDNLSKYTEAVATWPEGITPDLVQBACESELNEATGTKLAYETKVDLVOTSBALQE
SITPTAQLCPSFERARATFSPVLPDIVMEAPINSLLPSTGASVAQPSASPLEVPSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAAQEAEAPYISIACDLIKE
TKLSTEPSPEFSNYSEIAKFEKSVPDHCELVDDSSPESEPVDLFSDDSIPEVPQTQEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRLEFLVDDLVDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAla
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187
1
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Matches:
Conservative:
Mismatches:
  organism="Mus musculus"
                                                          db_xref="taxon:10090"
chromosome="11"
                                                                                                                                                                                                                         evidence=experimental
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                                                                                                                                                                                                                                                                                                                  codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3174. .4063
/gene="Rtn4"
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gene="Rtn4"
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                                                                                                                                                                                                                                                                                                                                                  AUCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATA 2556
                                                                                                                                                                                                                                                                                                                                                                                                                                2617 AAAGAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTG 2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2677 TIGATGIGGGTATTTACTTACGTIGGTGCCTTGTTCAATGGTTTGACACTACTGATTTTA 2736
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
1 (Dases 1 to 4063)
Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Genomic Structure and Functional Characterisation of the Promoters
of Human and Mouse nogo/rtn4
of Human and Mouse (2), 299-323 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                      SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
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Oertle, T. and Schwab, M.E.
Direct Submission
Submitted (07-MAX-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
                                                                                      2317 TCAGTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC
                                                                                                                                SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                          2377 AGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATT
                                                                                                                                                                                                                       41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                2437 GCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAAGGGTGTGATCCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                       1 SerValValAspLeuLeuTyrTrpArgAsplleLysLysTyrGlyValValPheGlyAla
US-09-830-972-2_COPY_975_1163 (1-189) x BC032272 (1-3815)
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Van der Putten, H.
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ROSGSSVPRAAABASLAPSLAPAAATLSKLEPDDEPPRPRPPARAABASPLAEPAPPSTPAAP
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KVVEEDGVASSFNGSSFNGSSAMLVENTERVTYKESTOKEDVAFA
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RANMESKVOKKCFEDSLEQKGHGKDSESRNENASPPRTPELVKDGSRAYITCDSFSSA
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TIDNISKYTERAVARHVEGIPDLVOGRAGESELMAAROTKIAYETKVDLVOTSBAIQE
TI YPTAQLCPS FEERATSPSPLYDI VMEAPLNSILPSTGASVAQPSASPLEVSPVS
YDGI KLEPENPPPYEEAMSVALKTSDSKEEI KEPESFNAAAQEAEAPY ISIACDLIKE
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                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3099 AGCITATICCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATT
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                            l. .4518
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Casavant, T., Soares, M.B.
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schemen, C.M., Schuler, G. Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wang, J., Hsieh, R.K.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonando, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstain, M.J., Usdin, T.B., Toshiyuki, S.,
Carnicci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosk, S.A., McEwant, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Villalon, D.K., Muzny, S.J., Soarcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Soderk, S.A., Lux, Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                       3084 CATTATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAGCAAAA 3143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCO56373 4518 bp mRNA linear ROD 08-OCT-2003
Mus musculus CDNA clone MGC:73436 IMAGE:6847916, complete cds.
                                                                                                           2964 TTGATGTGGGTATTTACTTACGTTGGTGCCTTGTTCAATGGTTTGACACTACTGATTTTA 3023
                                                                                                                                                                                                                   2904 AAAGAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTG 2963
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Trisue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo, Mr. F. Akabogu, I., Bair, J., Crouch, K., Davis, A.,
Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J.,
                                                      140
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 4518)
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Submitted (11-AUG-2003) National Institutes of Health, Mammalian
Submitted (11-AUG-2003) Cancer Genomics Office, National Cancer
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                                                    LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                            AlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAsp
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rroc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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VSKVPLLLPNVSALESQIEMGNIVKPKVLTKRABEKLJSPDTEKEDRSLTAVLSAELINK
TSVVDLLYMRDIKKTGVYFGASLFLLILSLTVPSIVSTAYIALLSVTISFRIYKGV
IQAIOKESDERPPRAYLESBVAISEBLVQKYSNSALGHYNSTIKELRRLFLVDDLVDS
LKFAVLMMVFTYVGALFNGLTLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDA
MAKIQARI PGAKRKAE"
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TKLSTEPSPEFSNYSEIAKFEKSVPDHCELVDDSSPESEPVDLFSDDSIPEVPQTQEE
AVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDAASNEIPTL
TKKETISLQMEBFNTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDD
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Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.
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LRSLSPLSTVGSKGAHGYLGNLSAVASTGGTIEETLNEAARELPERATNPPVNRSSAEF
                                                                                                        Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced. AY102284
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KVVKEDGVMSPEKTMDIFNEMKMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA
RANMESKVDKKCFEDSLEQKGHGKDSESRNENASFPRTPELVKDGSRAYITCDSFSSA
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TIDNISKYTRINVATKNEGLIPPLIVQEACESELNEATGTKI AYETKVIDVYJSERIQE
SI YPTAQLCPS FEERBATPSPVLIPDI VMEAPLINSLL PSTGAS VAQPSASPLEVPSPVS
SI YPTAQLCES FEERBANSVALKTSDSKEEI KRPESFNAAQEARAPY ISIACDLIKE
                                                   Oertle,T., Hubor,C., van der Putten,H. and Schwab,M.E.
Genomic Structure and Functional Characterisation of the Promoters
of Human and Mouse nogo/trn4
J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4627)
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
Location/Qualifiers
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Certle, T. and Schwab, M.E.
Direct Submission
Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
                        AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
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/strain="129/8vG7"
/db xref="taxon:10090"
/chromosome="11"
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/gene="Rtn4"
/note="synonym: nogo"
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/product="RTN4"
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/gene="Rtn4"
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/gene="Rtn4"
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Van der Putten, H.
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Submitted (05-DEC-2000) School of Biochemistry and Genetics, The Medical School, Newcastle University, Newcastle upon Tyne, Tyne and Wear NE2 4HH, UK
 987 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATA 1046
                                                                                                                                                                            1167 TTGATGTGGGTATTTACTTACGTTGCTGCCTTGTTCAATGGTTTGACACTACTGATTTTA 1226
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SYAYIALLSVTISFRIV
YYAYIALLSVTISELSVTISFRIVAVIQANVEHPFRAYLGSBVAISBELVQKYSNSA
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                           SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr11e 100
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 734)
                                                                                                      1107 AAAGAATTGAGGCGTCTCTTCTTAGTTGATTAGTTGATTCCCTGAAGTTTGCAGTG
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                                                  1047 TCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATA
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Mus musculus vp20/RTN4C protein mRNA, complete cds
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Mouse vp20/RTN4C cDNA
Unpublished to 734)
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Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.
Genomic Structure and Functional Characterisation of the Promoters
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                   Submitted (07-MAY-2002) Brain Research Institute, University Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland
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Matches:
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Mismatches:
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Oertle, T. and Schwab, M.E.
Direct Submission
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Van der Putten, H.
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Mismatches:
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Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.

Genomic Structure and Functional Characterisation of the Promoters of Human and Mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
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                                                   ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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Certle, T. and Schwab, M.E.
Direct Submission
Submitted (07-MAY-2002) Brain Research Institute, University
Surich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
      US-09-830-972-2_COPY_975_1163 (1-189) x AF326337 (1-734)
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Van der Putten, H.
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                                                              AY102281 2209 bp mRNA linear ROD 29-JAN-2003
Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.
AY102281
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RRGSGSVVDDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSYTAYIALLSVTISF
RTKGVJQA QKSDEGHPRAYLESEVAISEELVQKYSNSALGHVNSTIKELRLFLV
DDLVDSLKFAYLMWVFTYVGALFNGTLLLILALISLSFSIPVIYERHQAQIDHYLGGLAN
KSYKDAMAKIQAKIDGLKRKAE"
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 2209)
Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E. Genomic Structure and Punctional Characterisation of the Promoters of Human and Mouse nogo/rtn4
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Direct Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Submitted (08-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland
Location/Qualifiers
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Oertle, T. and Schwab, M.E.
Direct Submission
Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="NOGO-B; RTN4-B1; alternatively spliced"
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/db_xref="G1:23379811"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:10090"
chromosome="11"
CCTGGATTGAAGCGCAAAGCAGAA 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Rtn4"
/note="synonym: nogo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="129/SvcJ7"
                                                                                                                                              Mus musculus (house mouse)
                                                                                                              AY102281.1 GI:23379810
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'gene="Rtn4"
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/gene="Rtn4"
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Van der Putten, H.
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                                RESULT 21
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ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

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993 GAGGAATTGGTTCAGAAATATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 1052
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LYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYB
STREPENPPPYEEAMSVSLKKVSGITERIKEENENDMCFKKQKLLIYLLHVDLIKET
KLGAREPADPFSDVSEMAKVEQPVPHSELVEDSSPDSEPVDLFSDDSIPDVPCKQUET
WHLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKOTLLPDEVST
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAAACGGCCTACATTGCC
                                                                                               LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
  LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arussou
Homo sapiens brain my043 protein mRNA, complete cds.
AF063601
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/protein_id="AAG43160.1"
/db_xref="GI:12002034"
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Mao,Y.M., Xie,Y. and Zheng,Z.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="011a12"
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/dev_stage="fetus"
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ACCESSION
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AF063601
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WEVKOSKEDSDMLAAGGKIESNLESKVÜKKCPADSLEQTNHEKÖSESSNÜDTSFPST
PEGIKORSGATITCAPPINAATESITYNIPIPLICABPTSGENTYDEKKLESKAQIVTEK
PEGIKORSGATITCAPPINAATESITYNIPIPLICABPTSGENTYDEKKAQIVTEK
PEGIKORSGATITCAPPINAATESITYNIPIPLICAROPSELTYDIVQEAGESELNEY
TGTKIAYETKNDLVQTSEVNQESLYPAAQLCPSFESEATPSPVLPDIVWEAPLINSAV
PSGAGASIOJESSEPLEARSVYTESITHEPRINPPPYEBAMSVESKKKVSGOTKEBIKEPEN
INAALQETRAPYI STACDIITGTKLSAEPAPDFSDYSEMAKVEQPVEDHSSELVEDSSP
DSEPVDLFSDDSIPDVYCOTTLPPPSLAKKKIPALENFESFESMIEYKNDDSSP
YLESFKLSTONYKOTTLPPPTLISKTIOSFSKKARIPLGVGMELSTAYKSDDDLFISKALPPEGGKP
YLESFKLSTONYKOTTLPPPTLISKTIOSFSKLAREYTDLEVSHKSEIANRPGGAGSIPCTE
LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALATQAEISSIVKFKV
                                                                                                                                                                                                                                                                                             LVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLS
LTVBSIVSYTAXIALALLSVTISFRIYKGVIQA IQKSDEGPPRAYLESEVAISEELV
GYSBNSALGHYNCTI KELRRLFLADLUDSLKFAVLWWYFTYVGALFNGLTLLILALI
SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2614 AAGGAACTCAGGCGCCTCTTCTTAGTTGATTTTAGTTGATTCTCTGAAGTTTGCAGTG 2673
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      novel Nogo-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2374 AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGGCGTAACAGCCTAACACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2494 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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No
Developmentally-regulated alternative splicing in a Unpublished
                                                                                                  of Neurosciences,
China
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184
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_txef="taxon:9606"
1. .2883
/note="alternatively spliced"
                                        2 (bases 1 to 2883)
Jin,W.-L. and Ju,G.
Direct Submission
Submitted (12-NOV-2000) Institute
West Road, Xian, Shannxi 710032, C
Location/Qualifiers
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AF320999.1 GI:11878277
                    DSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIOPKVEEKISFSDD
FSKNGSATSKVLLLPPDVSALATQAEIESIVKPVLVKEAEKKLPSDTEKEDRSPSAI
FSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLIVFSIVSYTAYTALALLSVTIS
FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFL
VDDLVDSLKFRALLMWPTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLA
NKNVKDAMAKIQAKIPGLKRKAE"
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2883)
Jin,W.-L. and Ju,G.
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AF320999
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Homo sapiens
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LOCUS
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                    Pred. No.:
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1 (Dases I to 3491)

2hou, Z.M., Sha, J.H., Li,J.M., Lin,M., Zhu,H., Zhou,Y.D., Wang,L.R., Zhou,H., Wang,Y.Q. and Zhou,K.Y.

Expression of a novel reticulon-like gene in human testis

21857060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / translation="MOLKEQPCNTISAGQEDFPSVLLETAASLPSLSPLSAASFKEHE
YLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSP
KASSAVIVANDREELIVKTKOEEKLEVSNNTLLHONQQELPTALTKLVKEDEVSEKAK
DSFREKRVAVEAPMEERTADFPERVWEVVDSKEDSDMLAAGGKIESNLESVUDKG
PADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIPPL
                                                 AF333336 3491 bp mRNA linear PRI 27-MAY-2003
Homo sapiens testis specific reticulon 5 protein mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGDPTSENKTDEKKI EEKKAQI VTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE
SVVANNPEGLTPDLVQEACESBLSEVTOKTIATSTKNDLVQTSEVNGSELYPAQLCP
SPEESEATPSPVLD1 VMEAPLNSAVPSAGASVIQESSPLEASSVNYESI KHEPEND
PPYEERAMSVSLKKVSGI KEEI KEPENI NAALQETEAPYI SI ACDLI KETKLSAEPADD
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KIQAKIPGLKRKAE"
3402. .3407
2674 TIGAIGIGGCIAITIACCIAIGIIGGIGCCIIGIIIAAIGGICIGACACIACIGAITIIG 2733
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ETSPESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPL
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AIQKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLK
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Shaju,J.H., Zhou,Z.M., and Li,J.M.
Direct Submission
Submitted (04-JAN-2001) Key Lab of Reproductive Medicine, Nanjing
Medical University, Han Zhong Road 140, Nanjing, Jiangsu 210029,
                                   AlaLeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAgp
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product="testis specific reticulon 5 protein"
product="testis apacific"
productin id="AAK20831.1"
db_xref="GI:13377628"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="testis"
/dev_stage="adult"
179-_3139
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note="reticulon"
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AUTHORS
TITLE
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AUTHORS
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Nogo and nogo receptor derived peptides for
neuroprotection
Patent: WO 03002602-A 5 09-JAN-2003;
YEDA RESEARCH AND DEVELOPMENT CO. LTD. (IL.
Location/Qualifiers
1. .3576
/ organism="Homo sapiens"
/ mol_type="unassigned DNA"
/ db_xref="taxon:9606"
1. .3576
Length:
Matches:
Conservative:
Mismatches:
Indels:
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Sequence 5 from Patent WO03002602.
AX766050
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12NS/ PC
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PC C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/56//
G01N33/566//
PC C12P21/08,C12N15/00,C12N5/00
CC Protein similar to neuroendrocrine-specific protein, and C
9916898.1 PI
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Location/Qualifiers
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PR 22-JUL-1998 GB 9816024.5,19-JUL-1999 GB DAVID MICHALOVICH, RABINDER KUMAR PRINJHA
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Matches:
Conservative:
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source
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Or 20022200 AA.

Homo sapiens (human)

Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 3579)

Michalovich, D. and Prinjha, R.K.

Michalovich, D. and Prinjha, R.K.

Protein similar to neuroendrocrine-specific protein, and encoding patent: JP 2002522016-A 1 23-JUL-2002;

SMITHKLINE BEECHAM PLC
OS Homo sapiens (human)
PN JP 2002522016-A/1

PD 23-JUL-2002

PF 21-JUL-1999 JP 2000561310
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EDEDLEELEVLERREPAAGLSAAPVPTAPAAGAPIADFGNDFVPPAPRRGPLAAPPVAP
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QKYSNSALGHVNCTIKELRRLFLVDDLVDSLKPAVLMMVFTYVGALFNGLTLLILALI
SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
HERZEGOVINA
                                                                                                                                                                                                                                                              Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Nature 403 (6768), 383-384 (2000)
Homo sapiens mRNA for Nogo-A protein (Nogo gene)
AJ251383
AJ251383.1 GI:9408095
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/db_xref="taxon:9606"
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Nogo gene; Nogo-A protein.
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Michalovich, D.
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Alignment Scores:
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184
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184
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98.94
Mismatches:
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Query Match:
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US-09-830-972-2_COPY_975_1163 (1-189) x HSA251383 (1-3579)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        3070 AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAAACAGTCTACATT
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SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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/note="unnamed protein product; Human NogoA"
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Sequence 4 from Patent WO2004052932.
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/db_xref="GI:49732809"
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EFFSDSSEPTEI DEFPTLISSKTOSFSKLAREYTDLEVSHKESIANAPDGAGSLPCTE
LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALATQAEIESIVKPKV
LIVKABKKLPSOTTKERRSPSALFSAELSKTSVVDLLYWRDIKKTGVVPGASLFLLLS
LIVFSIVSYTSATIALLSVTISFRIYGVIQAIQKSDEGHPFRAYLESEVAISEELUS
SKYSNSALGHTWITKELRELPUDDLVDSLKRAVLMWYFTYVGALFSEVAISEELUS
SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRAE"
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TGTKLAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAV
PSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPEN
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LVKBAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLS
LTVPSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELV
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EDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLVAP
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SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                      Nogo receptor-mediated blockade of Patent: WO 0151520-A 5 19-JUL-2001; YALE UNIVERSITY (US)
                                                                                                                                                                                                                                                                                                                          /mol_type="unassigned RNA"
/db xref="taxon:9606"
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/db_xref="GI:15385810"
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/organism="Homo sapiens"
                                                                                                                                                                                                                               Location/Qualifiers
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Mammalia; Eutheria;
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                                                                                              Strittmatter, S.M.
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PSLSPLSAASPKEHFYLGNLSTVLPTEGTLQRINVSBASKEVSEKAKTLLIDRDLTEFS
ELYSEMGSSFSVSPKAEAVIVANPREEIIVKNXDEEKKLVSNNILHNQGELPTALT
KLYKEDERVYSSEKANSTSKARVATAAPMEEYADFKPFERWEVKSKEDSDMLAAG
GKIESNLESKVDKKCFADSLEQTNHEKOSESSNDDTSFPSTPEGIKORSGAYITCAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 4053)
Ohara, O., Suyama, M., Kikuno, R., Nagase, T. and Ishikawa, K.
Oharato, Suyama, M., Kikuno, R., Nagase, T. and Ishikawa, K.
Direct Submission
Liaboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
Location/Qualifiers
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                                                                                                                                     3624 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 3683
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
3444 AAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTG
                                     HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                           3504 TIGATGIGGGTATITACCTATGITGGIGCCTTGTTTAATGGICTGACACTACTGATTTTG
                                                                                                             AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                                                                                                                                                                                       AB020693 4053 bp mRNA linear
Homo sapiens mRNA for KIAA0886 protein, partial cds
AB020693
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'codon_start=1
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/clone_lib="pBluescriptII SK plus"
/dev_stage="adult"
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/protein_id="BAA74909.2"
/db_xref="GI:40788974"
                                                                                                                                                                                                                                                                                         3684 ATCCCTGGATTGAAGCGCAAAGCTGAA 3710
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hk07722"
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/gene="KIAA0886"
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ETDYVTTDMITTKVTEEVVANMPEGILFDLVOEACESELNEVTGTKIAYETKMDLVOTS
EWWGESIYPAAQICCPSFEESEATPSPVLPDIVWEAPLNSAVESAGSVIQPSSSPLEA
SSVNYESIKHEPENPPPYSEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIAC
DIJKETKLSAEPAPDFSDYSEMAKVEQPVEPHSELVEDSSPDSBPVDLFSDDSIPDVP
QKQDETVMLVKESLITETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLL
PDRVYTLSKKEKITPLQMEBLSTAYKSNDDLFISKRACYBSPT RETFETSBSSPTEILDBEPT
IJSSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKVIQPRVEEK
ISFSDDFSKNGSATSKVLLLPPDVSALATQAEIESIVVKRVLVKEAEKKLPSDTEKED
RSPALIESAELSKTSVVDLLYWRDIKKTGVVFGASIFLLLSLTVFSIVGSTATALAL
LSVTISFRIYKGVIQAIQKSDEAPPRAYLESEVAISEELVQCYSNSALGHVNCTIKE
LRRLFLVDDLVDSLKKFVLAMVFTYVGALFNGITLLILALISLFSVPVIYERHQAQID
HYLGLANKNVKDAMAKIQAKIPGLKRAE"
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Homo sapiens RTN4 isoform G (RTN4) mRNA, complete cds;
alternatively spliced.
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                                                                                                                                                                                                                                                                                                                           Homo sapiens Butazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4060) Certle, T., Huber, C., van der Putten, H. and Schwab, M.E. Genomic Structure and functional characterisation of the promoters of human and mouse nogo/rtn4
                                                                                                 2 (bases 1 to 4060)
Van der Putten, H.
Van der Putten, H.
Subriect Submissien

3 (base)

3 (bases 1 to 4060)

Oertle, T and Schwab, M.E.

Direct Submission

Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4060
184
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                     gene="RTN4"
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908.00
98.94%
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98.16%
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sapiens (human)
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Best Local Similarity:
Query Match:
                                                                                  22376540
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        ORGANISM
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AUTHORS
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SOURCE
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4070 bp mRNA linear PRI 23-SEP-2003 Homo sapiens RTN4 isoform F (RTN4) mRNA, complete cds; alternatively spliced.
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1 (bases 1 to 4070)
Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basesl, Swirtzerland
(bases 1 to 4070)
Oertle, T. and Schwab, M.E.
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Submitted (17-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
                                   2525 TCAGTTGTTGACTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGTTTGGTGCC
                                                                                                                                                           2585 AGCCTATTCCTGCTGCTGCTTTCATTGACAGTATTCCAGCATTGTGAGCGTAACAGCCTACATT
                                                                                                                                                                                                                                                                              2645 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 AlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAsp
SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                     SerLeuPheLeuLeuLeuSerLeuThrValPheSerlleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                                       61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                              41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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1. .4070
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Van der Putten, H.
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3 ServalvalAspLeuLeuTyrTrpArgAsplleLysLysThrGlyValValPheGlyAla 20
                                                                                                                 C12N5/10, C12P21/02, G01N33/15, G01N33/50, C12N15/00, A61K37/02, PC
                                                                                                                                                                                                   3015 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGGAAAA 3074
                                                                                                                                                                                                                                                                                                                                                 PAT 17-JUL-2003
                                                                                                                                                               161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                           141 AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 4093)
Valenzuela,D., Yuan,O., Hoffman,H., Hall,J. and Rapiejko,P. Secreted proteins and polynucleotides encoding them
Patent: JP 2002537757-A 32 12-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A61P31/04, A61P31/10, A61P31/12, A61P31/18, A61P35/00, A61P37/00,
                                       2895 TIGATGIGGGTATTIACCTATGTIGGTGCCCTTGTTTAATGGTCTGACACTACTTTTG
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Secreted proteins and polynucleotides encoding them.
BD270070
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Matches:
Conservative:
Mismatches:
Indels:
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JP 2002537757-A/32.
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Homo sapiens
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Best Local Similarity:
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BD270070
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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No:
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AUTHORS
TITLE
JOURNAL
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FTSFESMIEYENKEKLSALPPEGGKPVLIESFKLISLDNITCDTLLDDEVSTLSKKEKIPL
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KAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVVSSEKAK
DSFNEKRVAVEAPMREEYADFKRFERVWEVKOSKEDSDMLAAGGKIESKUVEKKV
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'note="RTN4-F; alternatively spliced"
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Matches:
Conservative:
Mismatches:
Indels:
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1. .4070
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                                                                                                                                              'note="synonym: NOGO"
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                                                                                                                                                         1. .143
/gene="RTN4"
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908.00
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                                                                        map="2p16"
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Best Local Similarity:
Query Match:
DB:
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/gene="RTN4" A
/note="RTN4" Aa; alternatively spliced"
/codon_start=1
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'gene="RTN4"
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Homo sapiens RTN4 isoform Aa (RTN4) mRNA, complete cds;
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Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland
1 (bases 1 to 4102)
Oertle,T. and Schwab,M.E.
Direct Submission
Submitted (17-MAY-2002) Brain Research Institute, University of Surich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland
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        SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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/chromosome="2"
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Van der Putten, H.
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                  SFEESEATPSPVLPDIVMEAPLANSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENP
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ETSPESMIEVENEKALSALPPEGGKPYLESPKLSLDNTKOTILLDDEVSTLSKKKEIPL
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FADSLEQTNHEKDSESSNDDYSPPSTPEGIKOKSAGATITGFPRPRAAFESIATNIPPL
LGDPTSENKTDEKKIEBKKAQIYTEKNTSTRYSNPEJVAAQDSETDYYTTDNITKVTB
EVVANMPEGILPDLVQEACESELNEVTGTKIAYETKODLVQTSEVMQESLYPAAQLCP
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KAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVVSSEKAK
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Oerses 1 to 4109)
Oersle, T., Huber, C., van der Putten, H. and Schwab, M.E.
Genomic structure and functional characterisation of the promoters
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AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                               HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
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Submitted (17-MAY-2002) Brain Research Institute, University
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
                                                                                                                                                                                                      Homo sapiens RTN4 isoform E (RTN4) mRNA, complete cds; AX123248
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'note="RTM4-E; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                     of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                              3107 ATCCCTGGATTGAAGCGCAAAGCTGAA 3133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inc., Basel, Switzerland
3 (bases 1 to 4109)
Oertle, T. and Schwab, M.E.
Direct Submission
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Homo sapiens
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Van der Putten, H.
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AUTHORS
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YTDLEVSHKKSILANAPDGAGGLPCTELPHDISLKNYOPKVEEKISFSDDFSKNGSATS
KVULLPPDVSALATQARIBSIVKPKYLVKGARKKLPSDTSKUSDSSTSTS
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ALOKSDBGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRELFUDDLVDSLK
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KTQAKIPGHEKRAB"

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Homo sapiens RTN4 isoform D (RTN4) mRNA, complete cds;
alternatively spliced.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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FAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA
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Genomic structure and functional characterisation of the promoters
of human and mouse nogo/trn4
J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                                                                                            2 (bases 1 to 4123)
Van der Putten,H.
Direct Submission
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland
3 (bases 1 to 4123)
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| 197. .3157
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4160 bp mRNA linear PRI 23-SEP-2003 Homo sapiens RTN4 isoform Ab (RTN4) mRNA, complete cds; alternatively spliced.
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1 (bases 1 to 4160)
Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E. Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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Van der Putten, H.
Direct Submission
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
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                                                                                                                                                                                                  2768 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
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                                                                                                             2708 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGAGTCTAAGGT
                                                                                                                                                                                                                                                   81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                                                                                                                                                                                                                                                                                                                          2888 AAGGAACTCAGGCGCTCTTCTTAGTTGATTATTAGTTGATTCTCTGAAGTTTGCTTGAAGTTTGCTGAAGTT
21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                    61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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3 (bases 1 to 4160)
Oertle, T. and Schwab, M.B.
Direct Submission
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| /note="reticulon family"
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Homo sapiens
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SFEESEATPSPVLPDI VMEAPLNSAVPSAGASVI QPSSSPLEASSVNYESI KHEPENP
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ERQPSWDFSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPWT
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YLESFKLSLDNTKDTLLPDEVSTLSKKEK I PLQMEELSTAVSNDDLFI SKEAQITRET
ETEDSSS I EI I DEFPTLI SSKTUSFSKRAREYTDLEVSHKSETANAPDGAGSLDCTB
LPHDLSLKNI OPKVERKI SFSDDSFRAGSATSKVLLLPPDVSALATQAE I ESI VKPKV
LVKEAEKKLI PSDTEKEDRSPSAI FSAELSKTSVVDLLYWRDI KKTGVVFGASLFLLLS
                                                                                                                                                                            HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bguchi, Y., Tagami, S. and Tsujimoto, Y.

Direct Submission

Submitted (12-MAR-2000) Yutaka Eguchi, Osaka University Graduate
School of Medicine, Biomedical Research Center, Department of
Medical Genetics; Yamadaoka 2-2, Suita, Osaka 567-0871, Japan

(E-mail:eguchi@gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363,

Fax:+81-6-6879-3369)

Location/Qualifiers
                                              141 AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
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/mol_type="mRNN"
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/tissue_type="brain"
/tissue_lib="human fetal brain"
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2 (bases 1 to 4632)
Zhou,Y., Yu,L. and Zhao,S.Y.
Direct Submission
Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of
Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3151 TCAGTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC
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QKYSNSALGHVNCTIKELRRLFLVDDLVDSLKPAVLMMVFTYVGALFNGLTLLILALI
SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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1 (bases I to 4632)

Yang,J., Yu,L., Bi,A.D. and Zhao,S.Y.
Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14-->2p13 by radiation hybrid mapping 2cytogenet. Cell Genet. 88 (1-2), 101-102 (2000) 20237542
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4789 bp mRNA linear PRI 23-SEP-2003
Homo sapiens RTN4 isoform A (RTN4) mRNA, complete cds;
alternatively spliced.
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                                        3554 AAGGAACTCAGGCGCCTCTTCTTAGTTGATTTAGTTGATGATGTTTCTCTGAAGTTTGCAGTG 3613
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/product=rrnv4 | asoform A"
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/db_xref="G1:26800573"
/db_xref="G1:26800573"
/fb_xref="G1:26800573"
/db_xref="G1:26800573"
/db_xref="G1:26800
                                                                                                                                                                                                                                                                                                     161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Genomic Structure and functional characterisation of the promoters
of human and mouse nogo/trn4
J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 4789)

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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
Location/Qualifiers
                                                                                                                                                                                                         141 AlaLeuIleSerLeuPheSerIleProValileTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                                                     LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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Direct Submission
Submitted (07-WAY-2002) Brain Research Institute, University
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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/organism="Homo sapiens
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1. .4789
/gene="RTN4"
/note="synonym: NOGO"
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/gene="RTN4"
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gene="RTN4"
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Homo sapiens
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Van der Putten, H.
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Patent: WO 2004076622-A 436 10-SEP-2004;
National Institute of Advanced Industrial Science and Tec hnology
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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Sequence 436 from Patent WO2004076622.
CQ874017
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/db_xref="taxon:9606"
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Homo sapiens
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PAT 26-SEP-2002

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3745 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 3804
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                                                                                                                                 Unclassified.
Unclassified.
1 (bases 1 to 4822)
S Jones, K.A., Volkmuth, W. and Walker, M.G.
Bone remodeling genes
AL Patent: US 6428186-A 106 30-JUL-2002;
Location/Qualifiers
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Mismatches:
Indels:
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LOCUS AY114152 3821 bp mRNA
DEFINITION Mus musculus nogo-A mRNA, complete cds.
                   AR220865
Sequence 106 from patent US 6426186.
AR220865.
AR220865.1 GI:23327742
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/mol_type="genomic DNA"
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SEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEKLI
VSNNILHNQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFER
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N. K.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Butterfield, X.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Chench, A., Schein, J. B., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                           1784 bp mRNA linear PRI 29-JUN-2004
Homo sapiens reticulon 4, transcript variant 4, mRNA (cDNA clone
BC016165
                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1784)

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Submitted (19-007-2001) National Institutes of Health, Mammalian
Submitted (19-0070). Cancer Genomics Office, National Cancer
Gene Collection (MGC). Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                   3346 GCTATCCAGAAATCAGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCC
                                                                                                                                                                                                                                                                   3466 ATAAAAAGAATTGAGGCGTCTCTTAGTTGATGATGATTTAGTTGATTCCCTGAAGTTTGCA
                                                                                                                    80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr
     60 AlalleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
Email:.cgapbs-r@mail.nih.gov
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TSVVDLLYMEDIKTSTOVY FORSLFLLISLIPPSIUSYTAYIALLSVTISFRIYK
VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRIFUDDLYD
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                                                                                                                                                                                                                                                                                                          J. (bases I to 3821)
Jin,W., Long,M., Li,R. and Ju,G.
Direct Submission
Submitted (17-MAY-2002) Institute of Neurosciences, 17 Chang Le Xi
Road, Xi'an, Shaanxi 710032, China
Location/Qualifiers
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3821)
Jin, W., Long, M., Li, R. and Ju, G. Cloning and expression of the mouse Nogo-A protein Unpublished
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/note="neurite outgrowth inhibition; RTN4; foocen"
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Conservative:
Mismatches:
Indels:
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                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="BALB/c"
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AY114152
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2389 bp mRNA linear PRI 23-SEP-2003 Homo sapiens RTN4 isoform B2 (RTN4) mRNA, complete cds; alternatively spliced.
977 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 1036
                                                                                                                                                             1337 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 1396
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Genomic structure and functional characterisation of the promoters
of human and mouse nogo/xtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
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                                                                      1037 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
                                                                                                                                                                                                                                                       1217 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG
                                                                                                                                      SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                                                                                                                                                                                                                                                                                    LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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                                                                                                                                                                                                                             101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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/organism="Homo sapiens"
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/evidence=experimental
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Oertle, T. and Schwab, M.E.
Direct Submission
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/note="synonym:
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/product="reticulon 4, isoform D"
/protectin_id="AAH16165.1"
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ERQPSWDPSPLYSTYVAAPSPLAAAAVSPSKLEDEDEPASAPRPAYPT
PRAAPPSTPAAPKRGSSGSVDETLFALPAASEPVIRSSAVVDLIYWRDIKKTG
VVPGASLFILISLTVPSIVSYTAXIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAY
ILSEEVAISBELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSIKFAVLWWVFTYVGAL
FNGITLLILALISLTVALIALISLTVGLANKNVKDAMAKIQAKIPGKRKAE
"RUGITLLILALISLTVALIALISLTVALIANKNVKDAMAKIQAKIPGKRKAE
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                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 23 Row: d Column: 19
This clone has the following problem: The cds is short compared to the longest cds in the locus.
Location/Qualifiers
                                                                                                                               Andy Chan, Starah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Parvanch Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Buane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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/db_xref="MIM:604475"
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Matches:
Conservative:
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                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                Prinjha, R., Moore, S.E., Vinson, M., Blake, S., Morrow, R. Christie, G., Michalovich, D., Simmons, D.L. and Walsh, P. Inhibitor of neurite outgrowth in humans Nature 403 (6768), 383-384 (2000)
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Matches:
Conservative:
Mismatches:
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Beecham, Third Avenue, Harlow, Essex, Ch
                                                                                                                                                                                                                                   Direct Submission
Submitted (29-NOV-1999) Michalovich
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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AJ251385
AJ251385.1 GI:9408099
Nogo gene; Nogo-C protein.
Homo sapiens (human)
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Mammalia; Eutheria;
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Best Local Similarity:
Query Match:
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                                                         ORGANISM
                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                   REFERENCE
AUTHORS
                                                                                                                                            TITLE
JOURNAL
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Matches:
Conservative:
Mismatches:
Indels:
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905.00
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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DEFINITION
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122 MetTrpValPhrThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAla 141 468 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACTGTTTTTGGCT 527 142 LeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHis 161	BC007109 BC07109 BC007109 BC007100 BC007100 BC00710		
8686866	RESULT 48 BC007109 LOCUS DEPINITION ACCESSION VERSION VERSION CEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL PUBMED REFERENCE AUTHORS	TITLE JOURNAL REMARK COMMENT
	Db S74 CCTGGATTCAAGCCGAAAGCTGAA 597 RESULT 47 RR028522 LOCUS AR028522 LOCUS AR028522 LOCUS ACCESSION AR028522 VERSION AR028522.1 GI:5940495 KEYWORDS SOURCE Unclassified Unclassified AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS JOURNAL AUTHORS JOURNA		22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41 168 [

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BD249448 11.22 bp DNA linear PAT 17-JUL-2003
Protein similar to neuroendrocrine-specific protein, and encoding
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1 (bases 1 to 1122)
Michalovich, D. and Prinjha, R.K.
Protein similar to neuroendrocrine-specific protein, and encoding Patent: JP 2002522016-A 3 23-JUL-2002;
SMITHKLINE BEBECHAM PLC
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                                         9916898.1 PI
                                                                                             TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
                         LeuileSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis
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Protein similar to neuroendrocrine-specific protein, and encoding cDNA
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/organism='Homo sapiens (human)'
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PR 22-JUL-1998 GB 9816024.5,19-JUL-1999 GB
DAVID MICHALOVICH, RABINDER KUMAR PRINJHA
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                                                                                                                                                            182 ProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                             CCTGGATTGAAGCGCAAAGCTGAA 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
JP 2002522016-A/3
23-JUL-2002
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JP 2002522016-A/3.
Homo sapiens (human)
Homo sapiens
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TITLE
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KEYWORDS
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BD249448
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 21 Row: h Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: The cds is short compared the longest cds in the locus.
Location/Qualifiers
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SVYXIALLILSVTISFRIY IYGVIQING TOKSDEPRAXLBSEVAISEELVQKYSNSA
LGHYNCTIKELRLSLYDDLYDSIKFAYLWWYFTYVGALFRGTLLILALISLFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRAE"
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(bases 1 to 1151)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
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Michalovich,D.
Direct Submission
Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
HERZEGOVINA
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                            735
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Catarrhini, Hominidae, Homo.
  TIGGCCCTGCTCTCTGTGACCATCATTAGGATATACAAGGGTGTGATCATCCAAGCTATC
                                                                                                736 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAAATCTGAAGTTGCTATATCT
                                                                                                                                                                                          796 GAGGACTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                                                                                                                                                                                                                                                        916 AIGIGGGTATITACCIAIGTIGGGCCTTGTITAAIGGTCTGACACTACTGATITIGGCT
                                                                                                                                                                                                                                                                                                    856 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                         GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prinjha,R., Moore,S.E., Vinson,M., Blake,S., Morrow,R., Christie,G., Michalovich,D., Simmons,D.L. and Walsh,F.S. Inhibitor of neurite outgrowth in humans Nature 403 (6768), 383-384 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp mRNA linear
protein (Nogo gene).
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/organism="Homo sapiens"
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/db xref="taxon:9606"
1. .1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N Homo sapiens mRNA for Nogo-B pr AJ251384
AJ251384.
I GI:9408097
Nogo gene; Nogo-B protein.
Homo sapiens (human)
Filtonian
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Mammalia; Eutheria; Primates;
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1.1122
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86 human secreted proteins.
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JP 2002514090-A/78.
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Best Local Similarity:
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Stapleton, M.; Soares, M.; Bonaldo, M. F.; Casavant, T. L., Stapleton, M.; Soares, M. B.; Bonaldo, M. F.; Casavant, T. L., Scheetz, T. E., Brownstein, M. J.; Usdin, T. B., Toshiyuki, S.; Carninci, P.; Prange, C.; Raha, S.S.; Loquellano, N. A.; Peters, G. J.; Abramson, R. D.; Mullahy, S. J.; Bosak, S. A.; McEwan, P. J.; McKernan, K. J.; Malek, J. A.; Gunaratne, P. H.; Richards, S.; Worley, K.C.; Hale, S.; Garcia, A. M.; Gay, L. J.; Hulyk, S. W.; Villalon, D. K.; Marny, D. M.; Sodergran, E. J.; Hulyk, S. W.; Fahey, J.; Helton, E.; Ketteman, M.; Young, A.; Young, A.; Shevchenko, Y.; Boutfard, G. G.; Blakesley, R. W.; Touchman, J. W.; Green, B. D.; Dickson, M. C.; Rodriguez, A. C.; Grimwood, J.; Schmutz, J.; Myers, R. M.; Butterfield, Y. S.; Krzywinski, M. I.; Skalbsk, U.; Smailus, D. B.; Schnerch, A.; Schein, J. B.; Jones, S. J.; and Marra, M. A.; Schein, J. B.; Jones, S. J.; and Marra, M. S.; More than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: c Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5902015 This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Blakesley.R., Agele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
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McDownell,J., Peargoon,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogf,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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186. .785
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (17-NOV-2000) National Institutes of Health, Mammalian
Submitted (17-NOV-2000) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Aug 19, 2003 this sequence version replaced gi:12654418. Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:12654418.
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LGHVNCTIKELRRLFLYDDLVDSLKFAVLMWYPTYVGALFNGLTLLILALISLFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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Moore, P.A., Shi, Y., Rosen, C.A., Ruben, S.M., Lafleur, D.W., Olsen, H.S., Ebner, R. Brewer, L.A., Young, P., Greene, J.M., Ferrie, A.M., Yu, G.L., Ni, J. and Feng, P.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                             TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                  548 GAACTCAGGCGCCTCTTCTTAGTTGATTTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                             MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAla
                                                                                                                                       LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis
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/db_xref="taxon:9606"
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Sequence 79 from Patent EP1439189.
CQ855235
CQ855235.1 GI:51510663
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/note="n equals a,t,g,
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PI AND M FERRIE.

PI AND M FERRIE.

PI CO7H21/02, C07H21/04, C12N5/00, C12N5/04, C12N5/06, C12N5/10 PC C7H21/02, C12N15/09, C12N15/09, C12N15/09, C12N15/09, C12N15/09, C12N15/09, C12N15/09, C12N15/09, C12N15/09, C12N15/09, C12N15/09, C12N15/10, C12N15/11, C12N15/12, C12P21/06, C12N15/09, C12N15/10, C12N15/11, C12N15/12, C12P21/04, C12P21/06
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/- .ranism="unidentified"
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86 human secreted proteins
                                                                           JP 2002514090-A/78
14-MAY-2002
11-JUN-1998 JP 1999503203
13-JUN-1997 US 60/0495
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86 human secreted proteins
Patent: JP 2002514090-A 78
HUMAN GENOME SCIENCES INC
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  TITLE
JOURNAL
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셤 ઠ 쉽 ઠે 셤 ò g ò 유 ઠે 셤

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DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M. Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAFSPLSAAAVSPSK
TEBDDBPARPAPRRGSSGSVVVDLL
YMRDIKTGVYRGASLFLLLSTTYSIVSVTAYIALALLSVTISFRYKGVIQAIQKS
DEGHPPRAYLESEVISESEVQKYSNSALGHVNCTIKELRLPLVDDLVDSLVFRAVIN
                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 58 Row: d Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24431932 This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOGO, ASY, NI220/250, NSP, RTN-X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  662 TIGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'tissue type="Eye, retinoblastoma"
'clone lib="NIH MGC_16"
'lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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// gene="RTN4"

// note="synonyms: NSP-CL, of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of th
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/db_xref="G1:47939582"
/db_xref="LocusID:57142"
/db_xref="MIM:604475"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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product="RTN4 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity:
Query Match:
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Homo sapiens reticulon 4, mRNA (cDNA clone IMAGE:4635625), complete
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-UNN-2004) National Institutes of Health, Mammalian
Submitted (10-UN-2004) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
                                                                                 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                                                                                                                            GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLys1leGlnAlaLys1le
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                                                                                                                                                                                                                                                                                                                                                                                                                                608 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparator: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccredarreaacccaaaccreaa 811
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 14 Row: n Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RTN-X"/db_xref="LocusID:57142"
/db_xref="LocusID:57142"
/db_xref="MIM:604475"
6. .1127
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Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                     This clone has the following problem: The cds is short compared the longest cds in the locus.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGluLeuValGlnLySTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                        1. .1485
/organiem="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3901353"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="Pancreas,
/clone_lib="NIH_MGC_70"
/lab_host="DH10B"
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/gene="RTN4"
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Strausberg A.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.K., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buttow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonddo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morkernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Murny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
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Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                            PRI 29-JUN-2004
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                                                                                                                                                                                 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1485)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1485 bp mRNA linear PRI 29-JUN-20
Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone
IMAGE:3901353), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                GluteuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                GAACTCAGGCGCCTCTTCTTAGTTGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                                                                                                                                                         human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                      GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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                                                                                                                                                                                                                                                                                                                          LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       615 GTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                        GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              915 GAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis
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Patent: WO 2003058021-A 303 17-JUL-2003,
Xantos Biomedicine AG (DE)
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CQ769577
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/organism="Homo sapiens"
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Best Local Similarity:
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Sugano, S. and Suzuki, Y.

Direct Submission

Submitted (Ja-Uu-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,

Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Science, University of Tokyo, Laboratory of Genome Structure, Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                     MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                          GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACAAAAG
                                     GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                               GAACTCAGGCGCCTCTTCTTAGTTGATGATTTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens
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REFERENCE AUTHORS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                    Key
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C12N15/00,A61K37/02,C12N5/00

Bone marrow secreted proteins and polynucleotides
Location/Qualifiers
source
1. .1610
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/organism='Homo sapiens (human)'
Location/Qualifiers
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Homo sapiens reticulon 4c mRNA, complete cds.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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PN JP 2002511231-A/3
PN JP 2002511231-A/3
PD 16-APR-2002
PF 18-DEC-1998 JP 2000526635
PR 30-DEC-1997 US 60/068958,24-SEP-1998 US 60/101603 PR 30-SEP-1998 US 60/102540
PR 31-DEC-1999 US 60/102540
PR 31-DEC-1999 US 60/102540
PR 31-DEC-1999 US 60/102540
PR 31-DEC-1999 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR 310-SEP-1998 US 60/101603 PR
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1610)
Lin,H. and Cao,L.
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                                                                                                                                                                                                                      671 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTTTGGTGCCAGC
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                Matches:
Conservative:
Mismatches:
Indels:
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JP 2002511231-A/3.
Homo sapiens (human)
Homo sapiens
                904.00
98.94%
97.34%
97.73%
                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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BD231889
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PRI 10-SEP-2003

Suzuki, Y.,

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Pax:81.3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1619)
Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:flodna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                    TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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                                    619 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC
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Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M.,
Sugiyama,T., Irie,K., Otsuki,T., Sato,H., Nishikawa,T.,
Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.
NEDO human CDNA sequencing project
                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens cDNA FLJ26295 fis, clone DMC07157.
AX129806
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Oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens
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/clone="mbororist"
/tissue_type="dermoid tumor"
/clone_lib="DMC"
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| organism="Homo sapiens"
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| db xref="taxon:9606"
| 106-..705
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| 1595
| 1608
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                                                                                                                 2 (bases 1 to 1617)
Yang J., Yu.L., Dai, F.Y., Cui, W.C., Zheng, L.H. and Zhao, S.Y.
Direct Submission
Submitted (17-AUG-1998) Lab of Human Gene Research, Institute of
Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCGTAACACACTACCT
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                                    chromosome
              Yang, J., Yu, L., Bi, A.D. and Zhao, S.Y.
Assignment of the human reticulon 4 gene (RTN4) to a post-2p13 by radiation hybrid mapping
Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
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Best Local Similarity:
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polyA_site
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Strausberg, R.L., Feligold, B.A., Grouse, L.H., Derge, J.G., Klausherg, R.L., Colling, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKerran, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, K.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Ghent, J. Schmutz, J., Morshing, M., Madan, A., Young, M. Schmutz, J., Myers, R.M., Ghent, J. Schmutz, J., Morshing, J. M., Schalk, J. Schmutz, J., Morshing, J. M., Ghen, B.D., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

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Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone
IMAGE:3862911), complete cds.
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                                                                                                                                                                                                                                                                                                                                    142 LeulleSerLeuPheSerlleProvallleTyrGluArgHisGlnValGlnIleAspHis 161
122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                          TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                     GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1668)
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                                                                                                                                                                                                                                                                                                                                                                102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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Contact: MGC help desk
Contact: MGC help desk
Tissul: rgcpbs-r@mail.nih.gov
Tissuc Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 ProGlyLeuLysArgLysAlaAsp 189
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAR Plate: 21 Row: h Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein
This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDEDIEELEVIERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP
BRQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWT
SPAPAPAAPSPETPAAPKRGSSGSVVVDLLYWBLIKKTGVYFGASLFTLLISLTVFSIV
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SPAPATIALLISVTISFFIXGSIGAPLAPKRAYLESEVAISEELVQKYSNSA
IGHVNCTIKELRRLEFUNDDLVDSLKPAVLMWYFTYVGALFNGITLLIALISLFSVPV
IYERHQAQIDHYLGILANKNVKDAMAKIQAKIPGIKRAKAE"
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                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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183
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/organism≂"Homo sapiens"
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Center code: BCM-HGSC
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/gene="RTN4"
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1. (Dases 1 to 1698)
2. (Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schefer C.F., Bhat, M.K., Hopkins, R.F., Zordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Gasavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Raky, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
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Lupublished

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E. (bases 1 to 1691)

S. (bases 1 to 1691)

Direct Submission

L. Submitted (27-FEB-1999) Pathology, University of Washington, 1959

Direct Submission

Location/Qualifiers

I. (59)

Pacific NE, Seattle, WA 98195, USA

Pacific NE, Seattle, WA 98195, USA

(nol type="mRNA" | // db_xref="taxon:9606" | // tisue type="mRNA" | // db_xref="taxon:9606" | // tisue type="mRNA" | // db_xref="taxon:9606" | // tisue type="skeletal muscle" | // tisue type="memory family and family muscle" | // tisue type="memory family and family muscle" | // tisue type="memory family and family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" | // tisue type="memory family muscle" |
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                                                                                                                                                                                  982 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 1041
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Catarrhini; Hominidae; Homo.
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                                    CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT
   GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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Homo sapiens foocen-s mRNA, complete cds.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   624
                           205 CTATTCCTGCTTCTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 264
                                                                                                         265 TIGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGTATCCAAGGTATC 324
                                                                                                                                                                                       325 CAGAAATCAGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  625 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAATC 684
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1 (Dases 1 to 1700)

Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Yu,J., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Novel human cDNA clone with function of inhibiting cancer cell
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Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
Yu,J. and Han,L.H.
                                                                                                                                                                GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                    LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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/note="Bynonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RIN-X"
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Submitted (17-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Prourement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M. A.G. E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadandsystemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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protein id="AAH14366.1"
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                                                                Submitted (122-MAR-2000) Yutaka Eguchi, Osaka University Graduate School of Medicine, Biomedical Research Center, Department of Medical Genetics; Yamadaoka 2-2, Suita, Osaka 567-0871, Japan (B-mail:eguchi@Gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363, Fax:+81-6-6879-3369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTATTCCTGCTTCCTTTCATTGACAGTATTCAGCATTGTGAGCGTAAACAGCCTACATTGCC
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Eguchi,Y., Tagami,S. and Tsujimoto,Y.
Direct Submission
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                          ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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Homo sapiens mRNA for RTN-xS,
AB040463
                                                                                                                                                                                                                                                      US-09-830-972-2_COPY_975_1163 (1-189)
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Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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ACCESSION
VERSION
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AUTHORS
TITLE
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MEDLINE
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1. (Dades 1 to 1/24).
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schender, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, W.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Rahs, S.S., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Malek, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, E., Ketteman, M., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,
Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1728 bp mRNA linear PRI 30-JUN-2004
Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone
BC068991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr11eLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 GAACTCAGACGCCTCTTCTTAGTTGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 639 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAATC 698
                                                                                                                                                                                                                                                                                                                                                                                                GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1728)

                                                                                                                                                                                        42 LeualaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnalaIle
                                                                                                                                                                                                                  TTGCCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC
                                                                                                                                                                                                                                                                                               339 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT
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                                                   GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
                                                                                                                                TTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAAATAGATCAT
                                                                                                         LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                           ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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Homo sapiens
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AUTHORS
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S Oertle, T. and Schwab, M.E.
Direct Submission
L Submitted (16-0CT-2002) Brain Research Institute and Department Biology, University of Zurich and ETH Zurich, Winterthurerstr.190, Zurich 8057, Switzerland
E 3 (bases 1 to 1721)
S Oertle, T. and Schwab, M.E.
Direct Submission
L Submitted (27-0CT-2003) Brain Research Institute and Department Biology, University of Zurich and ETH Zurich, Winterthurerstr.190, Zurich 8057, Switzerland
Sequence update by submitter
On Oct 27, 2003 this sequence version replaced gi:32331288.
Location/Qualifiers
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LGHYNCTIKELRRILSVTISPTIYGVIQAIGKSDEGHPFRAYLESEVAISEELVQKYSNSA
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
726. 1673
Protein_id="AAP47319.2"
'db_xref="GI:37992247"
'translation="MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIV
                                                                                                                                                                                                                                                                          MAM 27-0CT-2003
                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devines, T. to 1721)
1 (Deses I to 1721)
Oertle, T., Klinger, M., Stuermer, C.A. and Schwab, M.E.
A reticular rhapsody: phylogenic evolution and nomenclature of
                                                              TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                             AY164744 1721 bp mRNA 1:
Bos taurus RTN4-C (RTN4) mRNA, complete cds.
AY164744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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FASEB J. 17 (10), 1238-1247 (2003)
12832288
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/mol_type="mRNA"
/db_xref="taxon:9913"
1. .1721
                                                                                                                                                                       1340 CCTGGATTGAAGCGCAAAGCTGAA 1363
                                                                                                                                             182 ProglyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="RTN4-C"
                                                                                                                                                                                                                                                                                                                                    AY164744.2 GI:37992246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126. .725
/gene="RTN4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         726. .1673
/gene="RTN4"
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
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                                                                162
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
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JOURNAL
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COMMENT
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PRI 23-SEP-2003
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mumanlia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1800)
Oertle,T., Huber,C., van der Putten,H. and Schwab,M.B.
Genomic structure and functional characterisation of the promoters of human and mouse nogo/trn4
J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                     924 riedscicinscricterendacercaecriradeararacaaescicienteaaecrate 983
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1104 GAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
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                                                                                ValValAspLeufeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                              804 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                         82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                            LeuAlaLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                    62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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mRNA, complete
                                       US-09-830-972-2_COPY_975_1163 (1-189) x BC068991 (1-1728)
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Oertle, T. and Schwab, M.E.
Direct Submission
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LGHVNCTIKELRRLFLVDDUVDSLKPAVLMWVFTYVGALFNGLTLLILALISLFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRRAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiANL at: http://image.llnl.gov Series: IRAL Plate: 54 Row: c Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28557782
This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                Andy Chan, Steve S. Chand, Milliam Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Parkanol Barvaneh Sasedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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                                                                                                            Direct Submission
Submitted (05-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
  sequences
.. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone=TimaGE.4634389"
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/clone=Tib="NIH MGC_16"
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/note="Vector: pOTB7"
                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Matches:
Conservative:
Mismatches:
Indels:
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                         Proc. Natl. Acad. Sci.
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/gene="RTN4"
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904.00
98.94%
97.34%
  mouse cDNA
                                                                (bases 1 to 1728)
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                                                                                                                                                                                                                                                                                                                                                                                                  info@bcgsc.bc.ca
                                                                                     Strausberg, R.
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Best Local Similarity:
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1103

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1223

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PRI 03-SEP-1999
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Submitted (17-JUN-1998) Masuo Yutsudo, Osaka University, Dept. of
Tunor Virol., Res. Inst. Microb. Dis.; 3-1 Yamadaoka, Suita, Osaka
7565-0871, Japan (E-mail:yutsudo@biken.osaka-u.ac.jp,
Tel:81-6-879-8313, Fax:81-6-879-8315)
748 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 807
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                                                                                                                                                                                        Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
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Published Only in DataBase (1999)
2 (bases 1 to 2052)
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67. .1188
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                         182 ProGlyLeuLysArgLysAlaAsp 189
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                                                    CCTGGATTGAAGCGCAAAGCTGAA
                                                                                                              Homo sapiens ASY mRNA, AB015639
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Homo sapiens
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183
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/map="2p16"
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/note="synonym: NOGO"
              Location/Qualifiers
 Switzerland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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1 to, T. and Schwartz, S.M.
Cloning of a member of the reticulon gene family in human:
ubiquitous type
Unpublished
2 (bases 1 to 2276)
1 to, T. and Schwartz, S.M.
Direct Submission
Submitted (27-FFB-1999) Pathology, University of Washington, 1959
Pacific NE, Seattle, WA 98195, USA
1. .2276
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                                                                                                                                                                                                                                                                                                                                                                                      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                  Length:
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                   2.34e-83
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                                  904.00
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                                                                    Best Local Similarity:
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AUTHORS
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                                                                                                                                                                                                                                                                 LeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
                                                      101
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1 (Dases 1 to 2235)
Yang, J., Yu, L., Bi, A.D. and Zhao, S.Y.
Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14-->2p13 by radiation hybrid mapping
Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Gene Research, Institute of . 220 Handan Rd., Shanghai 200433,
                                                                        GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                           GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                           1042 CTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAATATAA
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CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT
                                                                                                                                                                                                                  ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
                                                    GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
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2 (bases 1 to 2235)
2 bases 1 to 2235)
Direct Submission
Submitted (05-MAY-1999) Lab of H
Genetics, Fudan University, No.
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Homo sapiens
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AF148538
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PPAPAPAPPSTPAAPKRGSSGSVVVDLYWRDIKKTGVVFGASLFLLLSLTVFSIV
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1367. 2332
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                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2332)

Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Genomic structure and functional characterisation of the promoters of human and mouse nogo/trn4

J. Mol. Biol. 325 (2), 299-323 (2003)
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            2 (Dases 1 to 2332)
Oerlle, T. and Schwab, M.B.
Direct Submission
Submitted (07-MAX-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="RTN4"
note="NOGO-B; RTN4-B1; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2332
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/map="2p16"
                                AY102277
AY102277.1 GI:26800561
     alternatively spliced.
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gene="RTN4"
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gene="RTN4"
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Van der Putten, H.
                                                                                                                                       Homo sapiens
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/db_xref="G1:4838517"
/translation="MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDBEEEEEEEED
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Homo sapiens RTN4 isoform B1 (RTN4) mRNA, complete cds;
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                                                                                                                            /note="member reticulon gene family"
/codon start=1
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Matches:
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'organism="Homo sapiens"
                           /mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="placenta"
180. .1301
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                 40
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1 (bases 1 to 2256)

1to.T. and Schwartz,S.M.

Cloning of a member of the reticulon gene family in rat: One of minor splice variants
Unpublished

2 (bases 1 to 2256)

Ito,T. and Schwartz,S.M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      804 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    684 AGCTTATTCCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AlaLeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAla
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                                                                                                                                                                                                                                                                                    2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValVal---PheGlyAla
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AF132046.1 GI:4838514
                                                                   1276
186
                                                                                                                                                                                                                                     x AY114153 (1-1276)
                                                                                                                  Conservative:
Mismatches:
Indels:
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                                                                     Length:
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                                                                1.63e-83
902.50
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                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                        CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 1039
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Ji (bases 1 to 1276)
Cloning and expression of the mouse Nogo-B protein
Unpublished
2 (bases 1 to 1276)
Jin, W., Li, R., Long, M., Shen, J. and Ju, G.
Jin, W., Li, R., Long, M., Shen, J. and Ju, G.
Direct Submission
Submitted (17-May-2002) Institute of Neurosciences, 17 Chang Le Xi
Road, Xi'an, Shaanxi 110032, China
Location/Qualifiers
                                               61
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                                                                                                                                                                                                                                                                                                                                    CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
                                            LeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValileGlnAlaile
                                                                                    920 TIGGCCCTGCTCTGTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                                                                                                                                                                                                                                        GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
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                                                                                                                                           GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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Corganiam=Mus musculus"
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/product="nogo-B"
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Mus musculus
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GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 1147
                                                                                                                                                                                                                                                                                                                                                                                                           /note="unnamed protein product"
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900.00
98.40%
96.81%
97.30%
                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                            Homo sapiens
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Best Local Similari
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    182
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DB:
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CQ783030
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                                                                                                                                                                                                                                                                                                     PAAPKREGSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSV
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ANKSVRDAMKIQAR FGLKRKAD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   813
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  University of Washington, 1959
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                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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Submitted (27-FEB-1999) Pathology, U
Pacifice NE, Seattle, WA 98195, USA
Location/Qualifiers
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901.00
98.94%
98.94%
97.41%
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Best Local Similarity:
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PAT 17-MAR-2004
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                        Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTGGTCAGC
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Research Association for Biotechnology (JP)
Location/Qualifiers
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Matches:
Conservative:
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Is 2 (Dases I to 1694)

Is 1 sogai, T. and Otsuki, T.

Direct Submission

Submitted (125-MAR-2002) Takao Isogai, Helix Research Institute,

Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology; cDNA library construction:

Institute of Medical Science, University of Tokyo, Laboratory of

Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass

sequencing and clone selection: Helix Research Institute (supported

by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                PRI 03-SEP-2002
                                                                                                                                                                             968 CAGAAATCAGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 1027
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                                                                                                                                                                                                                                     82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                            MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                                                                                                                                                     GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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Homo sapiens cDNA FLJ90558 fis, clone OVARC1001030.
AK075039
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Oligo capping; fis (full insert sequence).
Homo sapiens (human)
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Unpublished
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2868 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS HOMO sapiens (human)
PN JP 2002017375-A/2868
PD 32-JAN-2002
PP 07-JUL-2000 JP 200253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                1148 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTAGTTTTGGCT 1207
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                                                                                                             LeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N1S/00,C12N5/00
Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers

T CDS (479). (1351).
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YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
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Mismatches:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Primer for synthesizing
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JP 2002017375-A/2868.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity:
Query Match:
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1006 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 1065
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                                                                                                                                                                                                                                                                                                         human neuroblastoma with good prognosis, in comparion between
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         1. (Dases 1 to 1980)

Nucleic acid sequence characterized in that expression is potentiated in human neuroblastoma with good prognosis, in comparion between human neuroblastoma with good prognosis and neuroblastoma with bad prognosis

L. Patent JP 2001321175-A 22 20-NOV-2001;

CHIBA PREF HISAMITSU PHARMACEUTICAL CO INC

OS Home sapiens (human)

PN 97 20-NOV-2001

PP 12-MAY-2000 JP 2000140387

PI AKIRA MARAGAWARA

PC C12N15/09, C12Q1/02, C12Q1/68, G01N33/50, C12N15/00 CC Nucles of sequence characterized in that expression is CC potentiated in

CC human neuroblastoma with good prognosis, in comparion bet human

CC neuroblastoma with good prognosis and human

neuroblastoma with

CC prognosis

FT source 1. 1.1980

FT source 1. 1.1980

FT corrian/confisionalitiers

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Conservative:
Mismatches:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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898.00
98.41%
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97.08%
   to 1980)
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Query Match:
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REFERENCE
AUTHORS
TITLE
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Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="compared to AF148538, AF132047 and AC016171.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1088 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
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                   /tissue type="ovary, tumor tissue"
/clone_lib="OVARC1"
                                                 /note="cloning vector: pME18SFL3"
                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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96.81%
97.30%
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Best Local Similarity:
Query Match:
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KEYWORDS
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Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaile 80 Db 1186 ATCCGGAATCGAGGCCCCCCTTCGGGCCATTCGGGCATTTGGAGTTGTAATTGTACAGAAT 1305 Qy 101 LysGluLeuValGlnLysTycalGlyAaTTCTGCTCTTGGTCATGTGAACTGCACGATA 1305 Qy 101 LysGluLeuValGlnLysTycalGlyAalaCeuValAspSerLeuLysPheAlaVal 120 Db 1306 AAGGAACTCAGGGCCTCTTCTTAGTTGATTGATTGTTCTCTGGAGTTTGCAGTG 1365 Qy 121 LeuMetTrpValPheThrTytValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu 140 Db 1366 TTGATGTGGGGCTTTTGTTGTTGATTTATCTTGGAGTTTTGCAGTTTTGCAGTTTTGCAGTTTTTTTGCAGTTTTTTTGCAGTTTTTTTT	RESULT 81 BD139293 LOCUS LOCUS LOCUS ACCESSION BD139293 VERGION BLISO293 LOCUS ACCESSION BD139293 VERGION BD139293 VERGION BD139293 VERGION BD139293 VERGION BD139293 VERGION BD139293.1 GI:23234238 VERGION BD139293.1 GI:23234238 VERGION BD139293.1 GI:23234238 VERGION BD139293.1 GI:23234238 CORGANISM Homo sapiens Characa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE I (Dases I to 99) AUTHORS BOUQUELeret, L., Duclert, A. and Edwards, J.B.D.M. TITLE AUTHORS COMMENT CENSET COMMENT OS Homo sapiens (human) PN UP 2002508182-A 45 19-MAR-2002; PP 17-DEC-1998 JP 2000539136 PP 17-DEC-1998 JP 2000539136 PR 17-DEC-1998	CLZN1/21, CLZP21/02,CLZQ1/68,CLZN15/00,CLZ
OY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180	မ မ	Best Local Similarity: 89.00 Marches: 182

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Description: 1st strand CONA was primed with an oligo (dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with 5il and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct Draill sites of pME185-FL3. XNOI sites just outside the Draill sites can be used to isolate the cDNA insert. Libraries were constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CTGCTGCTGNAAAGCTGCG]; and primer [CTGACCTGNAAAAGCTGCG];
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VDSLRFAVLMWVFTYVGALFNGLTLIILALISLFSVPVIYERHQAQIDHYLGLANKNV
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brain cDNA library QnpA"
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                  pME18S-FL3 (Acc.No. AB009864)
Draili (CACTGTGTG)
Draili (CACCATGTG)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                          organism="Macaca fascicularis"
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                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 sex="male"
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895.00
98.94%
95.74%
96.76%
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                  Vector:
R. Sitel:
R. Site2:
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 Lab host:
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                                                                                                                                                                                                                                                                                         368 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTTG
                                                                                                                                                                                              LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                      LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
2 (bases 1 to 2162)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
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                                                                                      US-09-830-972-2_COPY_975_1163 (1-189) x BD139293 (1-994)
   Conservative:
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Gaps:
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Macaca fascicularis brain cDNA,
AB049853
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fis (full insert sequence)
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98.40%
96.81%
96.76%
Percent Similarity:
Best Local Similarity:
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Gallus gallus (chicken)

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Archosauria: Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus:

E (bases 1 to 1591)

S Boardman, P. E., Bonfield, J.K., Brown, W.R. A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humptray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblett, D., Overton, I.N., Rogers, J., Scott, C.E., Taylor, R.G., Tickle, C. and Wilson, S.A.

Direct Submission

I. Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire, CBLO 1SA, UK. E-mail enquiries: chickestebms.umist.ac.uk
                                                                                                                                                                                                              VRT 02-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing project.

This sequence is from the BBSRC/Dundes/Nortingham/Sanger/Sheffield/UMIST cDNA collection, Engage and Library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from brain, and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
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                                                                 245 AGCTIGITICITICITICATIAACAGIGITICAGCATCGIGAGCGIGACAGCITACAIT
21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                             1591 bp mRNA linear Gallus gallus finished cDNA, clone ChEST117m23.
BX934715.1 GI:41635243
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Mismatches:
Indels:
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/organiam="Gallus gallus"
/mol type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                      1851 CCCTGGGTTGAAGCGCAAAGCTGAA 1875
                                                                                                                181 eProGlyLeuLysArgLysAlaAsp 189
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/dev_stage="16 days"
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/clone="ChEST117m23"
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                  TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
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                                                                                                                                                                                                                                                                                                                                                           Unclassified.

1 (Dases 1 to 2610)

Cocks B.G., Stuart, S.G. and Seilhamer, J.J.

Cocks B.G., Stuart, S.G. and Seilhamer, J.J.

Compositions for the detection of blood cell and immunological response gene expression

response gene expression

Patent: US 6607899-4 382 19-AUG-2003;

Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 382 from patent US 6607879.
AR379837.1 GI:40087471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
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                                                                                                                                                                    1136 CCTGGATTGAAGCGCAAAGCTGAA 1159
                                                                                                                                                ProGlyLeuLysArgLysAlaAsp 189
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891.00
98.41%
96.83%
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IALALSVTISFITKGVIQAIQKSDEGHPFRAYLESDVAVSEELIGKYSSVVIJGHIN
GTVKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERH
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1. .119
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/note="NOGO"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
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Gallus gallus finished cDNA, clone ChEST11g8.
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92.06%
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Caltharp, S.A., Pira, C.U., McNeill, D.S., Liwnicz, B.H. and Oberg, K.C. Expression and Regulation of NOGO-A During Development of the Avian
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PPRKSEBQPJTJLINGKSVENIETDEDGRLVDJLSAATGKPVESERQDSELDSKKTTQ
PSEPTPAKI AKAEKI PLĢMEBLAALAY STDVSVAMEPKEGDSKGLSPSSPVSDDFY
MLVDPKTGTEFVAEVTDRETVHKNESKDI SNEIRDEKRQAPLTELPCDLSVRNVEVKT
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kpvtolcespedseaapspvlpdivmeaplssgtagaeastvoletsolgtfvttasy
Envkkeaekpplyoeavnmplioaoeakeeltlkkadresstspedletpyislacdl
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Waaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus
                                   ATCCAAAAGTCCGATGAAGGCCATCCATTAGGGCTTACTTGGAGTCTGATGTAGCTGTG
                                                                                                                                                   SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                                                                      LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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Linda, CA 92350, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="neurite outgrowth inhibitor NOGO-A"
protein_id="AAS18427.1"
db_xref="GI:41528325"
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Caltharp, S.A., McNeill, D.S., Pira, C.U. and Oberg, K.C. Direct Submission
Submitted (102-DEC-2003) Anatomy, Loma Linda Universit Stewart St. Evans Hall B09, Loma Linda, CA 92350, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY494005 2835 bp mRNA linear Gallus gallus neurite outgrowth inhibitor NOGO-A (partial cds.
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1. 2835
/organism="Gallus gallus"
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/db_xref="taxon:9031"
<1. 2835
                                                                                                                                                                                                                                                                                                              IleProGlyLeuLysArgLysAlaAsp 189
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AY494005.1 GI:42528324
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Gallus gallus
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Unpublished
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/gene="NOGO"
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1 (bases 1 to 1578)

Boardman, P.E., Bonfiteld, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Humt, P.J., Maddison, M., Mciaren, S.R., Tickle, C. and Wilson, S.M., Rogers, J., Scott, C.E., Taylor, R.G., Divect Submission
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657 TATTTGGGACTAGTGAACAAGAACGTCAAAGATGCGATGGCAAAGATCCAAGCAAAGATC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is from the BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from Rerebrum, and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript I KS(+); Site 1: EcoRI; Site 2: NotI Host: Escherichia coli DH10B. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 GTTGTTGACCTCCTTTACTGGCGAGACATTAAGAAGAAGACAGGAGTGGTGTTTGGTGCCAGC
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                                                                                                                                              linear
                                                                                                                                          CR353502 1578 bp mRNA line Gallus gallus finished cDNA, clone ChEST12704. CR353502.1 GI:45424789
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Matches:
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/mol_type="mRNA"
/strain="Compton_Line_151"
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/clone_lib="CSEQCHL15"
/dev_stage="adult"
                                   182 ProGlyLeuLysArgLysAlaAsp 189
                                                                     717 ccresecreaascecaaacreas 740
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Gallus gallus
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                1 (bases 1 to 1363)

Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Humbbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G., Direct Submission S.A.

Direct Submission

Submitted (0.2-FBB-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk

BBSRC/Dundee/Nortingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                                                                                                                  BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site_1: EcoRI, Site_2: NotI Host: Escherichia coli DH10B. Location/Qualifiers
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Mismatches:
Indels:
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Matches:
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C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2386)
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25-OCT-1996 US 08/740274
KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE,
                                                                                                                          TIGTTCCTGCTCCTCTTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTGCC
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PD 28-MAY-2002
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                                                                             US-09-830-972-2_COPY_975_1163 (1-189) x AY164737 (1-1597)
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   Conservative:
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LGHINGTVKELRLFLVVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPV
IYERHQADIYLGLVNKNVKDAMAKIQAKIPGLKRKTE"
                                                                                                                                                                                                                                                                                                                                                                                      VRT 30-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
Gallus.
1 (bases I to 1597)
Oertle,T., Klinger,M., Stuermer,C.A. and Schwab,M.E.
A reticular rhapsody: phylogenic evolution and nomenclature of the FRIK/Nogo gene family
FRASEB 3. 17 (10), 1238-1247 (2003)
                                                                                                                                                                                                                                                              713
                   473
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                                                                                                                                                                   TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Oertle,T. and Schwab,M.E.
Direct Submission
Submitted (16-077-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
Zurich 8057, Switzerland
Location/Qualifiers
                                                                                                                                                                                                                                                 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                 GAGCTGAGACGCCTCTTCCTCGTTGATGACTTGGTTGATTCTCTCAAGTTTGCAGTGTTG
                                                                                                                             534 ATGTGGGTGTTCACTTACGTTGGTGCCTTGTTTAATGGTCTGACATTACTGATACTGGTCT
                                                                                                          MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                           1597 bp mRNA linear
Gallus gallus RTN4-C (RTN4) mRNA, complete cds.
AX164737
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Matches:
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/mol_type="mRNA"
/db_xref="taxon:9031"
1. .1597
                                                                                                                                                                                                                                                                                             182 ProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                                                CCTGGGCTGAAGCGCAAACTGAG 737
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1. .125
/gene="RTN4"
126. .725
/gene="RTN4"
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Xenopus laevis RTN4.1-A3 (RTN4) mRNA, complete cd8; alternatively spliced. A7316195.1 GI:34809221
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
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Secreted proteins and polynucleotides encoding Patent: WO 0119988-A 41 22-MAR-2001; Genetics Institute, Inc. (US) Location/Qualifiers
                                                                                                                                         2386
179
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Mismatches:
Indels:
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Xenopus laevis
                                                                                                                                            Length:
Matches:
                                                  1. .2386
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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2001 ATCCCTGGATTGAAGCGCAAAGCTGAA 2027
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871.50
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Best Local Similarity:
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AY316195
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 TITLE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. 2386
1. Caganism="Hono capiens"
//organism="Hono capiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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2001 ATCCCTGGATTGAAGCGCAAAGCTGAA 2027
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Sequence 41 from Patent WO0119988.
AX099401 GI:13538524
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 Topology: Linear;
Key
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871.50
96.30%
94.71%
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Homo sapiens
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Best Local Similarity:
Query Match:
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Pred. No.:
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KEYWORDS
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AUTHORS
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Xenotor, A024 bp mRNA linear VRT 26-MAY-2004 Xenopus laevis RTM4.1-A1 (RTM4) mRNA, complete cds; alternatively AY316197
  2796 ATCCAGAAGTCAGAGGAAGGACCACCCATTCAGATCCATCTTGGAGTCCAACCTGGCGGTG 2855
                                                                                                                                                                                                                                                                             2856 CCAGAGGATCTGGTCCAGAAATACTGCAATGTGGCCCTGAACCATGTCAACTGCACAGC 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2976 TTGATGTGGGTCTTCACCTATATTGGTGCCTTGTTCAATGGTCTCACCCTGCTCATTGTG 3035
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Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus;
Xenopus; Xenopus; Xenopus; Xenopus;
Xinger,M., Diekman,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.
Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
                                                                                                                                                                                                                                                     81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr1le 100
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Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        2916 AAGGAGCTGCGGCACCTCTTCCTTGTAGAAGACCTGGTGGATTCCCTGAAGTTTGCAGTA
                                                                                                                                                            61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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                                                                        AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von
Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and
Stuermer, C.A.O.
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/mol_type="mRNA"
/b_xref="taxon:815"
/tissue_type="wholemount embryos"
/dev_stage="older than stage 50"
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/gene="RTN4"
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// db_xref="di:34809222" |
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SAPMEEPERPARDIEBEEBEBERGAWCDSLEPSPVEEBFGSIDSISPSESTD
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SEKGYVVDHPTSQQETISEHAKLYSQSAKEMPSGMLQSVAPPPROVOWFESSESENEIDSISDISP
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DLVQTAANVGEKVSPTAQAPARLEETDSVSSPVLDDIVMEAPLASALETVALKPDIS
PUTTALLPDSTDYDMFATVEQNIPFSFGGGHVAGNKTDEKKIEDIEAQKTSVGFGLKVA
TVNPPPTNSSAGSESTVTTHVATHVSTKPESPTDSIVOBAYBSERAPTOGIPKQKYESNI
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HEVVKDVRKPPDSKABDOSSKLPKKESKASTVSSSDFRNAVVDLIVMRNIKRSGVVFGAS
LFLLLSLSVFSILVSTVAGTTRELALLELVTTSLRIYKGTLOAIQKSEEGHPFRSILESNLA
VPEDLVQKYCNVALNHVNCTYKELRHHELVEDLVDSLKFAVTANVFYTIGALFNGITL
LIVALISLASVESIPVTRAES
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Kinger, M., Diekman, H., Heinz, D., Hirsch, C., Hannbeck von Kalnger, M., Diekman, H., Meinz, D., Hirsch, C., Hannbert, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A. Identification of two NOGO/RTM4 genes and analysis of Nogo-A expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
                                                                                                                                                                                                                                            Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
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Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.O.
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/gene="RTN4"
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variation 3337 /replace="RTN4"	/replace="a" variation 3553 /gene="RTN4" /replace="c" variation 3631 /gene="RTN4"	<pre>variation / Teplace="t" variation 3649 variation 3662 variation 3832 . 3837 variation 3855 variation 3855 variation 3855</pre>	1	Alignment Scores: Alignment Scores: 1.36e-68
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TPAVQKPDDSGKAVSDTFGGLDTTTKGGSAVHEVKVDKPKPPSKEDGSKLPKKESKA
STYSSSDFMNSVYDLIVMDITKSGVYFGASLFLLISLSSYPSIVSVLAYIAYIAYILLSVT
ISLRIYKGILQALQKSEGHPFRSILESNLAVPEDLVQKYCNVALMHVNCTVYKELRHI
FLVEDLVDSLKFAVLMWVFTYIGALFNGFTLLIVALISLFSIPVIXERHUA
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                                                                                                            note="reticulon-4; alternatively spliced"
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1. .110
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111. .3278
/gene="RTN4"
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AY316196.1 GI:34809223
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Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 4060)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hambeck von Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A. Identification of two NOGO/RIN4 genes and analysis of Nogo-A expression in Xenopus laevis
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Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitatestrasse 10, Konstanz 78457, Germany
Location/Qualifiers
                                                                                                                                                                                                                                         61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluUserGluValAlalle
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                      SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                  AlaLeuAlaLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAla
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Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.O.
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/dev_stage="older than stage 50"
1. .dov
/gene="RTN4"
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/mol_type="mRNA"
/db xref="taxon:8355"
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Arii6193 1758 bp mRNA linear VRT 25-MAY-2004
Xenopus laevis RTN4.1-B2 (RTN4) mRNA, complete cds; alternatively
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus;
1 (bases 1 to 1758)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A. Identification of two NOGO/RTN4 genes and analysis of Nogo-A
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Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
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                                                            193 AGCTTGTTCCTCCTCTCTCTGAGTGTGTTCAGTATTGTCAGCGGGGCTCCTCTATATT
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                                       1 ServalvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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Ininger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.B. and
Stuermer,C.A.O.
US-09-830-972-2_COPY_975_1163 (1-189) x AY316191 (1-1467)
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Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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/db_xref="MOSKWCAUDATA"
/db_xref="MOSKWCAUDATA"
/db_xref="MOSKWCAUDATA"
/dene="RTM4"
                                                                                                                                                                                                                                                                           AY316191 1467 bp mRNA linear VRT 25-MAY-2004 Xenopus laevis RTN4.1-N (RTN4) mRNA, complete cds, alternatively spliced.
                      3129 GCACTGATTTCCCTGTTCAGTATTCCTGTCATTTATGAAAGGCATCAGACTCAAGTGGAT 3188
                                                                                                                   3189 CACTACCTGGCACTCGTAAACAAGAATCTCAAGAGCACATCAGACCTGATTCTCTCTAAA 3248
                                                                              HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A. expression in Xenopus laevis and analysis of Nogo-A mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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Submitted (05-UNN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
  141 AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
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Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck Hanwhr, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuemer, C.A.O.
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/db xref="taxon:8355"
/tissue_type="wholemount embryos"
/dev stage="older than stage 50"
1. 1467
/gene="RTN4"
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Strausberg, L. Feingold, E.A., Grouse, L.H., Derge, J.G.,

Kausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Altschul, S.F., Zeeberg, B., Wagner, L., Schamen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Marny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Boutfard, G.G., Radriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)

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Direct Submission
Submitted (10-OCT-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20892-7510, USA
                                                   BC059960 1512 bp mRNA linear VRT 03-FEB-2004
Xenopus laevis hypothetical protein MGC68489, mRNA (cDNA clone
MGC:68489 IMAGE:4030449), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 128 Row: c Column: 9
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Bren,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1512)
Klein, S.L., Strausberg, R.L., Wagner, L.,
and Richardson, P.
                                                                                                                                                                                                      Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dev. Dyn. 225 (4), 384-391 (2002)
                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus; Xenopus.
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Contact: XGC help desk
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                                                                                                                                                                                                         note="reticulon-4; alternatively spliced"
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                                                tissue type="wholemount embryos"
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                                                                                                                                                                                                                                                                                                                Ariici92 1543 bp mRNA linear VRT 25-MAY-2004
Xenopus laevis RTN4.1-C (RTN4) mRNA, complete cds; alternatively
spliced.
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I (bases I to 1543)
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A. expression of two NOGO/RIN4 genes and analysis of Nogo-A Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
                                                                                  631
                                                                                                                        162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                                                                  Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
                                                             512 ATGIGGGICTICACCIATATIGGIGCCTIGTICAATGGICTCACCCTGCICATIGTGGCA
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Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von
Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and
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Xenopus laevis
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                                                                                                                                                                                                                                               692 CCCGGGCTGAACGCAAAGCTGAA 715
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AY316192.1 GI:34809215
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                                                                                                                                                                                                                                                                                                                                                                                      /product="MGC68489 protein"
/product="MGC68489 protein"
/brotein id="AAH59960.1"
/db_xref="G1:37747767"
/db_xref="LocalD:398819"
/translation="MACLPSGWKEKVVDLIYWRDIKRSGVVFGASLFLLLSLSVFSIV
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LNHVNCTVKELRHLFLVEDLVDSLKPANLMWVPTYIGALFNGLTLLIVALISLFSIPV
IYERHQTQVDHYLALVNKNLKSTSDLILSKVPGLKRRAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="MGC68489"
/note="Reticulon; Region: Reticulon. Reticulon, also know
as neuroendocrine-specific protein (NSP), is a protein of
unknown function which associates with the endoplasmic
reticulum. This family represents the C-terminal domain of
the three reticulon isoforms and their homologues"
/db_xref="CDD:pfam02453"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 TIGITICTCCTCCTCTCTCTGAGTGTGTTCAGTATTGTCAGCGTGCTCGCTTATATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuPheleuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                  1. .1512

/organism="xenopus laevis"

/mol_type="mRNA"

/db xref="teaxon:8355"

/clone="MGC:68489 IMAGE:4030449"

/tissue type="Kidney, adult Xenopus"

/clone_lib="NICHD_XGC_Kid1"

/lab host="DH108"

/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             x BC059960 (1-1512)
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                    1. .1512
/gene="MGC68489"
/db_xref="LocusID:398819"
119- .718
/gene="MGC68489"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
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78.72%
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Best Local Similari
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Pred. No.:
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                                                                 FEATURES
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8 셤 ò 셤 ઠે 유 ò 셤 ò 셤 ò 셤 ઠ

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                                                                                                                                                                                                                                                                                                                                                                             translation="MDEQSPDISSSHSGDERREPAQPGERKPWDDLDDVLDLTGGAGQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 GTTGTCGACCTTATTTACTGGCGGGACATTAAGAGATCCGGAGTGGTGTTTGGGGCAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 TTGTTCCTCCTGCTCTCTCTGAGTGTGTTCAGTATTGTCAGCGTGCTCGCTTATATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1701
148
21
19
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                                                                              /tissue_type="wholemount_embryos"
/dev_stage="older_than_stage_50"
1. .1701
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Mismatches:
Indels:
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Matches:
  organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                     /protein_id="AAQ82643.1"
/db_xref="GI:34809220"
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                         /mol_type="mRNA"
/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                      /codon_start=1
/product="RTN4.1-B1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-830-972-2_COPY_975_1163 (1-189)
                                                                                                                                                         gene="RTN4"
                                                                                                                                                                                                              'gene="RTN4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.17e-68
760.00
89.89%
78.72%
82.16%
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Best Local Similarity:
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DB:
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Xenopodinae; Xenopus; Xenopus;
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Submitted (05-JMN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
1. .1701
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KDBVSKLPKKESKAPSSTVPSSDFNSVVDLI YRNDI KREGVVFGASLFLLISISVPS
YVSLAY IALALLSVTISFRI YKGVLOAJ IQKSEGHPPRSILESNLALPEDVVQKHCT
VALNQVNRTVAELRELLEVEDIVNDSLKFAVLMWYFTY IGALFNGLTLLI VALISLFSI
PVI YERHQTQVDHYLALI NKNLKNTSDLI LAKVPGLKRKSE"
                                          AY316188 3886 bp mRNA linear VRT 25-MAY-2004
Xenopus laevis RTN4.2-A3 (RTN4) mRNA, complete cds; alternatively
spliced.
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/protein_id="AAQ82637.1"
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PARHWEEKEERDEDEEEDEKSWKESLEASPVLEDPGSTSGSSPTPHSPPEPSAPTEEP
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FSTGLAAMBALQBPTDNTVSASRSLIDTLETKALDQFKEEVIF8DKGVVBHPFSQQE
TISEBHAKLYSQSAKEMFSGALQSVAPPHEEFTDIKEVDYQYVDFKPFFFSKDIGY
EVKDVAEKLHVQRLILESTAKHEEKSSEREKEMISDDISDLISPLTPEVLSDSTDYREMPATV
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GATRVQVSTRAEGPTPDIVQBAYESEXTDTGIGSKINYEPRIDLVQTAFFSWQEKYSPT
AQVPALLEDSVSSPYLDIVWBAPLASTLCIETWALKPDISPVRIEPPARDEKTKAEP
EKPPSYEEAVTEVLQDQGPAAAADLGDSKQGAVVKEAEAPYISPYISIACDLIKGTQS
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MAQSFVIPEQKPGIDQKSEESSPSKPYLASFQPEIYVSKATDLFAKGLDTEISIPQER
HLHWEEFDEGLYSSKLPGSKYSPVSESPEFRLSPEELTSKHEEIQTHIAKHPEDKLQK
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

I (bases I to 3886)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hambeck von Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A. expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universited: Strasse 10, Konstanz 78457, Germany
Location/Qualifiers
1. .3886
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/gene="RTN4"
/note="reticulon-4; alternatively spliced"
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/mol_type="mRNA"
/db_xref="texon:8155"
/tissue_type="wholemount embryos"
/dev_stage="older than stage 50"
                                                                                                                                                                              Kenopus laevis (African clawed frog)
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/gene="RTN4"
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/gene="RTN4"
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Alignment Scores:

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Xenopus laevis RTM4.2-A1 (RTM4) mRNA, complete cds; alternatively apliced.
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Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and
Stuermer,C.A.O.
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                                                                                                    Conservative:
Mismatches:
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Xenopus laevis
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TITLE Direct Submission JOURNAL Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,	Universitaesestrasse 10, Konstanz 78457, Germany FEATURES Location/Qualifiers source 1.3943	/organism="Xenopus laevis" /mol_type="mRNA" /db_xref="taxon 835"	/tisbue_Cype="wnoiemount_embryos" /dev_stage="older than stage 50" gene 13943	S'UTR 118	/gene="Kin4" variation 59	/gene="K!N4" /replace="C" variation 101106	/gene="MIN4" /replace="" variation 109	/gene="RTN4" . / /replace="a" / rns 119 2017	/gene="R /note="r	/codon_start=1 /product=rRTN4.2-A1"	/protein id="AAQ82639.1" / Dax xxef==[ag1:348117.7" /+*3rq1a+ion= hwga/ocentrocoursernmysmann:num.num.num.num.num.num.num.num.num.num.	/ LIMITALE LOIS "PRESENCEDENGE STATE POLICIES OF THE PROPERTY	ASLSŠLPSLSSKEHVQTVAFSTGLAANBALQEPTDNTYSASRSLIDTLETKALDQFKE EVIFSDKGYVVEHPTSQQETISEEHAKLYSQSAKEMFSGMLQSVAPPHEEFTDIKEVD	YQYVDFKPFISSNSRDIGYEVKDVAEKLHVGRLNLESTAKHEEKSSEEKEMDISDIS PLTPEVLSDSTDYEMFATVEHSYPFSLGGSRVAGNKTDEKKIEDFEAQKTSVGFGLKV	ATVMPFYDESAQESEVTTGATRARVOVSTKAEGPTPDIVQEAYESEAVDTGISKLINYEP NIDLVQTAATSMQEKVSPTAQVPALLEDSVSSPVEDIVMPSPLASTLCLETMALKPD 1SPVRTEPDARDREFFKREDSKSPREVETJONGCRAAAAANTGISKGAVAFFAER	PY18PY18IACDLIKUTQSAASDFTEFSKFKQHEFDSQFMEFSDESSFDSELSEPSYK OWDSEVVRKETFTIKTESAMOSFVIPPOKROIJOKSEFSSSSSKFYASFOPPITVSK	ATDLFAKGLDTEISIPQERHLÄMEEFDEGLYSSKLPGSKYSPVSESPEFRLSPELTS KHEBIQTHIAKHPEDKLQKNKDKLDFLPENIEFTPIVQKADDFGKAASATHGGVDTTA	KGASEVHERKYTKEPEPSKKDEVSKLPKKESKAPSGTVPSSDFRNSYDLIYWRDIKR SGVVFGASLFLLLSLSVFSIVSVLAYIALLSVTISFRIYKGVLQAIQKSEEGHPFR SILESNLALPEDVVQKHCTVALNQVNRTVAETFLVDEDVDSLKFAVLMWVFTYIG ALFNGHTLLTALIYALISLFSIPVIYERHOTOVDHYTALINKNLKNTSDLILAKVPGLKRK	SE" SE" variation 167		Variation 231 / 2000="RTN4" / 2001 - 100	variation / Ceprace a /gene="RTN4"	/replace="" /replace="" / /replace="" / / / / / / / / / / / / / / / / / /		variation 737. 738 /gene="RTN4" /replace="ca"	variation 748 /gene="RTN4" /replace="t"	σ~~	<pre>variation 1017 /gene="RTN4" /replace="c"</pre>

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                          161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                            3188 GTCCCGGGGCTGAAGCGCAAATCAGAA 3214
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Gaps:
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Run

Sequence:

Title:

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Ad713955 Human NOG
Aad01174 Bovine ne
Add95550 Human NOG
Acc81048 Human NCG
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Ada23454 CDNA enco
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Abn86601 Human neu
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Adi31056 Human cDN
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AAZ36230
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AAS09453
ACC81048
ADP13574
AAA23454
ABV94680
ADG32772
ABX34563
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AAC64406
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AAF90323
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AAV23695
AAZ56888
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AAX04379
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1. .3492
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-De-CgnZ_1/USFTO_spool_p1/US09810972/runat_16062005_153944_18979/app_query.fasta_1.654
-DB=N Geneseq_16Dec04 -QFMT=fastap -SUPFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFWT=pc -NOSM=ext -HEAPSIZE=500 -MINLENE0 -MAXLENE=200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3163 TCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATA 3222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 AAAGAACTGAGGCGGCTTTTCTTAGTTGATTTAGTTGATTCCCTGAAGTTTGCAGTG 3282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACACTACTGATTTAA 3342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 1000nM. Also described: (1) a polymucleotide encoding the binding molecule; (2) an expression vector or system comprising the polymucleotide; (3) a host cell comprising the binding molecule or system comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence encodes rat NogoA, which is used in the exemplification of the present invention.
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                                                                                                                                                       New binding molecule that binds to the human NogoA polypeptide, NiG, NiC D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.
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                                                             Vitaliti A;
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Matches:
Conservative:
Mismatches:
Indels:
                                                             Schnell L,
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The present sequence is a cDNA encoding rat Nogo A protein which is a potent neural call growth inhibitor and is free of all central nervous sequence was generated by fusing Rol8037-3, R1-3021 cDNA sequence was generated by fusing ROL8037-3, R1-3021 cDNA sequences isolated from hexanucleotides-primed rat brain stem/Spinal cord library, and Olise EDNA from an oligo d(T)-primed rat oligodendrocyte library, Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharymgioma, ependyoma, pinealoma, haemangioblastoma, accoustic neuroma, oligodendroglioma, pinealoma, neuroblastoma or retinoblastoma and degenerative nerve consequence or Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue consequence or inhibit production of Nogo protein to induce regeneration of neurons or inhibit promote neurite
                                                       3403 CATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAAAATCCAAGCAAA 3462
HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; payperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertroly; neuronal regeneration; treatment; structural plasticity; screening; ss.
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             models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers
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 growth, regeneration or maintenance are deficient or desired. The animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                          3295 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAAGGGCGTGATCCAGGCT
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Mismatches:
Indels:
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Matches:
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nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; rat; gene; ds.
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                                                                                                                                              Cohen IR,
                                                                                                                                                               WPI; 2002-607255/65.
P-PSDB; ABB81074, ABB81076, ABB81077.
                                 Location/Qualifiers
253. .3744
                                                     /product= "Nogo-A"
                                                                                                                                              Hauben E,
                                                                                                   98IL-00124500.
98WO-US014715.
98US-00218277.
                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD
                                                                                        28-JUN-2001; 2001US-00893348
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                                                                                                                                              Eisenbach-Schwartz M,
                        norvegicus.
                                                                 US2002072493-A1.
                                                                                                         21-JUL-1998;
22-DEC-1998;
19-MAY-1999;
                                                                                                    19-MAY-1998;
                                                                             13-JUN-2002
                                                                                                                                                    Moalem G;
                        Rattus
                                    Key
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Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.

Disclosure; Page 40-44; 93pp; English.

The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central peripheral nervous system (NS). The metchod involves administerring (NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system (C combinations. The method is useful for promoting neurons system certains trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not autoimmune disease, or neoplasm. The disease results in a degenerative control method in the matter or both. The disease is not autoimmune disease, results in a degenerative control method in either gray or white matter or both. The disease is disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorse, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral dise hermiation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral curropathies associated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjorgen Lasson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, bilary cirrhosis, primary anyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-compathies, complications of various dutys (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcet-Marie-Tooth disease, pathies, complications of various dutys (e.g., metronidazole) and toxins celasgease, or lipoproteinemia. The present sequence represents a DNA cencelling and anylone. and Nogo-C), an example of NS-specific antigen

T; 0 U; 0 Other; 4684 BP; 1358 A; 1047 C; 1112 G; 1167 Sequence

Alignment Scores: Pred. No.: Score: Percent Similarity:	1.7e-100 925.00 100.00%	Length: Matches: Conservative:	4684 189 0
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Pinnock RD;

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Brooksbank RA, Dixon AK,
                  WPI; 2003-364994/35.
P-PSDB; ADB85283.
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                                                                                                                                                                             IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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07-FEB-2002; 2002GB-00002880
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Best Local Similarity:
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                                                                                                                                                                       Use of gene sequence that is down-regulated in response to streptozocin-induced diabetes, vector, host cell, animal, polypeptide and antibody, in screening of compounds for treating or diagnosing pain.
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                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated gene sequence that is down-regulated in the spinal cord in response to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence identity to a sequence whose expression products are kinases, phosphatases, ion channel proteins, receptors, transporters, G-protein coupled receptor proteins, DNA-binding proteins, proteases or enzymes, given in the specification. A gene of the invention has analgesic activity, and may have a use in gene therapy. The gene sequences, vector, host cell, animal, polypeptide and antibody are useful for screening of compounds for diagnosing or treating pain. The kits are useful for simultaneous, separate or sequential detecting and/or quantifying downsululation of a gene sequence in the spinal cord of a mammal in response to streptozocin-induced diabetes. The compound or pharmaceutical composition is useful as a medicament for treating or diagnosing pain.
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Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                          Chen MS
                                                                                          WPI; 2000-400052/34.
P-PSDB; AAY71312.
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Best Local Similarity:
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(CHEN/) CHEN M S.
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1751 CATTATCTAGGACTTGCAAACAAGGGTGTTAAGGATGCCATGGCCAAAAATCCAAGCAAAA 1810
                                                                                                                                                                                                                                                                                       Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roduct= "Nogo C protein (residues 40-238) flanked by 1-residues at the N-terminal and 239-522 residues at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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/note= "Start codon of Nogo C coding region"
715. .717
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/note= "Stop codon of Nogo C coding region"
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(pos:889. .891, aa:Xaa)
(pos:940. .942, aa:Xaa)
(pos:952. .954, aa:Xaa)
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.1230, aa:Xaa)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .87, aa:Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (pos:7. .9, aa:Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               does not end in a stop codon
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                                                                       1837
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                                                                                                                                                                                                                                                       growth inhibitor Nogo C cDNA
                                     IleProGlyLeuLysArgLysAlaAsp 189
                                                                     1811 Arcccrccarrcaaccccaaaccacar
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The present sequence is a cDNA encoding rat Nogo C protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelln material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, acoustic neuroma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma acoustic neuroma, oligodendrogloma, menagioma, chaemangioblastoma or retinoblastoma and degenerative nerve disease e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in disagnostic and screening methods for predisposition or prevent disorders and to screen for or test molecules which can treat or referred in claim 32 and SEQ ID NO: 29 in disolosure of the Process or the CNS in claim 2 and SEQ ID NO: 29 in disolosure of the content of process or the specification does not include sequences for the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content 
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Matches:
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Mismatches:
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Claim 23; Fig 14; 122pp; English.
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Best Local Similarity:
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               LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis
                                             TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
                                                               631 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGGAAAAAC
ATGTGGGTGTTTACTTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT
                                pre-diabetic, Type 2 diabetes, antidiabetic, gene therapy, insulin resistance, metabolic disease, mouse, gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moodie S, Waters S,
                                                                                                                                                                                Mouse CYP27 nucleotide sequence SEQ ID NO:87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 87; 209pp; English
                                                                                ProGlyLeuLysArgLysAlaAsp 189
                                                                                         CCTGGATTGAAGCGCAAAGCAGAT 714
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2002US-0386314P.
2002US-0386332P.
2002US-0386312P.
2002US-0386481P.
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2002US-0386512P.
2002US-0386518P.
2002US-038654P.
2002US-0386654P.
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                                                                                                                                ADF42781 standard; cDNA; 734
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                                                                                                                                                                                                                                                                                                         2002US-0386074P
                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-053469/05.
P-PSDB; ADF42782.
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511
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present invention describes a method for identifying an agent

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treating a diabetic or pre-diabetic individual. The method comprises contacting an agent to a mixture comprising a polypeptide encoded by a nucleic acid that hybridises under stringent conditions to a nucleic acid conditions to a nucleic acid encoding any of the 23 fully defined amino acid sequences given in the specification, and selecting an agent that modulates the expression or activity of the polypeptide. Also described: (1) a method of treating a diabetic or pre-diabetic animal, comprising administering to the animal acid sequence of introducing an expression cassette into a cell, comprising introducing into the cell an expression cassette comprising a promoter operably linked to a polynuclectide encoding a polypeptide, where the polynuclectide hybridises under stringent conditions to a nucleic acid encoding the above amino acid sequences; and (3) a method of diagnosing in a sample from the individual the level of the above-mentioned polynuclectide encoding the above-mentioned polynuclectide encoding the polypeptide or the level of the above-mentioned polynuclectide from the compared to a level of the polypeptide or comprising enter a modulated level of the polypeptide or comprise in either a lean individual indicates that the individual is diabetic. The method is useful in diagnosing and treating diabetic or pre-diabetic. The method is useful in diagnosing and treating diabetic or pre-diabetic. The compared to a level of the method may also be contacted the metabolic diseases in human subjects. The method may also be contacted the metabolic diseases in human subjects. The method may also be contacted the metabolic diseases in human subjects or pre-diabetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in identifying agents for treating diabetic or pre-diabetic individuals. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 GAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCTGAAGTTTGCAGTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 GAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA
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Matches:
Conservative:
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3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 3189
                                                                                                                                                                                                                     3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249
                                                                                                                                                                                                                                                                                                                                                                                                                                3370 TIGATGEGGTATTTACCTATGTTGGTGCCCTTGTTTAATGGTCTGACACTGATTTTG 3429
3010 TCAGTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 3069
                                                                                                                                                                                                                                                          SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                    3070 AGCCTATTCCTGCTGCTTCATTGACAGTATTCAGCATTGTGAGGCGTAACAGCTTACATT
                                                                                                          41 AlaLeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValileGlnAla
                                                                                                                                                                                                                                                                                                                                                       3310 AAGGAACTCAGGCGCCTCTTTAGTTGATTGATTAGTTGATTCTCTGAAGTTTGCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3490 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGGCTATGGCTAAAAATCCAAGCAAAA
                                SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                  IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                                              3250 TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACA
                                                                                                                                                                                                                                                                                                                                 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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24-JAN-2000; 2000GB-00001550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleotide is also useful for chromosome localization and for tissue expression studies. The present sequence represents a DNA encoding the human MAGI protein
                                                                                                                                                                                                                                                                         MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; stroke; cytostatic; cerebroprotective; neuroprotective; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "MAGI polypeptide"
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               ProGlyLeuLysArgLysAlaAsp 189
                                    CCTGGATTGAAGCGCAAAGCAGAA 663
                                                                                                                                                                                                                                    Human MAGI polypeptide encoding DNA.
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1. .3579
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                                                                                                                          AAZ56886 standard; DNA; 3579
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P-PSDB; AAYS6967.
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DB:
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NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuroprotective; nootropic; neuroleptic; antiparkinsonian;
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                                                                                                                                                                                                                             cerebroprotective; neuroleptic; diagnosis; therapy; ss
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SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

RESULT 9

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3129
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                                                                                                 The present sequence is that of cDNA encoding human NOGO-A (see AAB82349). NOGO-A is a previously known splice variant of the human NOGO pane on chromosome 2p21. NOGO-A cDNA was obtained by CFR amplification of human spinal cord cDNA. The invention relates to a novel splice variant, NOGO-C (see AAF90323). It provides NOGO-C polypeptides and polymuclectides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polymuclectides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Althemer's disease and Parkinson's disease, neuromuscular
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                                                                                                                                                                                                                                                                                            disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C
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                                                               Disclosure; Page 25-26; 25pp; English.
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE polypeptides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating acute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas), hyperpoliferative or dysproliferative disorders (e.g. neuroblastomas), hyperpoliferative, or dysproliferative disorders (e.g. cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may be useful in treating Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polynucleotide encoding the BACE polypeptide are useful in manufacturing a medicament for the treatment or prevention of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          responsive to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of a cancer. The polynucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present nucleic acid sequence encodes the human NogoA
                                                                                                                                                                           Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoA; Nogo-associated disease; metastasis; gene; ds.
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                                                                                  1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                            SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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                                                                                                                                                                                                                                                        SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                                                                                                                                                                                                                                                                  LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                   AlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neurotransmitter receptor protein Nogo encoding DNA.
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                                                              x ABK90134 (1-3579)
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         Conservative:
Mismatches:
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                                           Gaps:
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The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering (NS specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system (Trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or camages caused by surgery such as tumour excision. The disease is not autoimmune disease or neoplasm. The disease results in a degenerative conditionate demential and penetral sclerosis, non-arteritic optic neuropathy, and disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, anyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjorgen Larsson syndrome, peripheral compathy, chronic ataxic neuropathy, bilary cirrhosis, primary anyloidosis, obstructive lung diseases, acromegaly, malabsorption syndrome, polycythemia vera, immunoglobulin [IG)A- and IGG gamma- compathies, complications of various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjorgen Larsson syndrome, peripheral compathy, chronic ataxic neuropathy, bilary cirrhosis, primary anyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin [IG)A- and IGG gamma- compathy, disease, relangectasia, primary adrenomyeloneuropathy, Giant axonal neuropathy, and sisease, Fabry's disease, or lipoproteinemia. The present sequence represents a DNA and example of NS-specific antigen
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                                                                                                                                                                                                                                                                                                                                                                                   Beserman P, Mosonego A;
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                                                                                                                                                                                                                                                                                                                                                                                   Cohen IR,
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P-PSDB; ABB81078, ABB81079, ABB81080.
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                                                                                                                                   98IL-00124500.
98WO-US014715.
98US-00218277.
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21-JUL-1998;
22-DEC-1998;
19-MAY-1999;
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cc fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene in an expression of the gene in an expression of the gene in an expression of the gene in an expression of the gene in an expression of the gene collamnia a subject with the agent and identifying fat cell number or size in the subject. The agent comprises an antisense coligonucleotide. The subject. The agent comprises an antisense coligonucleotide to the agent, detecting binding of the agent to the polypeptide to the agent, detecting binding of the agent to the collypeptide to a change in an activity of the polypeptide, treating a subject with the agent and identifying fat cell number or size in the cumber or size comprises an antibody. A method of regulating fat cell subject number or size or number of a gent that changes the expression of a gene, and treating the subject containing fat cells and an agent that changes the expression of a gene, and treating the subject containing the subject con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
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                                                                                                                                                                                                                                                                                                                                                                          influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents human cDNA used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of identifying compounds that influence
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                                                                                                                                                                                  ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
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        GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGATCCAAGCT
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                                                                     AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                        IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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anorectic; antidiabetic.
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P-PSDB; ADO08103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a myelin-associated glycoprotein (MAG)

derivative comprising a mutation in or flanking MAG Ig-like domain 5

(Igd5), excluding the MAG derivative MAG (d1-3)-Fc, where the mutation
reduces or eliminates the ability of the derivative to regulate neurite
cutgrowth as compared to endogenous or soluble MAG without eliminating
promoting to neuronal surfaces. The inhibitors of MAG are useful for
promoting neural degeneration associated with injuries, disorders, or
treating neural degeneration associated with injuries, disorders, or
cliseases. The disorder, disease, or condition is associated with
apoptosis or results from a demyelinating disease and includes
amylotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
Kuru, multiple system atrophy, amylotrophic lateral sclerosis (fou
Gehrig's disease), or progressive supranclear palsy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New myelin-associated glycoprotein (MAG) derivative comprises a mutation in or flanking MAG Ig-like domain 5 (Igd5), excluding the MAG derivative MAG (d1-3)-Fc, useful promoting neural growth and regeneration.
                                                                                                        se; gene; human; myelin-associated glycoprotein; MAG; neural growth; neural regeneration; apoptosis; amylotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease; Huntington's disease; multiple sclerosis; Creutzfeldt-Jacob disease; kuru; multiple system atrophy; Lou Gehrig's disease; progressive supranuclear palsy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents the human NOGO-A cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 8; 81pp; English.
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1. .3579
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ADR13965 standard; cDNA; 3579 BP
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(DOME/) DOMENICONI M.
(CAOZ/) CAO Z.
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P-PSDB; ADR13966.
                                                                                 Human NOGO-A CDNA.
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                          ADR13965
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Conservative: Mismatches: Indels: Gaps:

1.31e-98 908.00 98.94% 97.35% 98.16%

> Best Local Similarity: Query Match: DB:

Percent Similarity:

Length: Matches:

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3010 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 3069
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US-09-830-972-2_COPY_975_1163 (1-189) x ADR13965 (1-3579)
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(CHEN/) CHEN M
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AlaLeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAsp

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dictivity are used in the treatment of nepplastry discusse of the treatment of nepplastry discussed of the treatment of nepplastry discussed on the treatment of pinealowa, haemangioblastoma, acoustic neuroma, oligodendroglioma, pinealoma, haemangioblastoma acoustic neuroma, oligodendroglioma, neuroblastroma or retinoblastroma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benjand dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or component plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in disquestive or desired for predisposition of disorders and to screen for or test molecules which can treat or provent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO. 29 in disclosure of the specification. However the specification does not include sequences for
                                                                                                                                                                                                                                                                                 The present sequence is a cDNA encoding bovine Nogo protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The present sequence was obtained from bovine spinal cord white matter CDNA library. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g.
                                                                                                                                             yo proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                   Claim 26; Fig 12; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           these SEQ ID numbers
                              Chen MS
                                                                                  WPI; 2000-400052/34
                              Schwab ME,
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Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 U; 0 Other;

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                184
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Length:
Matches:
Conservative:
                                                  Mismatches:
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97.35%
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Best Local Similarity:
Query Match:
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Sequence 3919 BP; 1168 A; 857 C; 890 G; 1004 T; 0 U; 0 Other;

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The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 1000nM. Also described. (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence encodes human NogoA, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                     binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder;
                                                                  2781 CATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA
2721 GCTCTGATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCGCAAAAAAT
                                               161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
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                                                                                                                                                                                                                                                                                                                   Human NogoA encoding cDNA SEQ ID NO:4.
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1. .3579
/*tag= a
/product= "NogoA"
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Zurini M;
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(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence (Genbank accession number AB0202693) encodes the human Nogo protein, a 250kDa myelin-associated axon growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of randal or cerebral trauma, spinal cord injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasis demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis, adrenoleukodystrophy, Palizaeus-Merzbacher disease, Spongy degeneration, viral infection and Krabbe's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease
                                                                                                                                                                                                                                                                                                                                                       Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central nervous system disorders.
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     /*tag= a
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26-MAY-2000; 2000US-0207366P.
29-SEP-2000; 2000US-0236378P.
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                                                                                                                                                                                                                                                                   3070 AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGGTAACAGCCTACATT
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135. .3713
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axonal growth by a central nervous system (CNS) neuron. The NgR polypeptide or an agent inhibits the binding of Nogo to NgR or NgR-dependent signal transduction in the central nervous system neuron may bused in treating central nervous system flasses, disorder or injury, egpinal cord injury. Expression of an NgR protein may be associated with inhibition of axonal regeneration following cranial, cerebral or spinal trauma, stroke or a demyelinating disease, such as multiple sclerosis, monophasic demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, or Krabbe's disease. The present sequence is used in the exemplification of the invention
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                                                                                           3563
                                                                                                                                                                                                                     The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (Pl, human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of Pl with 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive residues. The nucleic acid of the invention has neuroprotective activity. The polymucleotide may have a use in gene therapy. The nucleic acid is useful for decreasing inhibition of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy; axonal growth; central nervous system; CNS; Nogo; spinal cord injury; cranial trauma; serebral trauma; spinal trauma; stroke; Krabbe's disease; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
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                         AAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTG
                                                                             3504 TIGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG
                                                                                                                                                 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                              AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                       LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
     New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system neuron, or in treating central nervous system disease, disorder or
                                                                                                                                                                                                                                                                                           ATCCCTGGATTGAAGCGCAAAGCTGAA 3710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 126-131; 148pp; English.
                                                                                                                                                                                                                                                                      IleProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Human NogoA"
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                                                                                                                                                                                                                                                                                                                                                                             4053
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                                                                                                                              SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr11e 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; hamopolila; autoimmune disease; diabetes; inflammation; infection; fungal; bacterial; viral; HIV; allergy; arthritis; neurodegenerative disease; asthma; contraceptive; ss.
                                                                                                                                                                                                                                                            LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu
                                                                                  ATCCAGABAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
                  3264 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
                                                                 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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   41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                              LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                              AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding human secreted protein vb22_1, SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Human secreted protein vb22_1"
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98US-0103978P.
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99US-0113646P.
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28-SEP-1998;
25-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample (claimed) (M1) is useful for identifying sample is a whole blood sample (claimed) (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples is loolated at differentially expressed in peripheral blood samples (CC) and/or other solid tumors. This sequence corresponds to a gene that is fiferentially expressed and detected by the method of the invention. (Note: this sequence is not given as part of the printed specification (NCC) but was obtained from WIPO in electronic format at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3263
                peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3144 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC
                                                                                                                                                                                                                                                                                                                                                                             Stover JA;
ds; diagnosis; non-blood disease; solid tumor; gene expression;
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                                                                                                                                                                                                                                                                                                                                                                             Dorner A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-830-972-2_COPY_975_1163 (1-189) x ADP13574 (1-4053)
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Matches:
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03-APR-2003; 2003US-0459782P.
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                                                                                                                                                                                                                                                         TWINE N C.
BURCZYNSKI M E.
TREPICCHIO W L.
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STOVER J A.
SLONI D K.
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                                                                                                                                                                                                                                             WYETH
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LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu

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The invention relates to 40 human secreted proteins (AAY94981-795020),
and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
confine invention include those that are thought to be only partially
secreted, i.e., transmembrane proteins. The proteins of the invention may
cativity; cell proliferation; differentiation; immune modulation;
haematopoiesis regulation; tissue growth activity; activin/inhibin
activity; chemotactic/chemokinetic activity; activity/inhibin
activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
activity; anti-inflammatory activity; and tumnour inhibition activity. The
proteins may be administered to patients as vaccines, and the nucleotides
may be treated using the proteins or nucleotides of the invention include
autoimmune diseases; genetic disorders; haemophila; cardiovascular
diseases; cancer; bacterial, fungal and viral infections, especially HIV;
cuillain-Barre syndrome; insulin dependent diabetes mellitus; and
allergic reactions such as asthma and anaemia. They may also be used for
treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
diseases Alzheimer's disease, Parkinson's disease
and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin
sequences of the invention may be used in chromosome mapping, and as a
source of diagnostic primers and probes. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3219
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                                                                                                                   New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3160 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC
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                  Rapiejko P;
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                  Hall J,
                                                                                                                                                                                                   Claim 72; Page 321-322; 357pp; English.
                  Yuan O, Hoffman H,
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                  Valenzuela D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences that hybridize to (a), under moderately to (a); or (f) degenerate variants of (a). Polypeptides (ABF68596-ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting and stimulating and immune response. The polynucleotides cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and pancreatic tumor polypeptides, useful idiagnosing, preventing and/or treating cancer, particularly pancreatic
3520 TIGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG
                                                                                                                   161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
                                               141 AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Human pancreatic cancer expressed cDNA SEQ ID NO 53.
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09-FEB-2001; 20010S-0267568P.
28-APR-2001; 20010S-028713P.
16-MAY-2001; 20010S-0291631P.
12-UTL-2001; 20010S-039648P.
20-MG-2001; 20010S-0313999P.
27-NOV-2001; 2001US-0313626P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; tumour; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreas;
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 therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA differentially expressed in patients with SLE SeqID96
                                                      Other;
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This invention relates to novel methods for diagnosing and monitoring autoimmune and chronic inflammatory diseases. Specifically, it refers to autoimmune and chronic inflammatory diseases. Specifically, it refers to the identification of genes that have a clinical utility as diagnostic tools for the management of, in particular, patients with systemic lupus erythematosis (SLE) or rheumatoid arthritis (RA). Accordingly, the present invention describes a method for determining the levels of multiple differentially expressed genes of a patient, in a concerted manner, in order to achieve an improved diagnostic assay with sensitivity and specificity for the disease in question. As such, these genes are useful for the diagnosis of various other inflammatory disorders including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma, anylosing spondylitis, ulcerative colitis, primary sclerosing cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis. This polynucleotide is a DNA sequence representing human mRNA that is differentially expressed in patients with SLE, used in an exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing or monitoring autoimmune and chronic inflammatory diseases, such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, psoriasis and asthma by detecting the expression level of one
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                                    140
                                                                                                                                    HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                            MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarictioma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
            AAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTTAGTTGATTCTCTGAAGTTTGCAGTG
                                                                                    AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
, Hillman JL, Yu JY, Tuason O, Yap PB, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
i, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME;
                                    LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English
                                                                                                                                                                                                   3691 ATCCCTGGATTGAAGCGCAAAGCTGAA 3717
                                                                                                                                                                                     IleProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                   psoriasis; hepatitis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2001; 2001US-0279619P.
29-MAR-2001; 2001US-0280067P.
29-MAR-2001; 2001US-0280068P.
17-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291849P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-0299428P.
2001US-0299776P.
2001US-0300001P.
                                                                                                                                                                                                                                                             ABX34563 standard; cDNA; 4698
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                                                                                                                                                                                                                                                                                                               (first entry)
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Dufour GE, Hillman JL,
Daugherty SC, Dam TC,
Peralta CH, David MH,
Flores V, Marwaha R, L
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P-PSDB; ABU11573.
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, ceteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antipanemic, antipsoriatic and hepatotropic activity. The polynucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polynucleotides are particularly useful for diagnosing, treating or preventing cell particularly useful for diagnosing, treating or preventing cell consistence (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's disease, acquired immunodeficiency syndrome (ALDS), Goodpasture's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG 3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3155 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 3214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 11eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-972-2_COPY_975_1163 (1-189) x ABX34563 (1-4698)
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Matches:
Conservative:
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908.00
98.94%
97.35%
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This invention relates to a novel method for modulating the expression of a target gene in a cell. Specifically, it refers to the introduction into a cell of a polynucleotide that forms a duplex region with an mRNA transcribed from the target gene, where the duplex region omprises a mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that regulates mRNA at a post-transcriptional level. The present invention describes a method for controlling ontogenesis of a mammal, function of a mammalian cell in the post-transcriptional phase, which comprises introducing a plasmid vector comprising a promoter and nucleic acid molecule expressing an miRNA or siRNA silencing precursor to the miRNA. Accordingly, it provides a cell therapy method for treating cancer, immune disease, nerve disorder. (e.g. amyotrophic lateral sclerosis, Parkinson's disease, or Alzheimer's disease) or an inflammatory disease. The miRNA or the plasmid vector. As such, they can be developed into the cell that exhibit cytostatic, immunosuppressive, parkmaneral compositions that exhibit cytostatic, immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating expression of a target gene in a cell, for treating cancer, an immune disease, or a nerve disorder, comprises introducing into the cell a polynucleotide that forms a duplex region with an mRNA transcribed from
                                                                                                                                                                human; ds; miRNA; microRNA; ontogenesis; cell therapy; cancer; immune disease; nerve disorder; amyotrophic lateral sclerosis; Parkinson's disease; Alzheimer's disease; inflammatory disease; slikh silencing precursor; cytostatic; immunosuppressive; noctropic; neuroprotective; antiinflammatory; immunotherapy; reticulon 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4789 BP; 1422 A; 1052 C; 1075 G; 1240 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene whose expression is modulated by miRNAs of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
                                                                                                                          Human reticulon 4 DNA, target gene of miRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; SEQ ID NO 436; 865pp; English
ADR83534 standard; DNA; 4789 BP
                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-2004; 2004WO-JP001433
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                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       target gene
                                                                                                                                                                                                                                                                                               Homo sapiens,
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                                                                                 02-DEC-2004
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pharmaceutical compositions that exhibit cytostatic, immunosuppressive, nootropic, neuroprotective and antiinflammatory activities and hence can be used for immunotherapy. This polynucleotide sequence is a human target

1.97e-98

Alignment Scores:

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3254 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 3313
                                                                                                                                                   SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                   US-09-830-972-2_COPY_975_1163 (1-189) x ADR83534 (1-4789)
Length:
Matches:
Conservative:
Mismatches:
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            908.00
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                AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGGAGCGTAACAGCCTACATT
                                                                                                                                          ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
                                                                                                                                                                                                                                                         3554 AAGGAACTCAGGCGCCTCTTCTTAGTTGATTTTAGTTGATTCTCTGAAGTTTGCAGTG
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                                                                              3374 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
                                                                                                            IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                      SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                                                                                                                                                                                                                                                                                                            AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                      AlabeuAlabeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                  LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bone remodelling; osteoporosis; human; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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            expressed with genes known to be involved in bone remodelling and osteoporosis. The invention is used to diagnose disorders associated with bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
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                                                                                     BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;
substantially purified and isolated polynucleotides which are
                                                                                                                                 4822
184
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Conservative:
Mismatches:
Indels:
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                                                       remodelling genes of the invention
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908.00
98.94%
97.35%
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Best Local Similarity:
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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing a change in expression of the gene crelative to expression of the gene in an expression vector not exposed to the agent, treating a subject with the agent and identifying fat cell number or size in the subject. The agent comprises an antisense consprises providing a polypeptide and an agent, exposing the oligonucleotide. The subject comprises an ammal, preferably a human. The conjoquelocide ide agent, detecting binding of the agent to the agent, detecting binding of the agent to the agent comprises an antibody. A method of regulating a subject or a change in an activity of the polypeptide, treating a collippeptide or a change in an activity of the polypeptide, treating a comprises providing a subject containing fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents
                                                                                                                                                                                                                                                                                                                Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3492 BP; 1035 A; 800 C; 817 G; 840 T; 0 U; 0 Other;
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Mismatches:
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                                                                                 09-OCT-2002; 2002US-00267502.
                                                                                                                           2002US-00267502
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98.42%
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P-PSDB; ADO08105.
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Best Local Similarity:
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                                       15-APR-2004.
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2980 GCCAGCTTATTCCTGCTGTCTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTAC

20 AlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr

40 ilealaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln 60 AlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla

2920 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGTATTTTGGT

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1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValVal---PheGly

US-09-830-972-2_COPY_975_1163 (1-189) x AD007888 (1-3492)

Indels:

Query Match: DB:

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                                                                                                                                                                                                                                                                  139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirhumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; nucoprotective; antibacterial; virucide; fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; hyperproliferative disorder; neoplasm; cardiovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; skin aging; ocular disorder; corneal infection; wound healing; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human secreted protein is used medical condition.
                                     3160 ATATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACA
                                                                                                                                                                 ValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle
                                                                                                                                                                                                                                                                                                                  GTGTTGATGTGGGTATTTACTTACGTTGGTGCTTGTTCAATGGTTTGACACTACTGATT
IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr
                                                                                                                               100 IleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAla
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repropretedive; antibacterial; virtucide; fungicide; and opticality; carbonic processions and polymerical; carbonic condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arbhritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arreet, cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithalial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAR32690 to AAR32698 and AAB64421 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1220 TTGATGTGGGTATTTACCTATGTTGGTGCCCTTGTTTAATGGTCTGACACTACTGATTTTG 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1520 AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ServalvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1758 BP; 524 A; 380 C; 348 G; 504 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-1758)
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-830-972-2_COPY_975_1163 (1-189)
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Best Local Similarity:
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MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
94 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new member of the human neuroendocri
specific protein family, designated NSPH. The present sequence encodes
the human NSPH protein
                                                                                                                                         214 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT
                                                                      154 TIGGCCCTCCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                                                                                                                                                                                                    GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
                                                                                                                                                                                                                         GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
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                                   LeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                                                                                                                                                                              ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTTGACTACTGATTTTTGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC
                                                                                                                  62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Specific protein of human neuroendocrine, coding sequence and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NSPH encoding cDNA sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 CCTGGATTGAAGCGCAAAGCTGAA 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 14; 21pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
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                                                                                                                                                                                                                       stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
neuromuscular disorder; psychiatric disorder; developmental disorder;
neuroprotective; nootropic; neuroleptic; antiparkinsonian;
cerebroprotective; neuroleptic; diagnosis; therapy; ss.
                                                                                                                                                                                                    chromosome 2p21; neuropathy; spinal injury; brain injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValValAspLeuLeuTyrTrpArgAspIleLysLysThrClyValValPheGlyAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600 BP; 161 A; 113 C; 144 G; 182 T; 0 U; 0 Other;
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Matches:
Conservative:
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Indels:
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24-JAN-2000; 2000GB-00001550.
                                                                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-2000; 2000WO-GB004345.
                                         AAF90323 standard; cDNA; 600
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904.00
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97.73%
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P-PSDB; AAB82348.
                                                                                                                    (first
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                                                                                                                                                            Human NOGO-C cDNA.
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                                                                                                                                                                                                                                                                                                                                                                WO200136631-A1
                                                                                                                                                                                                    NOGO-C; human;
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                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                    23-JUL-2001
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                                                                               AAF90323;
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human neuroendocrine

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24-JUL-1997;
                               12-AUG-1996;
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19-FEB-1998
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                                                                                   LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                               CTATTCCTGCTGCTGTTCATTGATTCAGCATTGTGGGGGGTAACAGCCTACATTGCC
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                                                                                                                                                                                  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla11eSer
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This sequence encodes a human neuroendocrine-specific protein-like protein (NSPLP) of the invention. Recombinant cells transformed with the DNA are used to express the NSPLP proteins, which are used to treat cancer and neurodegenerative diseases such as amyotrophic lateral sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be used to inhibit activity of the NSPLP proteins. Antibodies specific for used to inhibit activity of the NSPLP proteins. Antibodies specific for NSPLP are used for disgnosis and monitoring treatment of diseases associated with NSPLP expression, in usual immunoassays, and to isolate NSPLP from natural sources. The NSPLP proteins, or their fragments can also be used in drug screening to identify NSPLP antagonists. The nucleic acid can be used diagnostically and for monitoring treatment (in hybridisation or amplification assays); to isolate closely related sequences; in gene therapy for both sense and antisense applications (including use of ribozymes) and for mapping the natural genomic sequence
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                                                                                                                                                                                                                                                                                             Human neuro-endocrine-specific protein-like proteins - useful for diagnosis, monitoring and treatment of cancer and neuro-degenerative disease.
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P-PSDB; AAW53947.
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                                                              TyrLeuGlyLeuAlaAsnLysSerVallysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                             588 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleoited is also useful for chromosome localization and for tissue expression studies. The present sequence represents a DNA encoding the human MAGI protein variant
              LeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis
                          MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; stroke; cytostatic; cerebroprotective; neuroprotective; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
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P-PSDB; AAY56969.
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1036 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTAATGGCTAAAATCCAAGCAAAAATC 1095
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Greene JM, Ferrie AM,
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R, Brewer LA,
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                                                                                                                                                                                                   The present sequence is that of cDNA encoding human NOGO-B (see AABB2350). NOGO-B is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel NOGO gene splice variant, NOGO-C (see AAF90323). It provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and disgnostic assessing to the seaso associated with inappropriate NOGO-C
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                                                                                                            New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
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Human RIN4B encoding cDNA SEQ ID NO 3.

04-MAR-2002

ABA05903;

Human; RTN4B; gene; ss

Homo sapiens

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CDNA; 1216

ABA05903 standard;

Location/Qualifiers 5. .1126

"RTN4B"

/product= /*tag=

> CN1311439-A 05-SEP-2001.

02-MAR-2000; 2000CN-00111791 02-MAR-2000; 2000CN-00111791

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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therappy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypurcleotides. Specific uses are described for each of the linker and the last are most highly expressed in (see AAX04311 for described uses)
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useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
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Mismatches:
Indels:
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Matches:
                                                 Claim 1; Page 235-236; 380pp; English.
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The invention relates to human RTN4B protein and coding sequence, useful for providing a cDNA sequence of human RTN4B. The protein is an isomer of RTN4 with RTN family members. The present invention also refers to polypeptide encoded by a nucleotide sequence and manufacturing method and application of the polypeptide and polypucleotide.
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                                                                                                                                                                                                                                                                                                                                                                preparation and
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TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC

ProGlyLeuLysArgLysAlaAsp 189

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treatment of e.g. tumors and degenerative disease, also related proteins,
antibodies and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis, cell death, cytostatic, neuroprotective; immunosuppressive; antiarthritic; dermatological; antianflammatory; hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian; vasotropic; verebroprotective; antialcoholic; gene therapy; tumour; autoimmune disease; degenerative disease; viral infection; leukaemia; carchnoma; sarcoma; multiple soleromis; rheumatoid arthritis; diabetes; lupus; hepatitis; influenza viruses; Alzheimer's disease; Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;
                                                                                                   MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAla
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 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                              GluLeuargargLeuPheLeuValaspaspLeuValaspSerLeuLysPheAlaValLeu
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therapy. The polynucleotides also related vectors, hosts (or their extracts), encoded polypeptide (or their receptors) and/or agents that inhibit their activity (including antisense sequences) are used for treatment or prevention of tunnours, autoimmune or degenerative diseases and viral infections, specifically leukaemia, carcinoma, sarcoma, multiple sclerosis, rhemmatoid arthritis, diabetes, lupus, or infection with hepatitis or influenza viruses, Alzheimer's, Huntington's or Parkinson's disease, reperfusion injury, stroke and alcoholic liver disease. Detection of the polymelectides and derived polypeptides can also be used for diagnosis of these diseases. This sequence encodes an apoptosis-associated protein described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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Matches:

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AAZJ6228-49 encode bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell lines, to regulate hematopoiesis, and to treat well and proliferation of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (GSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo.

C suppression, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoeitic stem cells, either in place of or in proliferation of hematopoeitic stem cells, either in place of or in proliferation of hematopoeitic stem cells, either in place of or in coppulate the stem cell compartment after irradiation or chemocherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage canduck an application in healing bone fractures.
                                        Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; erythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelo: colony stimulating factor; granulocyte; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer; bone fracture; cartilage damage; artificial joint; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations.
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cDNA encoding a bone marrow secreted protein designated BMS112.
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product= "bone marrow secreted protein"
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98US-0101603P.
98US-0102540P.
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Alignment Scores: Pred. No.:

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The invention relates to a method of detecting an autoimmune disorder in a subject comprising obtaining a biological sample, preferably a peripheral blood monourclear cell, from a subject, determining expression levels of at least two genes in the biological sample, and comparing the expression level of aach gene determined with a standard, where the comparison detects the presence of an autoimmune disorder in the subject. The method is useful for detecting or diagnosing an autoimmune disorder, e.g. rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, or type 1 (insulin-dependent) diabetes. The present sequence therease.
                                                                                                         Detecting an autoimmune disorder in a subject comprising comparing the expression level of each gene determined with a standard, where the comparing detects the presence of an autoimmune disorder in the subject.
                                                                                                                                                                                              Claim 10; SEQ ID NO 62; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the described method
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Sequence 1785 BP; 520 A; 316 C; 402 G; 547 T; 0 U; 0 Other;

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Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                                                                neuroblastoma, hyperproliferative disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoB; Nogo-associated disease; metastasis; gene; ds.
                                                                                                                                                                                                                                                /product= "Human NogoB protein"
                                                                                                                                                                                                                                                                                                                                                                                   Blackstock WP, Hale RS, Prinjha R, Rowley A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 50-52; 68pp; English.
CCTGGATTGAAGCGCAAAGCTGAA 810
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                   DNA encoding human NogoB protein.
                                       BP
                                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD.
(SMIK ) SMITHKLINE BEECHAM PLC.
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                                       ABK90133 standard; DNA; 2052
                                                                              (first entry)
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                                                           ABK90133;
                                                                                                                                                                                               Homo
                             Key
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE polypeptides, and determining if the test agent interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating caute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas, portains), hyperproliferative or dysproliferative disorders (e.g. cirrhosis, psoriais, Reloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may be useful in treating Nogo-associated diseases the modulators of Nogo or BACE polypeptides, and the polynucleotide encoding the BACE polypeptide are useful in creaning a medicament for the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polymucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy recombiques. The present nucleic acid sequence encodes the human NogoB of the invention

523 T; 0 U; 0 Other; Sequence 2052 BP; 511 A; 512 C; 506 G;

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                                                                                                                  ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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        Length:
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Conservative:
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        1.82e-98
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Alignment Scores:
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            Pred. No.:
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous centidates of (a); (d) sequences consisting of at least 20 contiguous stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABR68596. ABR68596. Consequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABR68596. Concern in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating panceatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           936
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diagnosing, preventing and/or treating cancer, particularly pancreatic
cancer.
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                                                                                                                                                              Jiang Y;
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Indels:
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09-FEB-2001; 2001US-0267568P.
21-MAR-2001; 2001US-0278651P.
28-ARR-2001; 2001US-0287112P.
16-MAY-2001; 2001US-0291631P.
12-UUJ-2001; 2001US-0339544P.
20-AUG-2001; 2001US-0333626P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                    Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour; stress-phosphorylated endoplasmic reticulum protein; cytostatic; gene therapy; cell growth; cellular stress response; neuron growth; regulator of oxidative stress; inhibitor of neurite outgrowth; axon regeneration; diagnosis; cancer; identification; ss.
                         MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis
                                                                                           TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                            .057 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
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Mismatches:
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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1268 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligonucleotide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
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                                                                                                                                                                                                                                                                                                        human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
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Nagai K, Kojima S, Otsuki T, Koga
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                                                                           1328 ccrecarreaaccccaaaccreaa 1351
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02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
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                                                                                                                                                                       synthesizing full length cDNA clones and their use
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                                                         Isogai T, Hayashi K, Ishii S, Kawai Y, a T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.
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                                                                               Wakamatsu A, Sugiyama
                   (HELI-) HELIX RES INST
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                                                         Nishikawa T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to nucleic acids (AA198058-AA198161) or their monologues expressed by human neuroblastomas useful for detecting genes expressed by neuroblastoma and for analysing their structure and function. The nucleic acids are useful for the diagnosis and prognosis of
                                        61
                                                                                                                    81
                                    GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                                                                                                                                                                                GAACTCAGGCGCCTCTTCTTAGTTGATTAGTTGATTCTCTGAAGTTTGCAGTGTTT
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CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
                                                                                                                GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                              GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
                                                                                                                                                                                                                                                                            GluteuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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(HISM ) HISAMITSU PHARM CO LTD.
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12-MAY-2000; 2000JP-00140387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; human; cytokine; cellular proliferation; cell movement; cellular differentiation; immune system regulator; anti-inflammatory; memacropoiesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy; genetic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
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                                                                                                                                                                                                                                                                                                           1006 TCAGTTGTTGACCTCCTGTACTGAGAGACATTAAGAAGACTGGAGTGGTGTTTGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1126 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1186 ATCCAGAAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                                                                                                                                                                                                                             SerLeuPheLeuLeuLeuSerLeuThrValPheSerlleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 AlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                                                                                                1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extended human secreted protein coding sequence, SEQ ID NO.
  U; 0 Other;
                                                                                                                                                                                                                                  US-09-830-972-2_COPY_975_1163 (1-189) x AAI98079 (1-1980)
                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
T; 0
  C; 423 G; 583
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  601 A; 373
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898.00
98.41%
96.30%
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  BP;
                                                                                                                                     Best Local Similarity:
Query Match:
DB:
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607

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The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and amethod of binding the bingspeptide to an antibody. The polymucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing human tissues and cells, and for distinguishing between human tissues and cells, and for calls from non-human clels that do or do not express the polymucleotides comprising the cDNAs. The polymucleotides and conceptions are useful in Grensic procedures or diagnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence represents a human secreted polymucleotide of the invention. Note: The sequence data for this patent did not form part of the printed segment of the printed segment of the printed segment.
128 AIGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide encoding secreted polypeptide, useful for gene therapy, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes.
                                                                                                                                              548 TATCTAGTACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC
                                      LeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis
                                                                                                                         TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
                                                                             488 crcarrrcacrcrrcagrgrrccrgrrarrrargaacggcarcaggcacagaraarcar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clusel C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; gene; ss; genetic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bougueleret L, Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 110; 113pp; English.
                                                                                                                                                                                                         ProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                                                                   608 CCTGGATTGAAGCGCAAAGCTGAA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted polynucleotide #110.
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99WO-IB000282.
2000WO-IB000951.
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15-SEP-2000; 2000US-00663600
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P-PSDB; ADP19259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of the investion. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may or can synchines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement tumour inhibition activity. The DMAS passed in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify the passed or cellular procedures to identify individuals or in diagnostic procedures to identify constructing a high resolution map of the human chromosomes. They constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              valvalaspieuLeuTyrTrpArgAspIleLysLysThrGlyValValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents an extended human secreted protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 991 BP; 280 A; 175 C; 232 G; 304 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                  Dumas Milne Edwards J;
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                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 185-186; 516pp; English.
                                                                                                                                                                                                                                                                                                                                                     New isolated human secreted proteins.
                                                                                                   97US-0069957P.
98US-0074121P.
98US-0081563P.
98US-0096116P.
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Crohn's disease; asthma; ulcerative collitis; hypereosinophila;
irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
                                                                                                           ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                           LeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle
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The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological cordetecting the altered expression of genes in an immunological cordetecting the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the invention of pan immunopathological condition in a sample, conditions to form one or more hybridisation complexes and comparising the plurality of cDNAs under conditions to form one or more hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The cnontoxing the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray for monitoring culcerative colitis, hypercosinophilia, irritable bowel syndrome, culcerative colitis, hypercosinophilia, irritable bowel syndrome, culcerative colitis, hypercosinophilia, irritable for some syndrome, carcinogenicity studies, forensics or pharmacogenomics. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of form to term the printed specification but was obtained in electronic format directly format directly format directly formation.
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                                                                                                                                                                                       A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
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                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 382; 50pp; English.
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or osteoarthritis.
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                                                                                                        characterisation, diagnostic or therapeutic use. They can also be used as tissue or mol.wt. markers, for chromosome identification, to identify genetic disorders, to isolate new related DNA, as sources of primers for proteins may also have many biological activities, e.g. cytokine, immunomodulator, haematopojesis regulating activity, tissue growth activity, activin or inhibin activity, chemotactic or chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, antinflammatory, adherin and tumour invasion suppressor activity, and tumour inhibition activity. The proteins can be expressed in vivo from DNA, introduced in gene therapy vectors
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                      specific proteins. Novel cDNA clones (see AAV30916-32) coding for human secreted proteins (see AAW58580-90) are claimed. These can be used for recombinant production of the secreted proteins for analysis,
to neuroendocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1941 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAA
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                                                                                                                                                                                                                                               GATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGC
                                                           sGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLe
                                                                                                           1611 GGAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTT
                                                                                                                                                                                uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAl
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/note= "putative leader/Bignal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein BG160_1 cDNA
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97US-00740274
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Spaulding V,
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24-OCT-1997;
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE polypeptides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating caute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas, cartenberal nerve damage, and in neoplastic (e.g. glioblastomas, cartenberal nerve damage, and in neoplastic (e.g. glioblastomas, cartenberal nerve damage, modificative or dysproliferative disorders (e.g. carrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may act as modulators or of BACE activity and in particular agents that may act as modulators or nogo or BACE polypeptides, and the polynucleotide encoding the modulators of Nogo or BACE polypeptides, and the polynucleotide encoding the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polynucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                                                                                                                                  Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; Nogoc; Nogo-associated disease; metastasis; gene; ds.
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/product= "Human NogoC protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                 DNA encoding human NogoC protein.
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(SMIK ) SMITHKLINE BEECHAM PLC.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

1e-93 864.00 97.88% 96.30%

Best Local Similarity: Query Match: DB:

Percent Similarity:

Score:

Alignment Scores:

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                                                       GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 307
                                                                                                     CTATTCCTGCTTCTTTCATTGACAGTATTCAGCATTGTAGAGCGTAACAGCCTACATTGCC 367
                                                                                                                                                              TIGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 427
                                                                                                                                                                                                                                   428 cagaaarcagargaaggccacccarrcaggccararcrggaarcrgaagrrgcrararcr 487
                                                                                                                                                                                                                                                                GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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                                                                                                                                              LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
                                                                                                                                                                                                       GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                    MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                    LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
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Spaulding V, Agostino MJ;
US-09-830-972-2_COPY_975_1163 (1-189) x ABK90135 (1-1798)
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Treacy M, Bowman MR,
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Merberg D,
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tuman cDNA clones represented in AAF98374 - AAF98489 encode secreted proteins AAB90667 - AAB90760. The CDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The polypeptides and nucleic acids may be used as nutrients or to modulate cytokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The CDNA sequence, proteins, their agonists and/or antagonists exhibit haematopoiesis proteins, their agonists and/or antagonists exhibit haematopoiesis celulating activity; tissue growth activity; activin/inhibit activity; chemotactic/chemokinetic activity, haemostatic and thrombolytic activity; chemotactivity; cadherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98490 - AAF98572 which are specific for the CDNA clones encoding the secreted
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                                               Isolated nucleic acids encoding polypeptides, useful for modulating e.g. cytokine and cell proliferation/differentiation activity, the immune
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Conservative:
Mismatches:
Indels:
                                                                            system and hematopolesis regulating activity.
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862.50
95.77%
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2001-244801/25
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Best Local Similarity:
                P-PSDB; AAB90682
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The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell. Transformed with the vector, the proteins encoded by the polynucleotides, antibodies that bind to the proteins and identification of modulators of the proteins or the proteins and identification of polynucleotides can be used as probes for the identification and isolation of full length conversion in the proteins can also be used as nutritional supplements. The protein is useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. cheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Albrimmer's also useful for treating neurodegenerative diseases (e.g. Albrimmer's also useful for treating neurodegenerative diseases (e.g. Albrimmer's also useful for treating neurodegenerative diseases (e.g. Albrimmer's also useful for treating neurodegenerative diseases (e.g. Albrimmer's also useful for treating neurodegenerative diseases (e.g. Albrimmer's also useful for treating neurodegenerative diseases (e.g. Albrimmer's also useful for treating neurodegenerative diseases (e.g. Albrimmer's also useful for treating neurodegenerative diseases (e.g. Albrimmer's also be also and allergic reactions and challergic for the also also also and allergic reactions and enconditions (e.g. asthma). They are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Six hundred and twenty five polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coagulation disorder; haemophilia; inflammatory disorder; ulcer; tissue regeneration; wound healing; haematopoiesis; myeloid deficiency; lymphoid cell deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; gene; secreted protein; immune deficiency; viral infection; bacterial infection; fungal infection; autoimmune disorder; burn; rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis; diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;
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sequences encoding a secreted protein
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                                                                                                                                                                                                                                                                                                            ABK34580 standard; cDNA; 1514
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; seppis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder;
                                                                                                                                                                                          IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla
                                                                                                                                                                                                                                                                                                                 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATTTA
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                                                                                            LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSer
                                                                                                                     AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC
                                                                                                                                            IleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArg
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                                                                                                                                                                                                                                                                   TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT
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/product= "Human secreted protein precursor"
/note= "CDS does not include start codon"
  172
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                                                                       x ABK34580 (1-1514)
           Conservative:
Mismatches:
Indels:
  Matches:
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                                                                    US-09-830-972-2_COPY_975_1163 (1-189)
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844.00
98.87%
97.18%
91.24%
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            Percent Similarity:
Best Local Similarity:
Query Match:
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AXD AAD08345-AAD08394 represent CDNAs corresponding to 50 human secreted

CC protein genes and AAE03998-AAE03947 represent the proteins they encode.

CAAE03948-AAE03936 represent human secreted protein fragments or variants.

CC The genes and their secreted proteins are useful for preventing, treating

CC or ameliorating medical conditions, e.g., by protein or gene therapy.

CC pathological conditions can be diagnosed by determining the amount of the

CC new protein in a sample or by determining the presence of mutations in

CC chased on the tissues in which they are most highly expressed, and include

CC developing products for the diagnosis or treatment of proliferative

CC developing products for the diagnosis or treatment of proliferative

CC developing products for the diagnosis or treatment of proliferative

CC developing products for the diagnosis or treatment allacines.

CC developing products for the diagnosis or treatment of proliferation

CC developing products for the diagnosis or treatment of proliferation

CC developing products for the diagnosis or treatment of proliferation

CC developing products for the diagnosis or treatment of proliferation

CC developing products for the diagnosis or treatment of products

CC disorders, schizophrenia, sthem, allergies,

CC disorders, disorders, diadney disorders, disease, Parkinson's disease),

CC cognitive disorders, endocrine disorders, parkinson's disease,

CC programory-related disorders, and cound healing and epithelial cell

CC proclines can also be used to aid wound healing and epithelial cell

CC proliferation, to prevent skin aging due to sunburn, to maintain organs

CC pregenerate tissues, to identify their cognate ligands or binding

CC professed on modify storage properties. Antibodies apporting tora

CC process and in chemotaxis, and can be used as a food additive or

CC process of the invention can be used in alleviating symptomes associated

CC radiousers remember and the disorders and in diagnostic immunosassy or environment seminar and an e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome.
                                                                                                                                                                                                                                                              "Mature human secreted protein"
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899. .1189
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Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;

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x AAD08386 (1-1683)
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                       US-09-830-972-2_COPY_975_1163 (1-189)
 7.61e-80
748.50
86.17%
84.57%
80.92%
                          Percent Similarity:
Best Local Similarity:
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716 GGCGCTAÁGAGGCACGCTGAG 736
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679.00
84.49%
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73.41%
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                                                                                                                        GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                            GlukeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                                                                                348 CTATTCCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
                                             LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                   GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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         LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                              Rat cDNA differentially expressed in MYCN activated cells SeqID 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                rat; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; MYCN activated cell.
                                                                                                                                                                        1088 GAACTCAGGCGCCTCTTCTTAGTTGATTTTAGTTGATTCTCTCTGAAGCT----
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NUCHTERN J G.
PLON S E.
SHOHET J M.
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This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to proceed the sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protoconcogene that is amplified in neuroblastoma cells and is common in small concogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as used for screening assays by identifying molecules or compounds that compositions at a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the printed specification but has been obtained in electronic format from the UN Patent Office at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 GCCGCACTCTCAGCCACCATCATACCGCATCTACAAGTCTGTTTTACAAGCAGTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1520 BP; 398 A; 354 C; 336 G; 432 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
SEQ ID NO 333; 27pp; English.
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CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGGTGGCGTGGCCTACCTGGCCCTG 1887

PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu

23

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LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82

63

83

43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln

GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102

3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu

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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the cells not expression of the gene crelative to expression of the gene in an expression vector not exposed to the agent, treating a subject with the agent comprises an antisense colligonucleotide. The subject comprises an antisense colligonucleotide. The subject comprises an antisense colligonucleotide. The subject comprises an antisense colligonucleotide are comprises an appropriate or the agent, detecting binding of the agent to the comprises of the agent to the agent of the agent to the agent and identifying fat cell number or size in the comprises an antishody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject comprises conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that containing or preventing                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
                                                                                                                                                                                                               Human, gene, 88; fat cell number, fat cell size, obesity, diabetes,
anorectic, antidiabetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 213; 275pp; English.
ADO07887 standard; cDNA; 2331 BP
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                                                                                                          (first entry)
                                                                                                                                                               Human polynucleotide #66
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P-PSDB; ADO08104
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                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                       01-JUL-2004
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                                                     AD007887;
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2128 IGGCTCCTGACCTACGTTGGCGCTCTCTTCAATGGCCTGACCCTGCTGCTCATGGCTGTG 2187

143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162

2068 CTGAGGAGGCTCTTCCTTGTCCAGGACCTGGATTCCTTAAAATTTGCAGTCCTGATG 2127 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142

LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet

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123

2248 CTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAAGATTCAGGCTAAAATCCCA 2307

2308 GGCGCTAAGAGGCACGCTGAG 2328 Сіугеціувагогуваї амвр 189

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AAX75770 standard; DNA; 3202

RESULT 52

AAX75770;

LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182

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Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer; disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; budquitin B; apolipoprotein B; MAP2; neurofilament-L; neurofilament-L; neurofilament-E; presenilin I; presenilin II; cellular tumour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bc1-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A;
                                                                                                                                                                                                                                                                                                                                                                                                        Human neuroendocrine-specific protein NSP-A DNA.
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(UYRO-) UNIV ROTTERDAM ERASMUS.
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US-09-830-972-2_COPY_975_1163 (1-189) x AD007887 (1-2331)

Gaps:

Length:
Matches:
Conservative:
Mismatches:
Indels:

2.86e-71 679.00 84.49% 67.91%

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores: Pred. No.:

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2370 crigidactrigricacarcacaraaargcrigricacdaaagarricaggcraaaarccca 2429
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                         143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr
                                                                                                 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                    Lung cancer related gene sequence SEQ ID NO:3237.
                                                                                                                                                                                                                    2430 eccernadadecacecreae 2450
                                                                                                                                                                               GlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                                   ВР
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25-SEP-2000; 2000US-02350424P.
25-SEP-2000; 2000US-02350424P.
25-SEP-2000; 2000US-0235134P.
26-SEP-2000; 2000US-0235280P.
26-SEP-2000; 2000US-0235387P.
26-SEP-2000; 2000US-0235387P.
27-SEP-2000; 2000US-023538P.
27-SEP-2000; 2000US-023580P.
27-SEP-2000; 2000US-023580P.
28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236034P.
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28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236031P.
29-SEP-2000; 2000US-0236031P.
02-OCT-2000; 2000US-0236031P.
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2000US-0234052P.
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2000US-0234567P.
2000US-0234923P.
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2000US-0209531P.
2000US-0233133P.
2000US-0233617P.
2000US-0234009P.
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2000US-0237425P.
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ABL64900
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                                                                                                                                                                                                                                                 This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegeneratives (e.g. Alzheimer's disease, Down's syndrome, wyotonic dystrophy, Huntington's disease, and theimer's alsease, Down's syndrome, wyotonic dystrophy, Huntington's disease, and mitiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disease. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated associated protein 2 (MAP2), neurofilament-L, neurofilament-M, neurofilament-P, resemilin I, presemilin II, glial fibrillary acidic protein (GRAP), the callular tumour antigen p53, B-cell leukemia/lymphoma protein-C (HMGP-C) and neuroendocrine specific protein A. This sequence encodes the wild type and mutant protein fragments represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2070 AAAACCGACGAACGCTTTTCAAGGCCTACTTGGAGCTTGAGATCACCCTTTCTCAG
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                                                                                                                    Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;
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Mismatches:
Indels:
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Matches:
                                         Burbach JPH;
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                                         Van Leeuwen FW, Grosveld FG,
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84.49%
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73.41%
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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent concerning for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 or ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an inti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, ossophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcer, infiltrating lobular cancer, sequamous cell carcinoma, neuroendocrine carcinoma and Wilm's
                                                                                                                                                                                                                                                                                 Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                           Horrigan S;
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                                                                                                                                                                        Ebner
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3237; 44pp; English
                                                                                                                                                                           Carter KC,
                    03-0CT-2000; 2000US-0237606P.
03-0CT-2000; 2000US-0237608P.
01-NOV-2000; 2000US-0244867P.
01-NOV-2000; 2000US-024687P.
03-OCT-2000; 2000US-0237604P
                                                                                                                                                                        Augustus M,
                                                                                                                                                                                               Weaver Z;
                                                                                                                             (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                        WPI; 2002-188264/24.
                                                                                                                                                             Young PE, A
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1950 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGGTGGTCGTGGCCTAGCCTGGCCTG 2009 2070 AAAACCGAGGAAGGCCACCCTTTCAAGGCCTACTTGGAGGTTGAGATCACCCTTTCTCAG 2129 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122 AlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaileGln 62 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82 2010 GCCGCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTCTGTTTTACAAGCAGTGCAG PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu US-09-830-972-2_COPY_975_1163 (1-189) x ABL64900 (1-3202) Length:
Matches:
Conservative:
Mismatches: Indels: 4.47e-71 679.00 84.49% 67.91% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: . 43 2130 103 23 63 83 윱 셤 g g ઠે ò ò ò 셤 È

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CTGAGGAGCTCTTCCTTGTCCAGGACCTGGTGGATTCCTTAAAATTTGCAGTCCTGATG 2249

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2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAAGATTCAGGCTAAAATCCCA 2429
                                                                                                                                      182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual detained anomal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated bNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                   22550 TGGCTCCTGACCTAGGCGCTCTTCAATGGCCTGACCCTGCTGCTGTATGGCTGTG
                                                                                    TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu
                                                                                                                                    LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro
                                                                   143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                Human soft tissue sarcoma-upregulated DNA - SEQ ID 1480.
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                                                                                                                                                                                                                             2430 GGCGCTAAGAGGCACGCTGAG 2450
                                                                                                                                                                                                      GlyLeuLysArgLysAlaAsp 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                          ADQ18661 standard; DNA; 3202
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ADR65814 standard; DNA; 3202
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                                                                                                                                                                                                                                                                                                                                            LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
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                                                                                                                                                                   2070 AAAACCGACGAAGCCACCCTTTCAAGGCCTACTTGGAGCTTGAGATCACCCTTTCTCAG
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                                                                                                                                                       LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu
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                                                                                                                    AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln
                                           ValAspLeuLeuTyrTrpArgAsp1leLysLysThrGlyValValPheGlyAlaSerLeu
                                                                                23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu
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                          x ADQ18661 (1-3202)
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                          US-09-830-972-2_COPY_975_1163 (1-189)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                           marker used in the method of the invention.
                                                                                                       Disclosure; SEQ ID NO 386; 226pp; English.
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Pred. No.:

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New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding
                             Human prostatic carcinoma derived DNA SEQ ID 10
                                        human, cytostatic; diagnosis; prostatic cancer; differential expression analysis; ds.
                                                                                                          27-FEB-2003; 2003DE-01009985.
14-MAY-2003; 2003DE-01022134.
                                                                                               22-FEB-2004; 2004WO-DE000433
                 (first entry)
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Beckmann G,
                                                                                                                                   DAHL E.
ROSENTHAL A.
HERMANN K.
PILARSKY C.
                                                                                                                                                                             Staub E;
                                                                                                                                                                                        WPI; 2004-653386/63.
                                                                                                                             (HINZ/) HINZMANN B.
                                                                      WO2004076614-A2
                                                           Homo sapiens.
                                                                                                                                                                      Schmitt A, F
Xinzhong L,
                 02-DEC-2004
                                                                                                                                                                Hinzmann B,
                                                                                   10-SEP-2004
     ADR65814;
                                                                                                                                   (ROSE/)
(HERM/)
                                                                                                                                                     (PILA/)
                                                                                                                                                                                                                 agents.
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Rosenthal A, Hermann K, Pilarsky C, Specht 3, Bruemmendorf T, Kinnemann H, Roepcke S;

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This invention describes novel cytostatic polynuclectide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Cor the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide, that binds to the polypeptide; non-human consolvant and tumonised or human; an anti-idotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated concernationally with anti-human CD4 murine monoclonal antibodies; between normal and tumorous tissues, with (over) expression being detected sequentially with anti-human CD4 murine monoclonal antibodies; between the diaminobearaidine as colour former (brown). The sequentially but non-malignant cells end, weakly. In 15 of 63 samples were counterstained with hemalum (blue). Malignant cells stained sequenced by much node metaatases were also stained. Delympia and polympetide sequences used in the method of the
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Claim 1; Page 160; 1607pp; German.
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Alignment Scores

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1950 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGGTGAGCGTCGTGGCCTAGCCTAGCCTTG 2009
                                                                                                                                                                                                                                                            2010 GCCGCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTCTGTTTTACAAGCAGTGCAG 2069
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                                                                                                                      2070 AAAACCGACGAACCTTTCAAGGCCTACTTGGAGGTTGAGATCACCCTTTCTCAG
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                                                                                             US-09-830-972-2_COPY_975_1163 (1-189) x ADR65814 (1-3202)
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Mismatches:
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14-MAY-2003; 2003DE-01022134.
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LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu

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This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody directed against Ab or any of the above derivatised (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated cancer patients, or subjects at risk, were incubated second antibody; streptavidin-conjugated horseradish percoxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 51 samples of defence of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR65954 represent the incubated and polypeptide sequences used in the method of the
                                                                                                                               Pilarsky C, Specht T;
mann H, Roepcke S;
                                                                                                                                                                                                                                                                   leic acids, and encoded proteins, from prostatic cancer tissue. for diagnosis, treatment and in screening for specific binding
                                                                                                                               Rosenthal A, Hermann K, Pilarsky
3, Bruemmendorf T, Kinnemann H,
                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1329; 1607pp; German.
                                                                                                                                                      Beckmann G,
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                                        ROSENTHAL A.
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HINZMANN B.
                                                             HERMANN K.
PILARSKY C.
                                                                                                                                    Hinzmann B,
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1890 ATTGACCTGTTGTATTGGCGGGACATCAAGCAGACGGCCATCGTGTTTGGGAGTTTCCTG 1949
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                                                                                                                                                                                                                                                                                                                                        AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln
                                                                                                                                                                                                 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSsrLeu
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Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;
                                                                                                                                                                     US-09-830-972-2_COPY_975_1163 (1-189) x ADR66747 (1-3202)
                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
2070 AAAACCGACGAACGCACCCTTTCAAGGCCTACTTGGAGGTTGAGATCACCCTTTCTCAG
                                                               83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu
                                                                                                                                             2190 crdaccaccrcrrcrrcrrcracaccrccrcarrcrraaaarrrccacrcrcarc
                                                                                                                                                                                                                                                  143 IleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHisTyr
                                                                                                                                                                                                                                                                      163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro
                                                                                                                                                                                 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu
                                                                                                                 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human soft tissue sarcoma-upregulated DNA - SEQ ID 5926
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acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu
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DNA methylation; matrix-assisted laser desorption/ionisation; MALDI;
electrospray; mass spectrometry; CpG dinucleotide; solid tumour.
                                                            Sequence 3305 BP; 828 A; 913 C; 843 G; 721 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human reticulon 1 (RTN1), transcript variant 1, cDNA:
                                                                                                                                                                                    US-09-830-972-2_COPY_975_1163 (1-189) x ADQ23106 (1-3305)
                                                                                               Length:
Matches:
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Mismatches:
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679.00
84.49%
67.91%
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The invention relates to a nucleic acid comprising at least 18 bases from a segment of the chemically pretreated DNA of genes associated with metastasis, i.e. any of ADS99709-ADS99306 human genomic sequences or any of the 19 sequences or any of the 19 sequences or any of the 19 sequences or any of the 19 sequences of SEQ ID 1,3,5 etc. Also included are an oligomer or peptide nucleic acid) comprising at least one base sequence of at least 9 bases which hybridises to (or is identical with) the sequence referred to above, producing an array of the oligomers on a carrier, obtaining genetic and/or epigenetic the oligomers on a carrier, obtaining genetic and/or epigenetic contents for diagnosis and/or therapy of diseases (or predisposition to them) by analysis of cytosine methylation and a kit comprising a pisulphite (disulphite or hydrogen sulphite) and the oligomers. In the method of above -bumethylated cytosines, then fragments of the converted chemically to uracii, or another base with hybridisation to the oligomers and a polymerase (preferably heat stable) to produce converted chemically to uracii, or another base with hybridisation to the oligomers and a polymerase (preferably heat stable) to produce the oligomers and a polymerase (preferably heat stable) to produce the oligomers and any hybridisation detected. The amplicons are labelled with fluorescent or radioactive markers, or with a detachable mass marker to allow their detection by mass spectrometry, specifically using the cimprove detection in the mass spectrometry, specifically using the complementary to (or identical with) parts of the nucleic acids listed above may be used as primers for amplification of the nucleic acids listed above may be used as primers for amplification of the nucleic acids listed above may be used as primers for amplification of the nucleic acids listed above may be used as primers for amplification of the nucleic acids listed above may be diseases associated with methylation of Coc determining very mass acondition of the nuclei
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                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid derived from chemically treated metastasis genes, for diagnosis of cancers by analysis of cytosine methylation, also
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                                                                                                                 06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01035529.
01-SEP-2000; 2000DE-01043826.
06-APR-2001; 2001WO-EP003970.
                                                                               21-JAN-2003; 2003US-00240485
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PIEPENBROCK
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01-JUL-2004 (first entry)
                                                    Claim 1; Page 171; 334pp;
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Best Local Similarity:
                                    diagnosing pain.
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                                                                                                                                               LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
                                    ValAspLeuLeuTyrTrpArgAspIleLysLysLysThrGlyValValPheGlyAlaSerLeu
                                              2037 CTGCTGCTTCTCCCTGACCCAGTTCAGCGTGGGGGGGCGTGGCCTACCTGGCCCTG
                                                                                                          2097 GCCGCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTCTGTTTTACAAGCAGCAGGAG
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P-PSDB; ADB79853.
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                                                                                                                                    The present invention relates to nucleotide sequences which are useful the screening of compounds for the treatment of pain, or for the diagnosis of pain. The nucleotide sequences are up-regulated in the spinal cord in response to streptozocin-induced diabetes. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 CTGCTGCTCTTCTCCCCTGACCCAGTTCAGCGTTGTGAGCGTCGTCGCCCTACCTGGCCCTG
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Use of isolated gene sequences and encoded polypeptides that are upregulated in the spinal cord in response to streptozocin-induced diabetes for screening compounds for the treatment of pain, or for
                                                                                                                                                                                                                                                        Sequence 1502 BP; 348 A; 392 C; 363 G; 399 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                             103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
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                                                                                                                            LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu
                                                                                                                                                                                                                                                             83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu
                                                                                                                                                                                                                                                                                                  2020 GAGCAGATCCAGAAGTACACAGACTGCCTGCAGCTGTATGTGAACAGCACTCTGAAGGAG
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43 AlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValIleGlnAlaIleGln
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11-JAN-2000; 2000US-00480902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42
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                                                                                              fat cell number; fat cell size; obesity; diabetes;
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Conservative:
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678.00
84.49%
67.38%
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                              Mouse polynucleotide #58.
                                                                                                                            anorectic; antidiabetic
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P-PSDB; ADO08106.
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                                                                                                 88;
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DB:
                                                                                              Mouse;
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rat; streptozocín; kinase; phosphatase; ion channel protein; receptor transporter; G-protein coupled receptor; GPCR; DNA-binding proteins; protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.

Rattus norvegicus

EP1284297-A2 19-FEB-2003.

C1-13 protein neuronal-specific gene SEQ ID NO:128.

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cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49347, or complements of them. Also included are i, (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid allowed as a promoter and a 3, non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cell polyadenylated ribonucleotides to a 3' end of the manner of polyadenylated ribonucleotides to a 3' end of the manner of comprising of the 15112 nucleic acid sequences or its complement cell or tissue comprementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the captementary nucleic acid is predictive of the capterning a level or pattern of the molecule in a bovine cell or tissue. CC tissue the detection of the molecule in a bovine cell or tissue. CC tissue are in sequence is one of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is nucleic acid is used for constructive for use in cattle gene expression, or reach and an analysis, cattle constr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     electronic format from the USPTO web site:
segdata.uspto.gov/sequence.html?DocID=20020137139
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Sequence 422 BP; 109 A; 79 C; 94 G; 140 T; 0 U; 0 Other;

Use of gene sequence that is down-regulated in response to streptozocin-induced diabetes, vector, host cell, animal, polypeptide and antibody, in screening of compounds for treating or diagnosing pain.

Pinnock RD;

К,

Lee

Dixon AK,

Brooksbank RA,

WPI; 2003-364994/35.

P-PSDB; ADB85246.

(WARN) WARNER LAMBERT CO.

26-JUL-2002; 2002EP-00255228. 27-JUL-2001; 2001GB-00018354. 07-FEB-2002; 2002GB-00002880. relates to a novel isolated gene sequence that is down-

Claim 1; Page 197; 256pp; English.

invention

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157 ValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLys 176
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                                                                                                                                                                                                          ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                                                                                                                                                                                      GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal
                                                                                                                                                                                                                                                                                       122 GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTT
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                                          Conservative:
Mismatches:
              Length:
Matches:
                                                                         Indels:
              7.91e-72
                         675.00
98.57%
97.14%
72.97%
                                       Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
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regulated in the spinal cord in response to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence identity to a sequence whose expression products are kinases, phosphatases, ion channel proteins, receptors, transporters, G-protein coupled receptor proteins, DNA-binding proteins, proteases or enzymes, given in the specification. A gene of the invention has analgesic activity, and may have use in gene therapy. The gene sequences, vector, host cell, animal, polypeptide and antibody are useful for screening of compounds for diagnosing or treating pain. The kits are useful for simultaneous, separate or sequential detecting and/or quantifying downregulation of a gene sequence in the spinal cord of a mammal in response to streptozocin-induced diabetes. The compound or pharmaceutical composition is useful as a medicament for treating or diagnosing pain. The present sequence represents a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 GCTGCCCTCTCTGCCACCATCAGCTTCCGCATCTACAAGTCCGTTCTACAAGCTGTGCAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTTGTAGAGGTCGTCGCCTACCTGGCCCTG 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
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Mismatches:
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DNA; 1473

ADB85247 standard;

RESULT 63

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Alignment Scores:
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                                               445
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                                                                                                                                                                                                         LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
                                                                                                                                                                                                                                   685
                                                                                                                                                            143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory; neuroprotective; gene therapy; cancer; immunopathology; neuropathology;
                                                                                                                              AAAACAGATGAGGGTCACCCTTTCAAGGCCTACCTGGAGCTGGAGATCACCCTGTCCCCAG
                                   |||| :::|||||||||| GAGCAGAGACTGCCTGCAGCTATACGTGAACAGCACTCTGAAGGAG
                                                                                  GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu
                                                                    LeuArgArgleuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet
                                                                                                                 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu
                                                                                                                                                                                                                        New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene is associated with a cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                 Human brain cell specific cDNA sequence SEQ ID NO:398
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to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2174 GAGCAGATTCAGAAGTACACGGACTGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2114 AAAACCGACGAAGGCACCTTTCAAGGCCTACTTGGAGCTTGAGATCACCCTTTCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 ulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHisTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine EST associated with lactation/muscle/fat deposition #11567
                                                                                                                                          Sequence 3279 BP; 814 A; 905 C; 850 G; 710 T; 0 U; 0 Other;
                                                                                                                                                                                                              3279
126
31
30
1
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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660.00
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67.02
71.35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA;
                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140

TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTG 363

304

ADR06965 standard; cDNA; 4607 BP.

04-NOV-2004 (first entry)

ADR06965;

LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120

184 rereaseastrestressaastracascaarrerscretestrestraacresaara

81

8 셤 ઠે 원 ò 셤 ₽ 셤

101

244 AAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAGTTTTGCAGTG 303

SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX4937, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the complementary nucleic acid permits the detection of the sold or pattern of the complementary nucleic acid permits the detection of the complementary nucleic acid is predictive of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the substance in a povine cell or the complementary nucleic acid sequence in cattle gene expression, or for genetically improving cattle. The present sequence is one of the selection of the molecule of sequence tell or the sequence as not shown in the specification but was obtained in constant from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 422 BP; 99 A; 85 C; 96 G; 142 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                         Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 11567; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                         Tao N,
                                                                                                                                                                       12-JAN-1999; 99US-0115707P.
11-JAN-2000; 2000US-00480902.
                                                                                                                         24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                                                                                                                                                                         Byatt JC, Mathialagan N,
                                                                                                                                                                                                                                           (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-110599/10.
                                                                                                                                                                                                                                                                       (MATH/) MATHIALAGAN
(TAON/) TAO N.
(WARR/) WARREN W C.
                       US2002137139-A1.
                                                                        26-SEP-2002
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Full length human cDNA useful for treating neurological disease Seq 471.

gene; ss; human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

Otsuki T;

Sugiyama T,

Nishikawa T, Isono Y, Nagai K, Irie R;

Isogai T, Yamamoto J, Wakamatsu A, Ishii S, WPI; 2004-583265/57. P-PSDB; ADR08921

> 1.17e-69 657.00 98.56% 97.12% 71.03%

> > Best Local Similarity:

Š 유 ò 유

Percent Similarity:

Alignment Scores:

(REAS-) RES ASSOC BIOTECHNOLOGY. 09-MAY-2003; 2003JP-00131452.

12-FEB-2004; 2004EP-00003145. 14-FEB-2003; 2003JP-00102207.

Homo sapiens. tranquiliser.

EP1447413-A2.

18-AUG-2004.

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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to cDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind antibodies, antisense molecules and siRNAs that can all be used to bind molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporoais, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 471; 2686pp; English.
GCCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCT 123
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Mismatches:
Indels:
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Matches:
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CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 2892
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             cytostatic and tranquiliser activities. This polymucleotide is a full length human TONA sequence of the invention. WOTE: This sequence is not given in the sequence listing of the specification but can be obtained CD-ROM from the European Patent Office, Vienna Sub-office.
 neuroprotective, nootropic, antiparkinsonian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaLeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAgp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HP02061; transmembrane domain; Saos-2; homology; neucoendooxine-specific protein C; antibody; assay reagent; diagnostic marker; primer; probe; antisense; gene therapy; agonist; antagonist; ligand; therapeutic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human transmembrane protein cDNA clone HP02061 coding sequence:
                                                                              Sequence 4607 BP; 1428 A; 944 C; 945 G; 1290 T; 0 U; 0 Other;
                                                                                                                         4607
1114
40
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                             Gaps:
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                                                                                                                       2.09e-64
625.50
81.05%
60.00%
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exhibit osteopathic,
                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                            Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the coding sequence of human cDNA clone HP02061 which encodes a 26 kD protein with two putative transmembrane domains. The cDNA was isolated from a Saos-2 (human osteosarcoma cell line) cDNA library. The protein has homology with the human neuroendocrine specific protein C (PIR Accession No. 160904), and may have a similar function. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically
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                                                                                                                                                                                                                                                                                                                                      control of cel.
e.g. cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 ATCCTGGCTCTTCTCTCTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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                                                      /*tag= a
/product= "Human transmembrane protein HP02061"
/note= "No stop codon given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 708 BP; 158 A; 195 C; 169 G; 186 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        Human proteins with transmembrane domains, involved in proliferation and differentiation, useful for treating
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                                                                                                                                                                  99WO-JP002226
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                                                                                                                                                                                             98JP-00119395
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(PROT-) PROTEGENE INC
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                            P-PSDB; AAY52387
                                                                                                                                                                                              28-APR-1998;
 sapiens
                                                                                                            WO9955862-A2
                                                                                                                                                                  27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                    inflammation
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HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                            SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                                                                                                                                                                                                                    SerValValAspLeuLeuTyrTrpArgAspIleLysLysTyrGlyValValPheGlyAla
                                                                                                                                                                 259 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT
                                                                                                                                                                                                                                                                                                                                          499 TTCATGTGGCTGATGACCTATGTTGTTGTTGTTTTTAACGGAATCACCCTTCTAATTCTT
                                                                                                                                                                                                                                                                                                                                                                                   AlaLeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAsp
                                                                                                           SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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                                                                                                                                                                                                                                                                                   LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLygPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 11; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:1935
 35
1
                                           US-09-830-972-2_COPY_975_1163 (1-189) x ADK67496 (1-711)
 Mismatches:
Indels:
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CTCCCTGGAATCGCCAAAAAAAAGGCAGAA 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; cDNA; 1330 BP
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59.47%
67.30%
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 Best Local Similarity:
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03-NOV-1999;
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DB:
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                                                                121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                                            160
                                                                                                                      HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide having BACE1 activity, useful in preparing a composition for treating amyloidosis or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polypeptide having BACE1 activity. The protein is RTN4 or RTN3 protein. The polypeptide is useful in preparing a composition for treating amyloidosis or Alzheimer's disease. This sequence corresponds to the RTN-3 gene.
                                                                            379 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTG
                                      LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                           AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                                                                                                                                                                    ds; neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3; amyloidosis; Alzheimer's disease.
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "RTN-3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. 711
/*tag= a
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                                                                                                                                                                                                                                                               ADK67496 standard; cDNA; 711
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622.50
81.05%
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                                                                                                                                                                                                                                                                                                                                Human RTN-3 cDNA sequence.
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P-PSDB; ADK67497.
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                                                                                                                      AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used into a host cell and culturing the cell to express the proteins. Or an be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N and persent pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
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                                            Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerValValAspleuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 ATCCTGGCTCTTCTCTCTGTGACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT
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Mismatches:
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Matches:
                                                                                Claim 1; Page 3443; 9803pp; English.
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622.50
81.05%
59.47%
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            2001-235357/24
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Best Local Similarity:
Query Match:
           WPI; 2001-235357/
P-PSDB; AAG75448.
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The invention relates to secreted proteins (AAY17219-228) encoded by polynucleotides obtained from human fetal kidney, adult lung, adult blood, adult testes, and fetal brain and murine adult borain, adult blood, adult testes, and fetal brain and murine adult bone marrow cDNA libraries. The secretd protein nucleic acid sequences (X6801-811) correspond to clones bd306-7, gj283-6, fK317-3, K213-2x, na316-1, nf93-20, np164-1, pe204-1, yal-1 and yb-1, (all clones are deposited as ATCC 98599); The PNS and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, hematopoiesis regulating activity, tissue growth activity, activin/ thrombolytic activity, receptor/ligand activity, and tumour activity, cadherin/cumour invasion suppressor activity, and tumour inhibition activity. The PNS are also stated to be useful for gene
CACTATGTTGGCATCGGCCGAGATCAGACCAAGTCGAAAAGATCCAAGCAAAA 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; kidney; lung; brain; blood; testis; bone marrow; nutritional activity; cytokine; cell proliferation; immune stimulation; hematopoiesis regulation; tissue growth; thrombolytic; gene therapy; anti-inflammatory; tumour invasion; ss.
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Steininger RJ, Wong GG,
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35
                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein encoding DNA (clone yb8-1).
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                                                       IleProGlyLeu---LysArgLysAlaAsp 189
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837 CTCCCTGGAATCGCCAAAAAAAGGCAGAA
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Treacy M, Agostino MJ,
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Query Match:
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Merberg D,
Fechtel K;
  777
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No.:
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22-MAR-2001; 2001WO-US009369.

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TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCATCAACAGGCCCTG 464
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                                                                                                                                                                                                                                                                                                61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
                                                                          1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
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                                                                                               21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                       41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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                                   US-09-830-972-2_COPY_975_1163 (1-189) x AAX60810 (1-1656)
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune coupressing activity, which is useful for the treatment of various immune configurations and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus cerythematosus, rhemmatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (QHHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory concesses, diseases of the peripheral nervous system. Alzheimer's, cell results and Shy-Drager syndrome, infections, infarction of cardiac and cisease, ulcers, bone regeneration. The protein, having activin- or inhibin related activities in well as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease contractogenesis in male mammals. The proteins and uncerted activities and mammals and nucleic acids are also contractogenesis.
                                                                                                                                                                               Clark H;
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                                                                                                                                                                                                                                                                                                       Secreted human proteins, useful as vaccine for treating various disc
such as autoimmune disorders (e.g. multiple sclerosis), and nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful as food supplements. The present sequence encodes a secreted
                                                                                                                                                       Mccoy JM, Lavallie E, Collins-Racie LA, Evans C;
Agostino MJ, Steininger RJ, Spaulding V, Wong GG,
Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                            such as autoimmune disorders (e. system disorders (e.g. stroke).
                                                           30-MAR-2000; 2000US-0053930
                                                                            04-DEC-2000; 2000US-00729674
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Query Match:
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61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 285 ATCCHGGCTCTTCTCTCTCTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT

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                                                                                          HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
                                             LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                         TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCTT
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ABA90885 standard; cDNA; 1656 **ABA90885**

ABA90885;

BP

Human polynucleotide SEQ ID NO 19.

(first entry)

14-FEB-2002

Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic lupus srythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophilia; cardiac infarction; stroke; sepsis; archritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; cohn's disease; chemotactic; neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.

Homo sapiens

US2001039335-A1.

08-NOV-2001

04-DEC-2000; 2000US-00729674 26-NOV-1997 04-DEC-1997

97US-0067454P. 97US-0068379P. 98US-0070346P. 98US-0070643P. 98US-0071304P. 98US-0071344P. 02-JAN-1998 07-JAN-1998 08-JAN-1998 13-JAN-1998 22-JAN-1998

98US-0073095P.

30-JAN-1998

98US-00197886 2000US-00539330 COLLINS-RACIE MCCOY J M. LAVALLIE E JACOBS 30-MAR-2000; (JACO/) (MCCO/) (LAVA/) (COLL/) (EVAN/) (MERB/) (TREA/)

EVANS C. MERBERG D. TREACY M.

The invention relates to isolated polymucleotides (ABA90876-ABA90968 and ABA9080) and encoded proteins (ABB55698-ABB5800), especially proteins (ABB51698-ABB5800), especially and encoded proteins (ABB55698-ABB5800), especially proteins SEQ ID NO 19 (ABB9085) and proteins SEQ ID NO 19 (ABB95707) contained in proteins bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 care deposited with the American Type Culture Collection (ATCC) with accession number 98599. The polymucleotides and encoded polypeptides have cycostatic, anti-inflammatory, immunomodulator, vulnerary, cartivin, inhibin, chemotactic, hAemostatic, thrombolytic and anti-inflammatory activity and acting as cytokine modulators, candearin suppressors. The polypeptides and polymucleotides are useful in gene therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial cor fungal infections, autoimmune disorders, cancer, systemic lupus cytoescarthritis; central and peripheral nervous system diseases and coercostencies; wound, burns, incisions and ulcers, osteoporosis or costeoarthritis; central and peripheral nervous system diseases and disease, amyotrophic lateral solerosis or Staft contral and peripheral contral and peripheral contral and peripheral contral and peripheral contral and peripheral contral and peripheral contral and peripheral contral and peripheral contral and peripheral contral and peripheral contral and peripheral contral and co disease; or tumours or cancers, pemphigus vulgaris or pemphigus foliaceus New secreted proteins and encoding polynucleotides, useful in gene therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or endotoxin lethality, arthritis, inflammatory bowel disease or Crohn's Collins-Racie LA, Evans C; Steininger RJ, Spaulding V; Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 U; 0 Other; Collins-Racie LA, Claim 13; Page 191-192; 349pp; English. Lavallie ER, Agostino MJ, Fechtel K; AGOSTINO M J. STEININGER R J SPAULDING V. WONG G G. Treacy M, Jacobs K, Pr.
Treac,
Clark H, F WPI; 2002-040725/05. FECHTEL K. P-PSDB; ABBS5707 inflammations. (WONG/) (CLAR/) (FECH/)

US-09-830-972-2_COPY_975_1163 (1-189) x ABA90885 (1-1656) Best Local Similarity: Query Match: DB:

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.14e-64 622.50 81.05% 59.47% 67.30%

Percent Similarity:

Alignment Scores:

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9 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 285 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT

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8 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle

production of other cytokines in certain cell populations

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584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 AlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; colony stimulating factor; granulocyte; erythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; myelo-emptyression; megakaryocyte; platelet; platelet disorder; thrombocytopenia; hematopositic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxymal nocturnal hemoglobinuia; bone grawth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer; bone fracture; cartilage damage; artificial joint; ss.
                                                                                                                         LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                     121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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/product= "bone marrow secreted protein"
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98US-0102540P
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strong 1 cells. The proteins can exhibit cytokine, cell proliferation, or strong 1 cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell lines, celliciencies. In addition, they may be used to support the growth and proliferation of erythroid progenitor cells, and to treat various anemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of megakaryocytes granulocytes, monocytes or macrophages, to prevent or treat myelosuppression, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation with platelet transfusions, to treat stem cell disorders conjunction with platelet transfusions, to treat stem cell disorders, conjunction with platelet transfusions, to treat stem cell disorders, conjunction with platelet conformal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and transfusions the presented the platement, and in the treatment of burnary in construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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Matches:
                                            Claim 11; Page 98-100; 120pp; English.
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622.50
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SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; protate; obseity; osteoclast; thynus; osteoporosis; arthritis; testis; lung; thyroid; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                               1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                               21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                                 460 GTACAGAAGTCAGAAGAAGAGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG
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                                       US-09-830-972-2_COPY_975_1163 (1-189) x AAZ38319 (1-1759)
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97US-0040161P.
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07-MAR-1997;
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                                       176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human proteins with transmembrane domains, involved in control of cell proliferation and differentiation, useful for treating e.g. cancer or
                         HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                                                                                                                                                                                                               HP02061; transmembrane domain; Saos-2; homology; detrocation procting proceduces, contibody; assay reagent; diagnostic marker; primer; probe; antisense; gene therapy; agonist; antagonist; ligand; therapeutic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Human transmembrane protein HP02061"
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Matches:
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                                                                             181 IleProGlyLeu---LygArgLysAlaAsp 189
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CTCCCTGGAATCGCCAAAAAAAAGGCAGAA 806
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(PROT-) PROTEGENE INC.
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Best Local Similarity:
Query Match:
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Pred. No.:
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161
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AAZ3831
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970S-0040133P
970S-0040334P
970S-0040331E
970S-0043312P
970S-0043312P
970S-0043313P
970S-0043313P
970S-0043315P
970S-0043569P
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97US-0051926P.
97US-0052874P.
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97US-0056631P.
97US-0056637P.
97US-0056637P.
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97US-0047593P.
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22-AUG-1997;
22-AUG-1997;
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11-APR-19
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Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                    970S-0056884P.
970S-0056886P.
970S-005688PP.
970S-005688P.
970S-0056899P.
                                                                                                                               970S-0056909P-
970S-0056910P-
970S-0057650P-
970S-0057669P-
970S-005761P-
970S-005781P-
970S-005781P-
97US-0056876P.
97US-0056877P.
97US-0056878P.
97US-0056879P.
                              97US-0056880P.
97US-0056881P.
97US-0056882P.
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97US-0056903P.
97US-0056908P.
                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                           WPI; 1998-506364/43.
P-PSDB; AAW74963.
                              22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
                                                                                    22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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02-OCT-1997;
                                                      22-AUG-1997
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22-AUG-1997
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05-SEP-1997
                      22-AUG-1997
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                                                                                                                                          22-AUG-1997
                                                                                                                                                                        05-SEP-1997
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New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

Claim 1; Page 473-474; 721pp; English.

This sequence represents a nucleic acid molecule designated Gene 92 from the human cDNA clone HAUBL57 (deposited as clone ATCC 97897 and ATCC 209043) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin protein as compared to the human protein only. The invention relates to compared to the human protein only. The invention relates to compared to the human protein only. The invention relates to les novel genes and their fragments (nucleic acid sequences: AAV59511-075912, amino acid sequences AAW7471-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polymucleotides.

Specific uses are described for each of the 186 polymucleotides, based on which tissues they are most highly expressed in (see AAV59511 for .

Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

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Conservative:
Mismatches:
Indels:
        Length:
Matches:
      1.25e-64
622.50
81.05$
59.47$
67.30$
                            Percent Similarity:
Best Local Similarity:
Aliqnment Scores:
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DB:
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US-09-830-972-2_COPY_975_1163 (1-189) x AAV59748 (1-1766)

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us-09-830-972-2_copy_975_1163.rng

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970S-0043313P
970S-0043313P
970S-004356P
970S-004356P
970S-0043576P
970S-0043576P
970S-0043578P
970S-0043572P
970S-0043572P
970S-0043572P
970S-0047590P
970S-0047591P
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970S-0049519P
970S-0056637P
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970S-005681P
        11-APR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
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22-AUG-1997
466
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                   140
                                                                                                                                                                                                                                                                                           SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                                                                                                                                                                                         647 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCTT 706
                                                                                                                                                                                                                                                                 9
                                                                                      21 SerieuPheleuLeuLeuSerieuThrValPheSerIleValSerValThrAlaTyrile 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; 88; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn; nervous system disorders; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive;
                                              41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                           407 ATCCTGGCTCTTCTCTCTGTCACCATCAGGATCTACAAGTCCGTCATCCAAGCT
                                                                                                                                                                     LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                      AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                              121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA #2 for novel secreted protein gene 92.
                                                                                                                                                                                                                                                                                                                                    181 IleProGlyLeu---LysArgLysAlaAsp 189
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                                                                                                                                                                                                                                                                                                                                                                                                  ABS73741 standard; cDNA; 1766 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0038621P.
97US-0040162P.
97US-0040163P.
97US-0040333P.
97US-0040334P.
97US-0040336P.
97US-0040336P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preservative; nutritional.
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6420526-B1
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11-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                              RESULT 76
ABS73741
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21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle

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407 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 466

41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla

61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlalle

SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

81

527 101

467

140

AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160

LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu

587

121

141 707 161

LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal

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ò 유 ACD82884 standard; cDNA; 1766 BP.

RESULT 77 ACD82884 ACD82884;

120 646

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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification, encoded by one of 309 cDNA sequences also given in the specification, encoded by one of 309 cDNA parmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include disorders e.g. neoplasms of the breast or liver, cardiovascular disorders of sorders e.g. nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to collurate or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a obbA derived from a gene encoding one of the novel human secreted broteins of the invention. Note: This sequence did not form part of the printed specification, but was conditions and also a processed to the condition of the condition of the processed the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           v isolated human secreted protein for diagnosing, preventing, treating
ameliorating medical conditions and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;
Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carter KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 254; 129pp; English.
97US-0056884P.
97US-0056886P.
97US-0056889P.
97US-0056889P.
97US-0056893P.
97US-005693P.
97US-0056903P.
97US-0056903P.
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970S-0056911P
970S-0057650P
970S-005761P
970S-0058761P
970S-0058781P
970S-005050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US004493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-634796/68.
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                                                                                          22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
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06-MAR-1998;
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Human; secreted protein; hyperproliferative disorder; leukaemia; breast cancer; wound; reproductive disorder; blood-related disorder; blasemophila; thrombocytopaenia; immunodeliciency; thymic hypoplasia; wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis; graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma; viral infection; bacterial infection; fungal infection; AIDS; sepsis; reapliatorder; kidney failure; cardiovascular disorder; cytostatic; angina pectoris; cerebral ischemia; congenital heart defect; respiratory disorder; neurological disorder; Alzheimer's disease; respiratory disorder; neurological disorder; Alzheimer's disease; immunosuppressive; antibammation; crohn's disease; vulnerary; anticoagulant; neuroprotective; thyromimetic; antiallergic; antiantimatic; virucide; fungicide; antiallergic; antianginal;
                                                                                                                      CDNA sequence #244 containing coding region of a human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           cerebroprotective; cardiant; nootropic; antiparkinsonian;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory; gene; ss
                                                                               22-SEP-2003 (first entry)
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1.25e-64

Percent Similarity:

97US-0056875P

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970S-0038621P.
970S-0040162P.
970S-0040334P.
970S-0040334P.
970S-00403312P.
970S-0043313P.
970S-0043313P.
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970S-0043313P.
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970S-0043568P.
970S-0043568P.
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07-MAR-1997;
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06-JUN-1997;
06-JUN-1997;
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23-MAY-1997
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New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral
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, Greene JM, Ferrie AM;
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Bndress GA, Yu G, Ni J, Reng P, Young PB, Greene JM, Ferrie AJ
Duan DR, Hu J, Florence R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                  9705-0056819P
9705-0056881P
9705-0056881P
9705-0056884P
9705-0056887P
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9705-005688P
9705-005689P
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9705-005691P
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98WO-US004493.
98US-00149476.
2000US-0190068P.
               97US-0056876P.
97US-0056877P.
97US-0056878P.
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NI J.
PENG P.
YOUNG P E.
GREENB J M.
FERRIB A M.
DUAN D R.
HU J.
FICCHER C L.
ENERR R A.
OLSEN H S.
FISCHER C L.
ENERR R A.
BREWER L A.
BREWER L A.
BREWER L A.
BLI Y.
LAPLEUR D W.
LI Y.
LLI Y.
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LEIN Y.
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
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P-PSDB; ABO34617.
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08-SEP-1998;
17-MAR-2000; 2
               22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
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(CART/)
(ENDR/)
(YUGG/)
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The present invention relates to the isolation of novel human secreted proteins and the polynucleotide sequences encoding them. The invention

Claim 4; SEQ ID NO 254; 260pp; English.

ADI22969 standard; cDNA; 1766 BP.

ADI22969

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also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polymucleotide sequences for the secreted proteins are useful for preventing, treating, ameliorating or diagnosing medical conditions such as hyperproliferative disorders (e.g. leukaemia or breast cancers), wounds, reproductive disorders (e.g. haemophilia or thrombocytopaenia), immunodeficiencies (e.g. haemophilia or thymic hypoplasia), autoimmune disorders (e.g. wiskott-Aldrich syndrome or thymic hypoplasia), autoimmune disorders (e.g. wiskott-Aldrich syndrome or thymic hypoplasia), autoimmune disorders (e.g. wiskott-Aldrich syndrome or thymic hypoplasia), autoimmune disorders (e.g. wiskott-Aldrich syndrome or thymic hypoplasia), cartainators (e.g. wind) infections (e.g. wind) or sepsis), respiratory disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina pectoris, cerebral ischaemia or congenital heart defects), respiratory parkinson's disease), and inflammations (e.g. Alzheimer's disease). The polymorphide may also be used as vaccine adjuvants.

ACDB2641-ACDB2950 encode human secreted proteins or their fragments.

Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         646
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                                                                                                                                                                                                                                                                                                                                                                                  USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
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cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.
                                              cDNA encoding novel human secreted protein seq id 254
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97US-0047502P.
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                                                                            Homo sapiens.
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23-MAY-1997;
23-MAY-1997;
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970S-0055724P.
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17-MAR-2000; 2000US-0190068P
16-MAR-2001; 2001US-00809391
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NI J.
FENG P.
FENG P. E.
GREENE J M.
FERRIE A M.
DUAN D R.
HU J.
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FISCHER C L.
BEBNER R.
BREWER L A.
MOORE P A.
SHI Y.
LAFLEUR D W.
LI Y.
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
23-MAY-1997;
06-JUN-1997;
06-JUN-1997;
13-JUN-1997;
                              08-JUL-1997;
16-JUL-1997;
18-AUG-1997;
22-AUG-1997;
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                                                                                                                                                                                                                                                              The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the CDNA sequence; a polynucleotide sequence encoding polympeptide, or its fragment, domain, epitope or species homologue, or apolympetide, or its fragment domain, epitope or species homologue, or polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medicament for diagnosing, preventing, treating or ameliorating a medicament for the invention.
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                                  Bednarik DP; ......TM, Ferrie AM;
                                                                                                                                                                                     diagnosing, preventing, treating or ameliorating a medical condition
                                             Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Bndress GA, Yu G, Ni J, Feng P, Young PB, Greene JM, Ferrie AM
Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                        New nucleic acid molecule, useful for preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;
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Best Local Similarity:
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(ZENG/) ZENG Z.
(KYAW/) KYAW H.
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161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

141 AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp

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Isolated nucleic acid molecules encoding human secreted proteins, useful for preventing, diagnosing and treating disorders associated with aberrant expression and activity.
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Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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9705-004761P
9705-0047632P
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97US-0056631P.
97US-0056632P.
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97US-0056662P.
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97US-0056893P.
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P-PSDB; ADH74280.
                                                              23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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 human, secreted protein, cancer; haematopoietic disorder; es; endocrine disorder; immune system disease; inflammatory disorder; es;
                           181 IleProGlyLeu---LyaArgLyaAlaAsp 189 :::|||||||::: |||||||:: | |||||| 827 CTCCCTGGAATCGCCAAAAAAAAGGGGAAA 856
                                                                                                                                        Human secreted protein cDNA #244.
                                                                                   ADH73971 standard; cDNA; 1766 BP
                                                                                                                                                                                                                                                                    970S-0038621P

970S-0040161P

970S-0040133P

970S-0040334P

970S-0040331P

970S-00403312P

970S-0043312P

970S-0043312P

970S-0043312P

970S-0043312P

970S-0043312P

970S-0043569P

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97US-0047596P.
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                                                                                                                                                                                                                US2003225248-A1.
                                                                                                                                                                                               Homo sapiens.
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11-APR-1997;
11-APR-1997;
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11-APR-1997;
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23-MAY-1997
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                                                                                                     ADH73971;
                                                                                                                                                                             gene.
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RESULT 80
                                          ADM3617
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                             The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPs) they encode. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e-g. cancer, haematopoietic disorders, diseases of the immune system, inflammatory and ordinary others. Full details of disorders that may be prevented, diagnosed and/or treated by the above methods are given in the proteins. The nucleic acid molecules may be used to produce their or proteins. The nucleic acid and it's complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the proteins. The nucleic acid in samples, and therefore which parients may be in need of restorative therapy. The SPs may also be used to presence of similar nucleic acids in samples, and therefore which parients may be in need of restorative therapy. The SPs may also be used to assays to identify modulators of SP expression and activity. The anti-SP antibodies and antagonists may also be used to down regulate expression and activity. The anti-SP antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATGAGTGTGGTTTCTTACCTC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SerieuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 ATCCTGGCTCTTCTCTCTGTGACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACTCATTATTCGTCTCTTTCTGGTAGAAGAICTGGTTGACTCCTTGAAGGTGGCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTGTT
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767 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;
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113
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Conservative:
Mismatches:
Indels:
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827 CTCCCTGGAATCGCCAAAAAAAGGCAGAA 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleProGlyLeu---LysArgLysAlaAsp 189
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Claim 3; SEQ ID NO 254; 142pp; English.
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622.50
81.05$
59.47$
67.30$
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Best Local Similarity:
Query Match:
DB:
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The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (1) of the RTM (reticulon)3 gene. Differential expression of RTM3 is a specific marker of neuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular disorders, specifically amountorphic lateral sclerosis (Abs) and myopathy. Also (i) antibodies specific for isoforms of RTM3 or oligonucleotides (antisense sequences or small interfering RMA) that can block/reduce expression of these isoforms express RTM3 are useful in screening for therapeutic agents. The present sequence is a RTM3 DNA sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing, prognosing and monitoring neuromuscular disease, particularly amyotrophic lateral sclerosis, comprises detecting modulation of the reticulon 3 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Tapia M, Larmet Y, Loeffler J;
Boutillier AL, Gaiddon C, Rene F;
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                                                                                                                                                                      Human RTN3 isoform VI coding sequence, SEQ ID 60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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/product= "RTN3 isoform VI"
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                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
   BP.
ADM36177 standard; DNA; 1911
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622.50
81.05%
59.47%
67.30%
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                                                                                                                03-JUN-2004 (first entry)
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Gonzales De Aguilar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-071743/07.
P-PSDB; ADM36178.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                         ADM36177;
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Liu C, Drmanac RT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                   382 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 441
                                                                                                                                                                                                 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                                                                                                                                                                                                                                                                                                     121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
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SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                                                                  61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                     41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                           622 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCTTCTAATTCTT
                                                                                                                                                                                                                                                                    LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; growth fehaematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immume disorder; cell culture; drug acreening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 IleproglyLeu---LysArgLysAlaAsp 189
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27-APR-2000; 2000US-00560875.
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB10981-ABB12330 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the nucleotides cathibodies against the polypeptides, methods of deetecting the nucleotides or polypeptides against the polypeptides of the invention have homology to known proteins, thereby compounds which bind to polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence complemental therapeutic applications. The polypeptides of the invention may have various activities including cytokine, cell proliferation or cell differentiation activities; nem cell growth factor activity; immunomodulatory activity; activity itsus growth activity; immunomodulatory activity; activity risus growth activity; immunomodulatory activity; activity risus growth activity; immunomodulatory activity; activity or light activities; or may be involved in oncogenesis, cancer cell proliferation or metaetasis.

Cohemotactic or chemokinetic activities; haemostatic, thrombotic or thromboty activities; preceptor or light activities; or may be involved in oncogenesis, cancer cell proliferation or metaetasis.

Conditions, e.g., by protein or gene therapy. Such conditions include cancers, headatopoietic disorders (e.g., metaetoid cell disorders) (conditions, e.g., by protein or gene therapy. Such conditions, e.g., by protein or gene therapy. Such conditions include and exercises, headatopoietic disorders (e.g., metaetoid cell growth. Polypeptides encoding them) may be used to promoce wound healing (e.g., of burns, incisions and ulcers), while those with care cell growth factor activity may be used in the treatment of viral, cancers land fungal infections in addition to immune diseases or accidental damage or properties and bused in culting the present sequence represents a collection of the above cond
                                                                                                                                        nan proteins and DNA encoding sequences useful for preventing, treating ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1915 BP; 492 A; 463 C; 411 G; 549 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention
                                                                                                                                                                                                                                                Claim 1; Page 838; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel human polypeptide of
                                                                        2001-457740/49.
                                                                                                                                              Human proteins and
                                                                                                  P-PSDB; ABB11960
                                                                                                                                                                                                 and cancer.
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1 ServalValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

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US-09-830-972-2_COPY_975_1163 (1-189) x ABA09204 (1-1915)

1915 113 41 35

Conservative: Mismatches:

1.4e-64 622.50 81.05\$ 59.47\$ 67.30\$

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

Indels:

Length: Matches:

347 ACGCTGATCATGCTGCTTTCCTGGCAGCTTTCAGTGTCATCAGTGTGTTTACCTC 406

21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

407 Arcchéscricricricristraccarcascricassaricracaasrccsricarcaascr 466

(HYSE-) HYSEQ INC.

41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding secretory proteins/membrane proteins, useful in
             AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                                                                                                                                                                        |||| ::: ::|||||||::|||||| || GCTGAAGTACAAGACCCAGATTGAT
                                                                                                                                                                                                                                     HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                                                                                                         IleGInLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                               SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                             LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                    Human cDNA encoding a membrane or secretory protein clone PSEC0103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; membrane protein; vaccine; gene therapy;
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CTCCCTGGAATCGCCAAAAAAAGGCAGAA 856
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therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
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Human, secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; observy architis; testis; lung; thyroid; settorid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                              AlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAsp 160
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SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
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                                                                                                                                                                                                                                                                                     121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu
                                                                                                                                                                                                           Human secreted protein gene 92 clone HAUBL57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human neuroencorine specific protein linked gene, hNSPL1, highly expressed in human nerve system. The protein is located in the endoplasmic reticulum membrane of cell, is highly expressed in normal nerve cell and has obvious difference in expression inside glia cell and inside glia cell tumour. It may have important some nerve system disease occurrence. The present sequence represents human neuroencocrine specific protein linked gene, hNSPL1, cDNA.
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                                                                                                                                                                                                               ss; gene; human; neuroencocrine specific protein linked gene; hNSPL1; glia cell; tumour; nervous system disease.
                                                                                                                                            Human neuroencocrine specific protein linked gene, hNSPL1, cDNA.
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22-AUG-1
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This sequence represents a nucleic acid molecule designated Gene 92 from the human cDNA clone HAUBLS7 (deposited as clone ATCC 97897 and ATCC 209043) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin C portion (e.g. AAV59502) for increasing the stability of the fused CC protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-C V58812; amino acid sequences AAW7731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein cor gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polynucleotides.

Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for
                                                                                                                                         Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;

dednarik Pp, Enderes GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 ACGCTGATCATGCTTGCTTTTCCTTTTCAGTGTCATCAGTGTGTTTTCTAGTGTCATGAGTGTTTTCTTACCTC 381
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                                                                                                                                                                                                                                                                                New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
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                  97US-0057669P.
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           121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                         HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                   Human; ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogeneals; necebran; nervous system disorders; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional.
                                                   AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                            622 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTTAACGGAATCACCCTTCTAATTCTT
                                                                                                                                                                                                                                                      Human cDNA #3 for novel secreted protein gene 92.
                                                                                                                                IleProGlyLeu---LysArgLysAlaAsp 189
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CTCCCTGGAATCGCCAAAAAAAAGGCAGAA 831
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97US-0040161P.
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                                                                                                                                                                                                                                                                                                                                                                                                                     disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to cuburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a cDNA derived from a gene encoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                      The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a pharmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441
                                                        Greene JM;
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                                                                                                                                                                                           New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or
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                                Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Gr Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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(HUMA-) HUMAN GENOME SCI INC.
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101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120

502 rccrcadaagcrirccaraarracargaargcroccargerocaccarcaacaggcccro

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141 AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
                                                                                                                                                                             HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                           742 cactatetregearcecegarcagaccaagrearrerreaaagarceaagaaa 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; hyperproliferative disorder; leukaemia; breast cancer; wound; reproductive disorder; blood-related disorder; breast cancer; wound; reproductive disorder; blood-related disorder; what hypoplasia; wiskott-Aldrich syndrome; almunodeficiency; thymic hypoplasia; graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma; viral infection; bacterial infection; fungal infection; AIDS; sepsis; renal disorder; kidney failure; cardiovascular disorder; cytostatic; angina pectoris; cerebral ischemia; congenital heart defect; respiratory disorder; neurological disorder; Alzheimer's disease; respiratory disoase; inflammation; Crohn's disease; vulnerary; antioacsupersesive; antibacterial; haemostatic; thrombolytic; anticathmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;
                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequence #245 containing coding region of a human secreted protein.
622 TTCATGIGGCIGATGACCTATGTIGGTIGCTGTTTTTAACGGAATCACCCTTCTAATICTT
                                                                                                                                 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerebroprotective; cardiant; nootropic; antiparkinsonian;
                                                                                                                                                                                                                                         181 IleProglyLeu---LysArgLysAlaAsp 189
                                                                                                                                                                                                                                                             802 CTCCCTGGAATCGCCAAAAAAAAGGCAGAA 831
                                                                                                                                                                                                                                                                                                                                         ACD82885 standard; cDNA; 2664 BP
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9703-00436749
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9703-0047581P
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22-AUG-1997;
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05-SEP-1997; 97US-0057669P.
12-SEP-1997; 97US-0057761P.
12-SEP-1997; 97US-0058765P.
09-CCT-1997; 97US-0061660P.
06-MAR-1998; 98WG-US004493.
08-SEP-1998; 98US-00149476.
                                                    RUBEN S M.
ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
YU G.
NI J.
YU G.
NI J.
YU G.
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YOUNG P E.
YOUNG P E.
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FISCHER C L.
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FLORENCE K A.
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LAFLEUR D W.
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KYAW H.
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Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP; Endress GA, Yu G, Ni J, Feng P, Young PB, Greene JM, Errie AM; Duan DR, Hu J, Florence RB, Disen HS, Fischer CL, Ebner R; Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; WPI; 2003-521800/49. P-PSDB; ABO34618.

New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral ischemia.

Claim 4; SEQ ID NO 255; 260pp; English.

The present invention relates to the isolation of novel human secreted proteins and the polynucleotide sequences encoding them. The invention also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polynucleotide for producing human secreted proteins are useful for preventing, treating, amplicating or disgnossing medical conditions such as hyperproliferative clisorders (e.g. pleukaemia or breast cancers), wounds, reproductive disorders (e.g. leukaemia or breast cancers), wounds, reproductive clisorders, blood-related disorders (e.g. haemophilia or thrombooytopaenia), immunodeficiencies (e.g. graff-versus-host disease, thymic hypoplasia), autoimmune disorders (e.g. graff-versus-host disease, cultiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma), ciral or bacterial or fungal infections (e.g. AIDS or sepsis), renal clisorders (e.g. kidney failure), cardiovascular disorders (e.g. angina pectoris, cerebral ischaemia or congenital heart defects), respiratory clisorders, neurological disorders (e.g. AIDS or sepsis). The partines disorders disease), and inflammations (e.g. AIDS or sepsis). The carboral ischaemia or congenital neart defects), respiratory confisorders, disease), and inflammations (e.g. Crohn's disease). The partined or polypeptide may also be used as vaccine adjuvants. ACMS2641-ACD8250 encode human secreted proteins or their fragments. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the cycle used site at seqdata.uspto.gov/psipablibEntry.html

us-09-830-972-2_copy_975_1163.rng

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97US-0040163P.
97US-004033P.
97US-0040331P.
97US-00403311P.
97US-0043311P.
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                                                                                                                                                                                     382 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 441
                                                                                                                                                                                                                                                                                                                    121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                                                                                                                                                                                                                                                                                                                         HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                262 GCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTTGTCTTTGGCACC 321
                                                                                                                                        442 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 501
                                                                                                                                                                                                                                                SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                                                                                                                                                                                                                                                  101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
                                                                                                                                                                                                                                                                                                                               622 TTCATGTGGCTGATGATCATGTTGTTGTTTTTTAACGGAATCACCCTTCTAATTCTT 681
                                                                                                                                                                                                                                                                                                                                                       141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
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                                                                                                      1 ServalValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
                                                                                                                                                                                                             61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                          41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.
Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding novel human secreted protein seq id 255
                                                                                    US-09-830-972-2_COPY_975_1163 (1-189) x ACD82885 (1-2664)
                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADI22970 standard; cDNA; 2664 BP
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                       2.23e-64
622.50
81.05$
59.47$
67.30$
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                                      Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                 Alignment Scores:
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                          . No. .
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ADI22970
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polypeptide, or its fragment, domain, epitope or species homologue; or a polymucleotide that hybridises under stringent conditions to any one of the sequences of (a) -(c). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer. The sequence encodes a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                 262 GCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 321
                                                                                                                                                                                                                                                                                                  322 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTTCTAGTGTTCATCAGTGTTGATTCATTAGCTC 381
                                                                                                                                                                                                                                                                                                                                                                                                                              SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                                                                                                                                                                                                                                      1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                                                                                                                                                    SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                 382 ATCCTGGCTCTTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                              LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; secreted protein; cancer; haematopoietic disorder; endocrine disorder; immune system disease; inflammatory disorder; ss;
  of the cDNA sequence; a polynucleotide sequence encoding a
                                                                                             T; 0 U; 7 Other;
                                                                                                                                2664
1113
41
35
1
                                                                                                                                                                                                                 US-09-830-972-2_COPY_975_1163 (1-189) x ADI22970 (1-2664)
                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 IleProGlyLeu---LysArgLysAlaAsp 189
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CTCCCTGGAATCGCCAAAAAAAGGCAGAA 831
                                                                                             Sequence 2664 BP; 707 A; 605 C; 566 G; 779
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                                                                                                                              2.23e-64
622.50
81.05%
59.47%
67.30%
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                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carter KC, Bednarik DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition
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g Z, Kyaw H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 255; 256pp; English.
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Yu G, Ni J, Fens
Iu J, Florence KA, C
97US-0056876P
97US-0056817P
97US-0056818P
97US-0056881P
97US-0056881P
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YOUNG P.
GREENE J. M.
FERRIE A. M.
DUAN D. R.
HU J.
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FISCHER C L.
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SHI Y.
LAFLEUR D W.
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P-PSDB; ADI23279.
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Hu J,
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(KYAW/) KYAW H.
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97US-0056630P.
97US-0056631P.
                                                              10-JUN-2002; 2002US-00164861
                          US2003225248-A1.
         Homo sapiens.
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(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP; Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM; Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R; Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; Ruben SM, Rober Endress GA, Yu

WPI; 2004-131264/13. P-PSDB; ADH74281.

Isolated nucleic acid molecules encoding human secreted proteins, useful for preventing, diagnosing and treating disorders associated with aberrant expression and activity.

Claim 3; SEQ ID NO 255; 142pp; English.

The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPs) they encode. The proteins and nucleic acids may be used in the prevention, disgnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoietic disorders, chiseases of the immune system, inflammatory endocrine disorders diseases of the immune system, inflammatory cancers and many others. Full decails of disorders that may be used as proteins. The nucleic acid molecules may be used to produce their specification. The nucleic acid molecules may be used to produce their specification. The nucleic acid molecules may be used to produce their specification. The nucleic acid molecules may be used to proteins. The nucleic acid in samples, and therefore which used as DNA probes in diagnostic assays to detect and quantitate the prosence of similar nucleic acids in samples, and therefore which presence of similar nucleic acids in samples, and therefore which assays to identify modulators of SP expression and activity. The anti-SP antibodies may also be used as diagnostic and activity. The anti-SP antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The present sequence

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(PROT-) PROTEIN DESIGN LABS INC.
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26-NOV-2003; 2003WO-US038193
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                                                                                                                                                               The invention relates to a novel method for detecting soft tissue sarcome which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and domparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for predicting a toxic effect
of a compound. The method comprises preparing a gene expression profile
of a tissue or cell sample exposed to the compound, and comparing the
gene expression profile to a database comprising SEQ ID 1-4925, where
differential expression of the gene indicates at least one toxic effect.
The method is useful for predicting at least one toxic effect of a
compound, identifying an agent that modulates the onset or
progression of a toxic response, predicting the cellular pathways that a
compound modulates in a cell, and identifying an agent that modulates at
least one activity of a protein. The method and compositions of the
present invention using a database of genes having liver toxin-induced
differential expression, are useful in identifying toxicity markers in
liver tissues or cells for drug screening and toxicity markers in
liver tissues or cells for drug screening and toxicity assays. Note: The
specification, but was obtained in electronic format directly from WIPO
                                     HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                         800 CACTATGTTGGCATCGCCCGAGATCAGCCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
740 GCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                  Toxic; toxin; gene expression profile; hepatotoxicity; liver; drug screening; toxicity assay; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 G; 789 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castle A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
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                                                                                                                181 ileProGlyLeu---LysArgLysAlaAsp 189
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                                                                                                                                         860 CTCCCTGGAATCGCCAAAAAAAAAGGCAGAA 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 3915; 1156pp; English.
                                                                                                                                                                                                                                                                                                                                                               Toxicity-related gene, SEQ ID 3915.
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                                                                                                                                                                                                                                       ADB58889 standard; DNA; 2773 BP
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2002US-0364055P.
2002US-0436643P.
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622.50
81.05%
                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) GENE LOGIC INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
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15-MAR-2002;
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                                     161
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Percent Similarity:

Pred. No.:

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327 ACGCTGATCATGCTCTTCTCTGCTGCTTTTCAGTGTTATCAGTGTGTCTTTACCTC 386
                                                                                                                                                                                                                                                              446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisTyrLeuGlyLeuAlaAsnLysSerValLysABpAlaMetAlaLysIleGlnAlaLys 180
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CACTATGTTGGGATTGCCCGGGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAG 806
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                                                                                               1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
                                                                                                                                                                                                                                                387 ATCCTGGCTCTACTCTCTGTCACCATCAGCTTCAGAGTCTACAAGTCTACCAAGCT
                                                                                                                                                                                                                                                                                             SerieuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                             41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                            SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCATGTGGCTGATGACCTACGTCGGTGCTGTTTTTAACGGAATTACCCTTCTGATTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                              LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuroprotective, Myotropic, neuromuscular disease, RTN3; reticulon 3; amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.
                                                               (1-2773)
   32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human RTN3 isoform III coding sequence, SEQ ID 54
Mismatches:
Indels:
                                                               x ADB58889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleProGlyLeu---LysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCCTGGAATCGCCAAAAAAAAGGCAGAA 836
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                                                                                                                                                                                                                                                                                                           The present invention relates to a method for diagnosing, or evaluating progression of, a neurcomuscular disease. The method comprises detecting modulation of the expression of a product (I) of the RTM (reticulon)3 gene. Differential expression of RTM3 is a specific marker of neuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular disorders, specifically amyotrophic lateral sclerosis (ALS) and myopathy. Also (1) antibodies specific for isoforms of RTM3 or oligonucleotides (antisense sequences or small interfering RNA) that can block/reduce expression of these isoforms are useful for treating neuromuscular diseases and (ii) cells that express RTM3 are useful in screening for therapeutic agents. The present sequence is a RTM3 DNA sequence used to illustrate the invention.
                                                                                                                                                                               prognosing and monitoring neuromuscular disease, particularly lateral sclerosis, comprises detecting modulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 GAACTGCTCATTTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                          De Tapia M, Larmet Y, Loeffler J;
Boutillier AL, Gaiddon C, Rene F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1968 BP; 496 A; 482 C; 411 G; 579 T; 0 U; 0 Other;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                      Claim 35; SEQ ID NO 54; 116pp; French.
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621.50
80.95$
59.79$
(UYPA-) UNIV PASTEUR LOUIS.
                                       Dupuis L, Di Scala F,
Gonzales De Aguilar J,
                                                                                                           WPI; 2004-071743/07
                                                                                                                                                                          Diagnosing, progno
amyotrophic latera
reticulon 3 gene.
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                                                                                                                                     P-PSDB; ADM36172
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the present through a comprision (a) the full-length coding region of (a); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% captuence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above (a)-(c). Also described: (1) an expression vector comprising the above comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide (comprising) (a) an amino acid sequence encoded by any of the above comprising the above polypeptide (a) or (b); (5) a chimeric polypeptide (baving at least 80% identical to (a) or (b); (5) a chimeric polypeptide; (a) an isolated antibody, that binds to the above polypeptide; (6) a comprising the antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated antigonic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above p
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TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                    human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an isolated tumour-associated antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tumour-associated antigenic target (TAT) cDNA sequence #1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c acid molecule and encoded polypeptide, for diagnosing, or treating cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1279; 5504pp; English
                                                                                                                    ProGlyLeu---LysArgLysAlaAsp 189
                                                                                                                                                                           862 CCTGGAATCGCCAAAAAAAGGCAGAA 888
                                                                                                                                                                                                                                                                                                ADQ84465 standard; cDNA; 2250 BP.
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   162
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mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCTGTA 180
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                                                                                                                        cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.
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TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAAGATCCAAGCAAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                           Seguence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;
                                                                                                                                                                                                                       2250
113
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                                                                                                                                                                                                                                                                                                       Gaps:
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621.50
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current (TAMT) nucleic acid comprising: (a) any of 4622 nucleotide antigenic target (TAMT) nucleic acid comprising: (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% acquences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (c). Also described: (l) an expression vector comprising the above (a)—

(c). Also described: (l) an expression vector comprising the above correction of a process for producing a polypeptide; (4) an isolated polypeptide (comprising: (a) an amino acid sequence encoded by any of the above correction of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-correction sequences; (b) an amino acid sequence encoded by the full-corporation of the above polypeptide; (d) or (b); (5) a chimeric polypeptide; (c) an isolated antibody that binds to the above polypeptide; (d) a number above polypeptide; (g) a tumour-associated antipolic target (TAT) and compression of matter comprising the above polypeptide; (l) a tumour-associated antipolic target (TAT) antibody, (l) a tumour-associated antipolic target (TAT) antibody, (l) a tumour-associated antipolic target (TAT) antibody, (l) a tumour-associated antipolic target (TAT) antibody, (l) a tumour-associated antibody the polypeptide or TAT binding organic molecule that binds to the above polypeptide; (l) a composition of matter comprising the above polypeptide or TAT binding organic molecule, in combination of matter comprising the composition of matter contained within the container; (12) methods of the cell is a least in part dependent upon a growth the composition of matter contained within the container; (l) a method of potentialing effect of the above protein; (l1) a method of determining the protein in a sample suspected of containing the protein in a sample suspected of containing the protein in a sample suspected of containing the protein and (l1) a method of binding an antibody, oligopeptide or a protein and (l1) a method of binding an antibody, oligopept
TAT; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes an isolated tumour-associated antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
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Conservative:
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human; tumour-associated antigenic target; cancer; cell proliferative disorder; gene;
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                                                                 Homo sapiens.
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Query Match:

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                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour-associated antigenic target; TAT; cytostatic; gene therapy; cell proliferative disorder; gene; ss.
                                                                                                                                                                                           102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                              LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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                               ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                         GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
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               US-09-830-972-2_COPY_975_1163 (1-189) x ADQ86409 (1-2250)
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New nucleic acid molecule and encoded polypeptide, for diagnosing, propression to treating cell proliferative disorders such as cancer.

May seventing or treating cell proliferative disorders such as cancer.

May separe (TMT) mucleic acid comprising: (a) any of 4622 mucleotide estences (see SEQ ID Noil to 6422); (b) the full-length coding region of (a) or (b); (d) a sequence that has 80% esquence (see SEQ ID Noil to 6422); (b) the full-length coding region of (a) or (b); (d) a sequence that has 80% esquence (see SEQ ID Noil to 6422); (b) the full-length coding region of (a) or (b); (d) a sequence that bybridises to (a)-(c). Also described: (1) an expression vector comprising the above comprising the above (c) and manno acid sequence encoded by the full-ength coding region of the above mucleotide sequences; (b) an amino acid sequence encoded by the full-ength coding region of the above mucleotide sequences; (b) an amino acid sequence encoded by the full-ength coding region of the above mucleotide sequences; (c) a sequence comprising the above polypeptide; (a) a chimeric polypeptide; (c) a chimeric polypeptide; (c) a chimeric polypeptide; (d) a chimeric polypeptide; (d) a chimeric polypeptide; (d) a chimeric polypeptide; (d) a chimeric polypeptide; (d) a chimeric polypeptide; (d) a composition of matter comprising the above polypeptide; (d) a composition of matter comprising the above polypeptide or TMF binding organic molecule that in mid correlation of matter comprising the above polypeptide or TMF binding organic molecule. The composition of matter contained within the container; (11) an exticle of manufacture comprising a container and thinking the growth of the call that expresses the above polypeptide or the growth of the cell is at least in part dependent upon a growth containing the above polypeptide or composition of matter contained within the container; (11) a method of cite above polypeptide or composition and mannal; (16) a method for treating or treating or treating or treating or treating or treati
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Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

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Query Match:
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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (l) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by the above nucleotide sequences; (b) an amino acid sequences encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide.
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                  CICATTAITCGICTCTITCTGGIAGAAGAICTGGTIGATCTCTIGAAGCTGGCTGTCTTC
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(ZHOU/)
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comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process cor producing the antibody; (8) an isolated olipopeptide that binds to the above polypeptide; (9) a tumour-associated antigence target (TAT) binding organic molecule; that binds to the above polypeptide; (10) a composition of matter comprising the above (chimmeric) polypeptide; (10) a composition of matter comprising organic molecule; in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein; where the growth of the cell is at least in part dependent upon a growth cell that express the above protein; (13) a method of determining the presence of a protein in a sample suspected of containing the protein cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein cannow, (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above.

The TAT sequences have cytostatic activities, and can be used in gene and preventing and methods are useful for diagnosing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
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ADM36175 RESULT

Key

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1705 CTGGCTCTTCTCTCTCTGTCACCTTCAGGATCTACAAGTCCGTCATCCAAGCTGTA 1764
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2065 TATGTTGGCATCGCCCGAGATCAGACCAATTGTTGAAAAGATCCAAGCAAAACTC 2124
                                                                                                                                               1945 Argregergargacciargriggrecrerrirraacegaarcacccricraarrcriger 2004
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                                   ValvalaspieuLeuTyrTrpargaspileLysLysThrGlyValvalPheGlyAlaSer 21
                                                                                                                         LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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US-09-830-972-2_COPY_975_1163 (1-189) x ADM36175 (1-3231)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human RTN3 isoform II coding sequence, SEQ ID 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
124. .2211
/*tag= a
/product= "RTN3 isoform II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing, prognosing and monitoring neuromuscular disease, particularly amyotrophic lateral sclerosis, comprises detecting modulation of the reticulon 3 gene.
481 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAACTC 540
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Boutillier AL, Gaiddon C, Rene
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                Human RTN3 isoform V coding sequence, SEQ ID 58.
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/product= "RTN3 isoform V"
                                         182 ProGlyLeu---LysArgLysAlaAsp 189
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Gonzales De Aguilar J,
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Query Match: DB:

141

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US-09-830-972-2_COPY_975_1163 (1-189) x ADM36179 (1-4092)
                  182 ProGlyLeu---LygArgLysAlaAsp 189
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9
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                                                                                   RESULT
                                               셤
                                                                                                                                 The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (I) of the RTN (reticulon)3 gene. Differential expression of RTN3 is a specific marker of neuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular disorders, specifically amyotrophic lateral sclerosis (ALS) and myopathy. Also (il) antibodies superific for isoforms of RTN3 or oligonucleotides (antisense sequences or small interfering RNA) that can block/reduce expression of these isoforms
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                                                                              prognosing and monitoring neuromuscular disease, particularly lateral sclerosis, comprises detecting modulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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                                                                                                                                                                                                                                                                                                                                             small interfering RNA) that can block/reduce expression of these isoforms are useful for treating neuromuscular diseases and (ii) cells that express RNN3 are useful in screening for therapeutic agents. The present sequence is a RTN3 DNA sequence used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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 Rene F;
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 Gaiddon C,
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Conservative:
Mismatches:
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Boutillier AL,
                                                                                                                                            Claim 35; SEQ ID NO 52; 116pp; French.
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80.95%
59.79%
67.19%
Gonzales De Aguilar J,
                             WPI; 2004-071743/07.
P-PSDB; ADM36170.
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Best Local Similarity:
                                                                            Diagnosing, prognamyotrophic later reticulon 3 gene.
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The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (1) of the RTN (reticulon)3 gene. Differential expression of RTN3 is a specific marker of neuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular diseases, specifically amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies specific for isoforms of RTN3 or oligonucleotides (antisense sequences or small interfering RNA) that can block/reduce expression of these isoforms are useful for treating neuromuscular diseases and (ii) cells that express RTN3 are useful in screening for therapeutic agents. The present sequence is a RTN3 DNA sequence used to illustrate the invention.
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C, Rene
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163. .3015
/*tag= a
/product= "RTN3 isoform VII"
2182 CCTGGAATCGCCAAAAAAAGGCAGAA 2208
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Boutillier AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 35; SEQ ID NO 62; 116pp; French.
                                                                                                                                     ADM36179 standard; DNA; 4092 BP
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Gonzales De Aguilar J,
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Best Local Similarity:
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                                                                                                                                                                                                 ADM36179;
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WPI; 2004-071743/07

P-PSDB; ADM36174

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2566 CTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCTGTA 2625
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2926 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAACTC 2985
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21
                                                                                                                     LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                        2506 CTGATCATGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGGTTTCTTACCTCATC
                                                                                                                                                                                                                                       LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
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Boutillier AL, Gaiddon C, Rene F;
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/product= "RTN3 isoform IV"
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Gonzales De Aguilar J,
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                                                                                                                                                                The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (I) of the RTN (reticulon)3 gene. Differential expression of RTM3 is a specific marker of neuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular disorders, specifically amportant sclerosis (ALS) and myopathy. Also (i) antibodies specific for isoforms of RTM3 or oligonucleotides (antisense sequences or small interfering RMA) that can block/reduce expression of these isoforms express RTM3 are useful in screening for therapeutic agents. The present sequence is a RTM3 DNA sequence used to illustrate the invention.
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                                                                Diagnosing, prognosing and monitoring neuromuscular disease, particularly amyotrophic lateral sclerosis, comprises detecting modulation of the reticulon 3 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 LeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4239 BP; 1282 A; 925 C; 890 G; 1142 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                       Claim 35; SEQ ID NO 56; 116pp; French.
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80.95$
59.79$
67.19$
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Best Local Similarity:
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2 yalValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

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The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (I) of the RTM (reticulon)3 gene. Differential expression of RTM3 is a specific marker of neuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular disorders, specifically amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies small interfering RNA) that can block/reduce expression of these isoforms are useful for treating neuromuscular diseases and (ii) cells that express RTM3 are useful in screening for therapeutic agents. The present sequence is a RTM3 DNA sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing, prognosing and monitoring neuromuscular disease, particularly amyotrophic lateral sclerosis, comprises detecting modulation of the reticulon 3 gene.
                                                                                                                                                                                                                                                           Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3; amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4296 BP; 1290 A; 944 C; 895 G; 1167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Tapia M, Larmet Y, Loeffler J;
Boutillier AL, Gaiddon C, Rene F;
                                                                                                                                                                                                                       Human RTN3 isoform I coding sequence, SEQ ID 50
                                                                                                                                                                                                                                                                                                                                                                                                          /product= "RTN3 isoform I"
                   3133 CCTGGAATCGCCAAAAAAAGGCAGAA 3159
ProGlyLeu---LysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 35; SEQ ID NO 50; 116pp; French.
                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
                                                                                                          ADM36167 standard; DNA; 4296 BP
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Gonzales De Aguilar J,
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P-PSDB; ADM36168.
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                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                   03-JUN-2004
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 182
                                                                                                                                              ADM36167;
                                                                      RESULT 100
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2650 GTGCACGATCTGATTTTCTGGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACCACG 2709
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                                                                                                                                                                                                                2830 CAGAAGTCAGAAGAAGGCCATCCATTCAAGGCCTACCTGGACGTAGACATTACTCTGTCC 2889
                                                                                                                                                                                                                                                                                 2890 TCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTGAAA 2949
                                                                                                                                                                                                                                                                                                                                                        3130 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAACTC 3189
                                                                                                                                                                                                                                                                                                                                                                                                      MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                                                                              82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                  102 GlubeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                                                                                                       61
                                                                   LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                         2770 CTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCTGTA
                                               22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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Search cor Job time

US-09-830-972-2_COPY_975_1163 (1-189) x ADM36167 (1-4296)

Length:
Matches:
Conservative:
Mismatches:
Indels:

5.75e-64

Alignment Scores:

Pred. No.:

Score:

621.50 80.95% 59.79% 67.19%

Percent Similarity: Best Local Similarity:

Query Match

Gaps:

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102, App 1419, Ap 117588, 117589,

40170, A 119336, 1905, Ap 117609,

407, App 149, App 1, Appli

Appli

OM protein

Run on:

Sequence:

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NAME/KEY: unsure

LOCATION: 33, 21, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,

S. OTHER INFORMATION: a, t, c, g, or other

US-09-484-970B-106
                                                                                                                                                                                                                                                                                                                                          Sequence 703, App
Sequence 48087, A
Sequence 178, App
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4281, nr.
Sequence 100, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 149,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 572:
Sequence 407,
Sequence 407,
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                Sequence
Sequence
Sequence
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Sequence 1
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OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
            US-09-949-016-1419

US-09-949-016-117588

US-09-949-016-117588

US-09-949-016-117589

US-09-949-016-12651

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US-09-949-016-12651

US-09-949-016-11335

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Matches:
Conservative:
Mismatches:
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US-09-484-970B-106
Sequence 106, Application US/09484970B
Patent No. 6426IBC
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Johnath, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SEQ ID NO 106
LENGTH: 4822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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261
13906
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
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336.9
336.9
30.9
30.9
30.5
30.5
30.5
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285
282.5
282.5
278.5
278.5
278.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command line parameters:
-MODEL=frame+p2n.model -DEV=x1p
-MODEL=frame+p2n.model -DEV=x1p
-MODEL=frame+p2n.model -DEV=x1p
-DE-CGPG_1 J/USPTO spool p/US09830972/runat 16062005 153942 18915/app_query,fasta_1.654
-DB=ISBUEd_PatenTe NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -START=1 -END=1 -NATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=loO -THR MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFNT=pto -NOEME=pct -THR MAX=100 -THR MIN=0 -MAXLEN=200000000
-WORDE=LOCAL -OUTFNT=pto -NOEME=xt -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-NOEMBAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-NO MARP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 106, App
Sequence 2, Appli
Sequence 3253, Ap
Sequence 3109, Ap
Sequence 3109, Ap
Sequence 298, App
Sequence 254, App
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Sequence 13561, A
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2464.194 Million cell updates/sec
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925
1 SVVDLLYWRDIKKTGVVFGA......VKDAMAKIQAKIPGLKRKAD 189
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/cgn2 6/ptodata/1/ina/5B_COMB.seq:*
/cgn2 6/ptodata/1/ina/6A_COMB.seq:*
/cgn2 6/ptodata/1/ina/6B_COMB.seq:*
/cgn2 6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2 6/ptodata/1/ina/PCTUS_COMB.seq:*
                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                         nucleic search, using frame_plus_p2n model
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US-08-700-607-2
US-09-949-016-3253
US-09-949-016-3309
US-09-949-016-1127
US-09-949-016-2988
US-09-149-476-254
US-09-149-476-255
US-09-149-476-254
US-09-149-476-254
US-09-149-476-254
US-09-149-476-254
US-09-179-1111
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Perfect score:
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Sequence 3253, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
PILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGTGGTGTTTGGTGCCAGC 167
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Mismatches:
Indels:
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Matches:
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904.00
98.94%
97.34%
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHRACATERISTICS:
LENGTH: 799 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                          Consensus
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Best Local Similarity:
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US-09-949-016-3253
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                           3265 TCAGTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 3324
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    SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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APPLICANT: Bandman, Olga
APPLICANT: Al-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S.
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SOFTWARE: FASTSEQ VETSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELESPERENCE/DOCKET NUMBER: PF-0114
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08700607
Patent No. 5858708
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
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US-08-700-607-2
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ITLE OF INVENTION:
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Patent No. 6607879
Patent No. 6607879
Patent Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Joffrey J. Salilamer
APPLICANT: Joffrey J. Salilamer
APPLICANT: Joffrey J. Salilamer
APPLICANT: Joffrey J. Salilamer
APPLICANT: Joffrey J. Salilamer
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 3253
LENGTH: 1669
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904.00
98.94%
97.34%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3253
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1311 GTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 1370
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  TITLE OF INVENTION:

NUMBER OF SEQUENCES:

ADDRESSEE: INCTTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: BALSENIA
COUNTRY: USA
ZIP: 94304
COUNTRY: USA
ZIP: 94304
COUNTRY: USA
SITATE: CALIFORNIA
COUNTRY: WORD PERFECT 6.1 For Windows/MS-DOS 6.2
COUNTRY: WORD PERFECT 6.1 For Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERWITH
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 37,071
REGISTRATION OF SEQUENCE,
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 382:
SEQUENCE CHARACTERISTICS:
TENORATION POR SEQ ID NO: 382:
TENORATION POR SEQ ID NO: 382:
TENORATION POR SEQ ID NO: 382:
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183
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Matches:
Conservative:
Mismatches:
Indels:
EXPRESSION
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891.00
98.41%
96.83%
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STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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CLONE: 1508778
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Best Local Similarity:
Query Match:
DB:
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sequence 1127, Application US/09949016

gequence 1127, Application US/09949016

general incomparitor.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 1127

LENTH: 3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr11eLysGlu
1950 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGAGCGTGAGCGTGAGCCTACCTGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2010 GCCGCACTCTCAGCCACCACCATTCCGCATCTACAAGTCTGTTTTACAAGCAGTGCAG
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Matches:
Conservative:
Mismatches:
Indels:
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679.00
84.49%
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Best Local Similarity:
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US-09-949-016-1127
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DB:
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Sequence 3309, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEX ID NOS: 207012

SOSTHARRE: FREASEQ for Windows Version 4.0

SEQ ID NO 3309

LENGTH: 2069
               1791 TTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT 1850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnSerThrIleLysGlu
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                                                                            aLeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHi
                                                                                                                                       STyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIl
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Matches:
Conservative:
Mismatches:
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679.00
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-3309
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HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                                                                                                                                                                                                                     367 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTTAACGGAATCACCCTTCTAATTCTT
                                                                                                                                                                                                                                                                                                                             LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: POOL2P1
CURRENT APPLICATION NUMBER: US/09/149, 476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
APPLICATION NUMBER: 60/040,336
APPLICATION NUMBER: 60/040,336
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APPLICATION UNDRER: 60/047,615
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,597
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,584
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,600
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APPLICATION NUMBER: 60/047,583
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APPLICATION NUMBER: 60/047,617
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APPLICATION NUMBER: 60/047,592
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Patent No. 6420526
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Sequence 2988, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PRILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SEC ID NOS: 207012

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Best Local Similarity:
Query Match:
DB:
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R APPLICATION NUMBER: 60/048,974
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R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,886
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R APPLICATION NUMBER: 60/047,632
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,601
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R APPLICATION NUMBER: 60/043,580 R APPLICATION NUMBER: 60/043,314
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,598 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 APPLICATION NUMBER: 60/056,879 APPLICATION NUMBER: 60/056,880 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 PPLICATION NUMBER: 60/056,888 997-08-22 FILING DATE: 1997-04-11 1997-08-2 997-08-2 1997-05-2 EARLIER
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,631
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RR APPLICATION NUMBER: 60/056,845
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APPLICATION NUMBER: 60/047,592
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Matches:
Conservative:
Mismatches:
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Patent No. 6420526
GENERAL INFORMATION:
PPLICANT: Rosen et al
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 IleProGlyLeu---LysArgLysAlaAsp 189
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER PILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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Best Local Similarity:
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A PPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-22
A PLICATION NUMBER: 60/056,892
R FILING DATE: 1997-08-22
A APPLICATION NUMBER: 60/057,761
R APPLICATION NUMBER: 60/057,761
R APPLICATION NUMBER: 60/047,595
R FILING DATE: 1997-05-23
                R APPLICATION NUMBER: 60/043,672
R FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,315
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/048,974
R FILING DATE: 1997-06-66
R R PILING DATE: 1997-06-66
R PILING DATE: 1997-08-22
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,880
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,894
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911
R FILING DATE: 1997-08-22
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,874
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,910
R PILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/047,588
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APPLICATION NUMBER: 60/047,585
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APPLICATION NUMBER: 60/047,586
RILING DATE: 1997-05-23
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,630
R APLING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,878
R FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,872
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APPLICATION NUMBER: 60/056,882
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,589
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100 262 GCGGTGCAGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 321 322 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCTC 381 21 SerieuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60 1 ServalvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20 382 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT US-09-830-972-2_COPY_975_1163 (1-189) x US-09-149-476-255 (1-2664) Length:
Matches:
Conservative:
Mismatches:
Indels: R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/056,632
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
FILING DATE: 1997-04-11
APPLICATION NUMBER: 61/043,576 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,875 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,908 FILING DATE: 1997-08-22 FILING DATE: 1997-06-13 APPLICATION NUMBER: 60/061,060 FILING DATE: 1997-10-02 FILING DATE: 1997-04-11 APPLICATION UNMBER: 60/047,501 ELING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,670 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/057,650 APPLICATION NUMBER: 60/049,610 FILING DATE: 1997-09-05 APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 APPLICATION NUMBER: 60/056,862 APPLICATION NUMBER: 60/048,964 1997-09-05 997-08-22 FILING DATE: 1997-08-1.5e-76 622.50 81.05% 59.47% 67.30% LING DATE: Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: EARLIER 1 EARLIER 1 EARLIER 1 EARLIER 1 EARLIER 1 EARLIER 1 EARLIER 1 EARLIER 1 EARLIER 1 EARLIER PEARLIER F BARLIER RARLIER RARLIER BARLIER red. No.: 셤 ò g 엄 8 ð ò 120

502 İCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTG

LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal

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3146 TCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTGAAA 3205
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     3026 credererrerereresecareacerreagareraeareraeaaereeareeareerera 3085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3266 ATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTTGTTTTTGCT 3325
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                                                                                                                                                                                                                                                                                  82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                              102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                                          42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
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SOFTWARE: FRACEGO Version 1.
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/70
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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3506 GTTGAAAG 3514
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OPERATING SYSTEM:
SOFTWARE: FASTSEQ
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STATE: CA
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US-08-700-607-4
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TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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Indels:
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CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: DL_FL_genes Version 2.0
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Patent No. 6783969
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Ma, Yunging
Yamazaki, Victoi
Chen, Rui-hong
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Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
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Wang, Jian-Rui
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Xue, Aidong J
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ORGANISM: Homo sapiens
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; LOCATION: (196)..(654)
US-09-799-451-111
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Alignment Scores:
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Patent No. 6703491

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-034

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                     41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLy8GlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                    449 ATCCTGGCTCTTCTCTCTGTCACCTTCAGGTCTACAAGTCCGTCATCCAAGCT
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Mismatches:
Indels:
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                                                                                                                                                          Length:
Matches:
                                                                                                                                                           2.03e-63
1095 base pairs
                                                                                                                                                                        524.50
72.77$
53.40$
56.70$
             TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: THPINOBO1
CLONE: 31870
                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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ValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 CGTCTGTTTCTTGTTGAGGATATCATCGATTCGATCAAGTTCGGCGTCATTCTGTGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAlaIleGlnLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 LeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644 CIGGIGCGCAGCAAATIGACAGAAATCACCGACAAGAICCGAGIGGCCAICCCC 697
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93
41
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Mismatches:
Indels:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
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CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
                                                                                                     Length:
Matches:
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Patent No. 6420526
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13561
                                                                                                                                                                                                                                                      US-09-830-972-2_COPY_975_1163 (1-189)
                                                                                                4.43e-62
518.00
75.28%
52.25%
56.00%
                                                                                                                                              Percent Similarity:
Best Local Similarity:
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US-09-149-476-102
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RELING DATE: 1997-05-23
A APPLICATION NUMBER: 60/047,615
R FILING DATE: 1997-05-23
A APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
A APPLICATION NUMBER: 60/047,502 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,633 APPLICATION NUMBER: 60/047,617 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,618 LING DATE: 1997-05-23 PLICATION NUMBER: 60/047,503 LING DATE: 1997-05-23 LING DATE: 1997-05-23 PLICATION NUMBER: 60/047,500 NG DATE: 1997-05-23 ICATION NUMBER: 60/047,598 NG DATE: 1997-05-23 G DATE: 1997-05-23 CATION NUMBER: 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 G DATE: 1997-04-11 CATION NUMBER: 60/043,315 APPLICATION NUMBER: 60/040,336 APPLICATION NUMBER: 60/047,600 APPLICATION NUMBER: 60/047,583 TLING DATE: 1997-05-23 ING DATE: 1997-05-23 PLICATION NUMBER: 60/047,581 LING DATE: 1997-05-23 PLICATION NUMBER: 60/047,584 CATION NUMBER: 60/047,587 ILING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,492 CATION NUMBER: 60/047, 582 'ILING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,612 APPLICATION NUMBER: 60/047,632 LING DATE: 1997-04-11 PLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 TLING DATE: 1997-04-11 PPLICATION NUMBER: 60/043,312 G DATE: 1997-04-11 CATION NUMBER: 60/043,672 PLICATION NUMBER: 60/047,592 LICATION NUMBER: 60/047,613 APPLICATION NUMBER: 60/047,596 TILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,601 CATION NUMBER: 60/043,314 APPLICATION NUMBER: 60/043,569 APPLICATION NUMBER: 60/043,671 CATION NUMBER: 60/043,313 APPLICATION NUMBER: 60/048,974 1997-05-23 1997-03-07 1997-05-23 1997-05-23 1997-05-23 1997-04-11 1997-04-11 LING DATE: 1997-04-11 1997-04-13 1997-05-23 EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER SARLIER SARLIER SARLIER

APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,893 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,878 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 ION NUMBER: 60/056,886 APPLICATION NUMBER: 60/056,877 APPLICATION NUMBER: 60/056,882 APPLICATION NUMBER: 60/056,637 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 APPLICATION NUMBER: 60/056,880 APPLICATION NUMBER: 60/056,636 PLICATION NUMBER: 60/056,910 APPLICATION NUMBER: 60/056,845 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,588 APPLICATION NUMBER: 60/047,590 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,894 APPLICATION NUMBER: 60/056,911 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 APPLICATION NUMBER: 60/056,631 APPLICATION NUMBER: 60/057,761 APPLICATION NUMBER: 60/047,595 PPLICATION NUMBER: 60/047,599 APPLICATION NUMBER: 60/047,585 APPLICATION NUMBER: 60/047,586 APPLICATION NUMBER: 60/047,589 APPLICATION NUMBER: 60/047,593 APPLICATION NUMBER: 60/047,594 LING DATE: 1997-08-22 ILING DATE: 1997-08-22 FILING DATE: 1997-08-22 ILING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 997-05-23 FILING DATE: 1997-08-22 LING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 997-05-23 FILING DATE: 1997-08-2 LING DATE: 1997-08-2 FILING DATE: 1997-08-2 FILING DATE: 1997-08-FILING DATE: 1997-08-FILING DATE:

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Sequence 1419, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTEN.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION WINBER: US/09/949,016
TITLE APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-08
NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE OF WINGOWS Version 4.0
SEQ ID NO 1419
LENGTH: 2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIelleLeuAla 141
                                                                      160 spHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180
                                                                                                         791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlalleSer 81
                                                                                              2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 LeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValIleGlnAlaile
   euAlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-1419 (1-2181)
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Matches:
Conservative:
Mismatches:
Indels:
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70.33%
50.55%
51.35%
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-1419
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Pred. No.:
     140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 SerieuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 ACGCTGATCATGCTTTCCCTGGCAGCTTTCAGTGTCATCARTGTGGGTTTCTTAMCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 eAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : CATCCTGGCTCTTCTCTGTCACCATCARCTTCAGGATCTACAAGTCCGTCATCCAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-830-972-2_COPY_975_1163 (1-189) x US-09-149-476-102 (1-794)
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101
38
41
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Matches:
Conservative:
Mismatches:
ER APPLICATION NUMBER: 60/047,501
ER FLING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/043,670
ER PLING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/056,632
ER FLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,841
ER FLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,881
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,881
ER APPLICATION NUMBER: 60/056,891
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,993
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,975
ER FLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,862
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,862
ER APPLICATION NUMBER: 60/056,862
ER APPLICATION NUMBER: 60/056,903
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,903
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,903
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,903
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/056,884
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,669
ELING DATE: 1997-09-05
APPLICATION NUMBER: 60/049,610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
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509.50
76.37%
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Best Local Similarity:
Query Match:
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                    EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER | EARLIER |
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                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-117589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-14995
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ORGANISM: Human
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US-09-949-016-117589/c
; Sequence 117589, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                         ||||::||||||||
1642 TATGTGGGGTTGGTGACCAATCAGTTGAGCCACATCAAAGATCCGAGCTAAAATC 1701
1522 TTCTACATCTTGACCTTCGTGGGTGCCATCTTCAATGGTTTGACTCTTCTCATTCTGGGA 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 LeuPheLeuLeuLeuSerLeuThrValPheSer1leValSerValThrAlaTyrIleAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 LeuAlaLeuLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAlaile 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 45
                                                                              TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-117588 (1-601)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 CAGAAATCAGATGAAGGCCACCCATTCAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indel8:
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Patent No. 6812339
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Query Match:
DB:
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US-09-949-016-117588/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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Pred. No.:
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Sequence 15051, Application US/09949016

Sequence 15051, Application US/09949016

Patent No. 6812339

HINTER NO. 6812339

TITLE OF INVENTION:

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TITLE OF INVENTION:

TITLE OF INVENTION:

PRIOR RAPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

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PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-08

NUMBER OF SEQ ID NOS: 2077012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12-07
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Conservative:
Mismatches:
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OTHER INFORMATION: Xaa= * or Gly or Arg
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Best Local Similarity:
     ; Uther 13-999C-3784
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ORGANISM: Human
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APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
PRIER REPERBNCE: 59.032.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ. ID NOS: 36681
SOFTWARE PATENT.
                                                    US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-14995 (1-42075)
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Indels:
Gaps:
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OTHER INFORMATION: BEQ VFGSFLLLLFSLT/QF
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LOCATION: 96..239
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LOCATION: 96..437
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NAME/KEY: UNSURE
LOCATION: 41
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Sequence 40169, Application US/09949016
Patent No. 6812339
Facent No. 6812339
Facent No. 6812339
FACENTAL INFORMATION:
TERRITOR INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
FILE REPERENCE: 2000-04-14
FRIOR PELICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/237,768
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-09
FRIOR FILING DATE: 2000-10-09
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                                                           91175 GTGCAGAAAACCGACGAAGGCCACCCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC
                                                                                                                                                             21 SerLeuPheleuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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Gaps:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40169
LENGTH: 601
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Fatent No. 6812339

GENERAL INFORMATION:
FAPLICART: VENTER, J. Craig et al.
FILE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: 06/241,755
FILE REPLICATION NUMBER: 60/241,755
FRIOR PILING DATE: 2000-10-20
FRIOR PILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-09-08
FRIOR PILING DATE: 2000-09-08
FRIOR SEQ ID NOS: 207012
SEQ ID NO 12869
FRIOR PILING DATE: 2000-09-08
FRIOR PILING DATE: 2000-09-08
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FRIOR PILING DATE: 2000-09-08
122296 GCCCTGGCCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTCTGTTTTACAAGCA 122355
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US-09-949-016-12869
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Pred. No.:
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ORGANISM: 1
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                                         21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 61 IleGlnLysSerAspGluGlyHisProPheArg-----
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166 ATTGCTTTGTTGAGTTTTCATATGTAT----
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REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
APLILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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Patent No. 5858708
GENERAL INFORMATION:
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US-08-700-607-9
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## TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
## TILE OF INVENTION WIMBER: US/09/949,016
## CURRENT APPLICATION NUMBER: US/09/949,016
## CURRENT FILING DATE: 2000-04-14
## PRIOR APPLICATION NUMBER: 60/241,755
## PRIOR APPLICATION NUMBER: 60/241,755
## PRIOR APPLICATION NUMBER: 60/241,498
## PRIOR APPLICATION NUMBER: 60/231,498
## PRIOR PELING DATE: 2000-09-08
## NUMBER OF SEQ ID NOS: 207012
## SEQ ID NO 111335
## LENGTH: 601
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Matches:
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Patent No. 6812339
GENERAL INFORMATION:
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Sequence 13161, Application US/09949016
; Betent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT PAPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PLILNG DATE: 2000-10-03
; PRIOR PLILNG DATE: 2000-10-03
; PRIOR PRILNG DATE: 2000-0-10-03
; RIOR PLILNG DATE: 2000-0-10-03
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US-09-949-016-13161
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTUON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTUON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES.
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 14730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 CAGAAATCAGATGAAGGNCACCCATTCAGGGCATATCTGGANTCTGAAGTTGCTATATCT 181
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; Sequence 14730, Application US/09949016
; Patent No. 6812339
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271.00
87.32$
70.42$
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276.00
89.71%
86.76%
TELEFAX: 415-845-4166
INFORMATION FOR ESO ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: SPLNFET01
CLONE: 28742
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Best Local Similarity:
Query Match:
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US-09-949-016-14730
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Pred. No.:
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RESULT 27

US-09-949-016-40170/c

Sequence 40170, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-04-14

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARD: PSEC OF Windows Version 4.0

LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 CAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTAAGGCTAAAATC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTvrGluArgHisGlnVal
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Matches:
Conservative:
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243.00
98.08%
92.31%
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 11198
LENGTH: 200
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64.44%
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CORGANISM: Homo sapiens
US-09-513-999C-11198
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US-09-949-016-40170
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                         9697 GACCCCGACTCATCTTGATCATTTTTCATCCCGATCCCCTAACCTACCCTTCAATCCTAA 9756
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Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION VMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLys-----
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Sequence 117609, Application US/09949016

Sequence 117609, Application US/09949016

Betent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPREMENCE: CLOOD1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRAEESE for Windows Version 4.0

LENGTH: 601

LENGTH: 601
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                                                                                                                                                                                                                                                                              TCAACCACTGATTTTTGACTTGGAAGAACCCAATCAAAACTGGTAAAGTTTTTGGTTCC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 GCTTACATTGGTTTA---TTGATCTCTGCTGCTGAA-----TATTCCGGT--- 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------AAATTGATTACTGGTAAAGGGTTCCTTGCTAATTTCAAACCA--- 393
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------ACTGGTAAATTGTACGCTAAAAGATTCAATGATGAAGTATTGCCAGAATTG 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 GluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAsp 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 IleGlnAlaIleGlnLygSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu 77
                                                                                                                                                                                                                              SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrdlyValValPheGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                      38 AlaTyrileAlaLeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 ValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer------AlaLeu
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    Alignment Scores:
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Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPBUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-13
PRIOR PEPLICATION NUMBER: US 60/074,725
PRIOR PEPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR PEPLICATION NUMBER: US 60/096,409
PRIOR PEPLICATION NUMBER: US 60/096,409
PRIOR PEPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
NUMBER PO SEQ ID NOS: 28208
SEQ ID NO 1905
LENGTH: 1125
                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERBENCE: CL001307
CURRENT APPLICATION NUMBER: 05/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PLILNG DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 119336
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  x US-09-949-016-119336 (1-601)
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Mismatches:
Indels:
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Matches:
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                                                                                                                                 Sequence 119336, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-830-972-2_COPY_975_1163 (1-189)
111 AspleuValAspSer 115
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; ORGANISM: Candida albicans
US-09-248-796A-1905
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Best Local Similarity:
                                                                                                             -09-949-016-119336/c
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US-09-248-796A-1905
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Pred. No.:
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DB:
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RESULT 32

US-09-949-016-48087/C

j Sequence 48087, Application US/09949016

j Patent No. 6812339

j GENERAL INFORMATION:

j TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

j TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

j TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

j TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

j FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

j FILE OF ILLING DATE: 2000-04-14

j PRIOR APPLICATION NUMBER: 60/231,768

j PRIOR FILING DATE: 2000-10-03

j PRIOR FILING DATE: 2000-00-08

j PRIOR FILING DATE: 2000-00-08

j PRIOR FILING DATE: 2000-00-08

j PRIOR FILING DATE: 2000-00-08

j PRIOR APPLICATION NUMBER: 60/231,498

j PRIOR APPLICATION NUMBER: 60/231,498

j RIOR FILING DATE: 2000-00-08

j PRIOR APPLICATION NUMBER: 60/231,498

j RIOR APPLICATION NUMBER: 60/231,498

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j RIOR APPLICATION NUMBER: 60/231,498

j RIOR APPLICATION NUMBER: 60/231,498

j RIOR APPLICATION NUMBER: 60/231,4
                                                                                                                 124 ValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIle 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20 :::||| |||||||||||||| :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
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                                                  US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-48087 (1-601)
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APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5. ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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102.00
70.00%
52.50%
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Best Local Similarity:
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; ORGANISM: Human
US-09-949-016-48087
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US-08-905-223-178
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Pred. No.:
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US-09-313-294A-703
i Sequence 703, Application US/09313294A
i Sequence 703, Application US/09313294A
i Patent No. 6476212
i GENERAL INFORMATION:
i APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Braman, Bradley K.
ITILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
ITILE REPERBENCE: DL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 703
LENGTH: 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 CTAACTGCTGACTTCAGAATAGAGCACTCACTCTATTACATGGGATTTACGGATGTATTA 386
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                                                                                                                                                                                                                                                                                                             141 AlaLeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnVal---
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ORGANISM: Zea mays
FEATURE:
NAMB/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700549677H1
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Matches:
Conservative:
Mismatches:
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Matches:
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Mismatches:
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Best Local Similarity:
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; ORGANISM: Human
US-09-949-016-117609
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PRATURE:

NAME/KEY: other

LOCATION: 88.189

IDENTIFICATION METHOD: blastn

OTHER INFORMATION: region 1..102

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OTHER INFORMATION: region 14..343

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OTHER INFORMA
                                                OTHER INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ISTABLED.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECHANICATION INFORMATION:
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NAME/KEY: other
LOCATION: 73.317
IDENTIFICATION HERDED: blastn
OTHER INFORMATION: dest tegion 1..245
OTHER INFORMATION: est tegion 1..245
OTHER INFORMATION: est tegion 1..245
OTHER INFORMATION: est tegion 243.305
OTHER INFORMATION: dentity 98
OTHER INFORMATION: id HUMSOGF10B
OTHER INFORMATION: id HUMSOGF10B
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OTHER INFORMATION: id HUMSOGF10B
OTHER INFORMATION: est tegion 243..305
OTHER INFORMATION: id HUMSOGF10B
OTHER INFORMATION: est tegion 243..305
OTHER INFORMATION: est tegion 1..131
OTHER INFORMATION: identity 99
OTHER INFORMATION: identity 95
OTHER INFORMATION: est tegion 254..341
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                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOCTAME: Patentin Release #1.0, Version #1.25
SUGTAMEN: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/1247
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY AGENT INFORMATION:
FILING DATE: 03-APR-1990
ATTORNEY AGENT INFORMATION:
FILING DATE: 03-APR-1990
ATTORNEY AGENT INFORMATION:
FILING DATE: 03-APR-1990
ATTORNEY AGENT INFORMATION:
FREERENCE DOCKET NUMBER: 6362-9951
TELEFONNENTION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LIBNGTH: 1828 base pairs
WANDE: MARCE: G19-238-0062
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LIBNGTH: 1828 base pairs
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COCATION: 155..1561
COCATION: 155..1561
CHER INFORMATION: /product= "ALPHA-5 SUBUNIT"
19.08-487-596-7
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Matches:
Conservative:
Mismatches:
Indels:
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
San Diego
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Best Local Similarity:
Query Match:
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                            STATE: C. COUNTRY:
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APPLICANT: Elliot, Steven B.
APPLICANT: Elliot, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NETRONAL
TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
CARRESPONDENCE BLOWN, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 35
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Mismatches:
Indels:
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Matches:
                                                             DENTIFICATION METHOD: blastn
OTHER INPORMATION: identity 96
OTHER INPORMATION: identity 96
OTHER INPORMATION: identity 96
OTHER INPORMATION: id HSC16E081
FEATURE:
NAME/KEY: other
LOCATION: 85..186
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: id AA157365
OTHER INFORMATION: identity 99
OTHER INFORMATION: identity 90
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10.81%
                                              LOCATION: 397..426
IDENTIFICATION METHOD:
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-08-487-596-7
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Sequence 5725, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
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1376 ATGAAGGAAATGATGTCCGTGAGGTTGTTGAAGATTGGAATTCATAGCCCAGGTTCTT 1435
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1472 ---ATTGTTGGATCTCTTGGGCTTTTT---GTTCCTGTTATTTATAAATGGGCAAATAA 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 LeulleLeuAlaLeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnVal 157
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                                                                                                                                                                                                                                                                         1828
41
33
61
56
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Matches:
Conservative:
Mismatches:
Indels:
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NAME/KEY: Coding Sequence
LOCATION: 155...1561
OTHER INFORMATION: alpha5 s
OTHER INFORMATION: nicctini
NAME/KEY: 5.UTR
LOCATION: 1...154
OTHER INFORMATION:
NAME/KEY: 3.UTR
LOCATION: 1562...1828
OTHER INFORMATION:
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38.74%
21.47%
10.27%
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Best Local Similarity:
Query Match:
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                            1376 ATGAAGGAAAATGATGTCCGTGAGGTTGTTGAAGATTGGAAATTCATAGCCCAGGTTCTT 1435
                                                                                                                                                                                                                                                                                                                                                                             1472 ---ATTGTTGGATCTCTTGGGCTTTTT---GTTCCTGTTATTATAAATGGGCAAATATA 1525
                                                                                                                       1316 TCTTCTAGAAACACATTGGAAGCTGCGCTCAATTCTATTCGCTACATTACAAGACACATC 1375
                                                                                  TyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPhe 107
                                                                                                                                                                                                                                                   119 ---AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu 137
                                                                                                                                                                                                                                                                                                                                    LeulleLeuAlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnVal 157
      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08660451A
Patent No. 6524789
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME.
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                   108 Leu------ValAspAspLeuValAspSerLeuLysPhe---
  72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGln-
                                                                                                                                                                                                                                                                             1436 GATCGGATGTTTCTGTGGACTTTTCTTTTCGTTTCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1526 TTAATACCAGTTCATATTGGAAATGCAAATAAG 1558
                                                                                                                                                                                                                                                                                                                                                                                                                      158 GlnileAspHisTyrLeuGlyLeuAlaAsnLys 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Brown, Martin, Haller & McClain CITY: San Diego
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OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/484,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/46
FILING DATE: 06/07/95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
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SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 619-238-0062
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US-08-660-451A-7
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Percent Similarity:
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No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         905 TCTTCTAGAAACACATTGGAAGCTGCGCTCGATTCTATTCGCTACATTACAAGACACATC 964
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565 AAAGTCATACCTCTAATTGGAGAGTATCTGGTATTTACCATGATTTTGTGACACTGTCA 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 785 ATGGCGCCTTTGGTCCGCAAGATATTTCTTCACACGCTTCCCAAACTGCTTTGCATGAGA 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 TyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPhe 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------SerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSer
                                                                                                                                                                                                                                                                                                                                                                                              US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-5725 (1-1273)
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41
32
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
CURRENT FILING DATE: 2000-04-14

PRIOR PLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0

SOFTWARE: 1273
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                                                                                                                                                                                                                                                                                           94.00
38.22%
21.47%
10.16%
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Query Match:
DB:
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US-08-956-171E-407/c
                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                           US-09-949-016-5725
                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                         TYPE: DNA
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APPLICANT: Charles Kunsch Gil H. Choi Patrick S. Dillon

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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ArgileTyrLysGlyValileGlnAlaileGlnLysSerAspGluGlyHisProPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         947 GCTGTTATTATTGGATTGAAATTTCAATTAAACCTGCCGATCGAAATCATCCTTAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 AlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1-1722)
                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDGS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle-
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                               ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 407:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 407: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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94.00
48.87%
27.07%
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Query Match:
DB:
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Sequence 149. Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
PAPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRIE: Maryland
COUNTRY: USA
    890 GGCCATTTGAAGTCTGAAAATATTTCTTCA-----TTATTGGTGTCATTTGTCATTATG 837
                                          92 AlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
                                                                               836 TTTGTAGGT---ATCCAAGTAGTTATTCAAAATGCACCTCGTTTGTTCAAAGAAGATGAC 780
                                                                                                                    LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
                                                                                                                                          --GCAATAACAATTATCGTCAGCTTA 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
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                                                                                                                                                                                                                    743 ATCAGTGGTCTTGTAATGTTGATTGTATTTGCAGTCAAT 705
                                                                                                                                                                                               132 PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSer 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
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Matches:
Conservative:
Mismatches:
Indels:
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ATTONERY/AGENT INFORMATION:
NAME: BTOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REPRENCE/OCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELECHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
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779 GTTGTACCTAAC-----
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92.50
46.99%
24.70%
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                   US-08-961-527-149
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                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              947 GCTGTTATTATTGGATTGAAAATTTCAATTAAACCTGCCGATCGAAATCATCTTAT--- 891
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                                                         132 PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSer 144
                                                                               ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 407:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/781,986A FILING DATE:
                                                                                                                                  RESULT 38
US-08-781-986A-407/C
; Sequence 407, Application US/08781986A
; Patent No. 6737248
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779 GTTGTACCTAAC----
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27.07%
10.16%
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Best Local Similarity:
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US-08-781-986A-407
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Sequence 4281, Application US/09949016

Sequence 4281, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOOL307

CURRENT PPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFFMARE: FastSEQ for Windows Version 4.0
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-----ATCAAAGCTGTGGGGG 1941
                                                                                                                                                                                                                                                                                2110 ATTCTGGTGCAGGCCTACCAGAGAGATGAACGTCTTCAAGGGAAACCCTGGATCAGCAG 2169
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                                                                                                                                                                                                           86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArg 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 LeuPheLeuValAspAsp-----106 LeuPheLeuValAspSerLeu 116
                                                                                                                                                                                    -----SerLeuPhe 146
                                                   ---LeuValAspSerLeu 116
                                                                                                                                                                                                                                                       147 SerileProValileTyrGluArgHisGln------ValGlnIleAspHisTyr 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 ServalThrileSerPheArgileTyrLysGlyValileGlnAlaileGlnLysSerAsp 65
                                                                                                                                          117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaileSerGluGluLeuVal
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Matches:
Conservative:
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Indels:
LeuPheLeuValAspAsp-----
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Best Local Similarity:
Query Match:
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US-09-949-016-4281
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LENGTH: 4661
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                                                                                      SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                                                                                                                                                                                                             S72 ATTCTCTGG------TATCAAGGTGCCTTGTTTATGGCAACGGTGCAACTGGTCATC 622
                                                                                                                                                                                                                                                                                                                                                            161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                  ----GAGAGCTTGTTTGGAGTT 496
                                                                                                                                                        101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
                                                                                                                                                                                                                         121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                                                                                                                                                                                                                           141 AlaLeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAsp 160
                                                                                                                                                                                                                                                                                                                           623 ATTGCTCTTCTACTTTATGGATTGACCTTGGCAGGGATTTCTACCTTACTAAGTGTCGTC 682
                   61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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                                                                                                                        ------CTCAGACCAGTGTTA
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TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease CURRENT PRENTER. 4239-5399.

CURRENT APPLICATION NUMBER: US/09/462,136

CURRENT FILING DATE: 2000-06-01

PRIOR PILING DATE: 1998-07-02

PRIOR PILING DATE: 1998-07-02

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 13
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Matches:
Conservative:
Mismatches:
Indels:
                                                   158 GGGATTCGCTTAATAGCTGGT----
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Patent No. 6426198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 748
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                                                                                                          497 GCT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 CTCCCT---CTCAAACGT
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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; LOCATION: (1).
US-09-462-136-1
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR PILE REFERENCE: PL-0017 US
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Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 ValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSer 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 LeulysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeu 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ATCAACAGGGCTTTGCTACCTTGAGGGAGATTGGACATGGACACGATCTAAAGAAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 ATCTTCGATGAGAAGTGCCTATCGAAGATTCCAAAGGGCCTCAAGGATAAG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-972-2_COPY_975_1163 (1-189) x US-09-313-294A-81 (1-296)
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OTHER INFORMATION: Incyte ID No. 6476212 700548479H1
NAME/KEY: unsure
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                                                                 LeuGlyLeuAlaAsnLysSerValLysAspAlaMet 174
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Conservative:
Mismatches:
Indels:
147 SerIleProValIleTyrGluArgHisGln---
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/313,294A CURRENT FILING DATE: 1999-05-14 NUMBER OF SEQ ID NOS: 7600 SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other
                                                                                                                                                           ; Sequence 81, Application US/09313294A; Patent No. 6476212; GENERAL INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
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Best Local Similarit
Query Match:
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                                                                                                                                RESULT 43
US-09-313-294A-81
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TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT APPLICATION NUMBER: 60/214,870
PRIOR APPLICATION NUMBER: 60/214,870
                                                                                                  2231 ATTCTGGTGCAGGCCTACCAGAGAGATGAACGTCTTCAAGGGGAAACCCTGGATCAGCAG 2290
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                                                                             ----SerLeuPhe 146
                                                                                                                                               ---ValGlnIleAspHisTyr 162
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            117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr
                                                ----CCCTTGACC
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                                             2291 CTGGGCAGGGTCCTAGGAGAAGTGGCTCCCCAGTATG 2326
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Matches:
Conservative:
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                                                                                                                                            147 SerIleProValIleTyrGluArgHisGln----
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                                                                             LeuLeulleLeuAlaLeuIle-----
                                                                                                                                                                                                                                                                                                       Sequence 100, Application US/09814915A Patent No. 6750015 GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 100
LENGTH: 4673
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Horwitz, Kathryn APPLICANT: Richer, Jennifer
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Query Match:
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Pred. No.:
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Patent No. 6593114
GENERAL INFORMAT
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280 GGCGTCATGAAAGGCGCTGCTGAAATGAAACAAGGCTTAAAAATAACATCTTTTCCAATT 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------Ala 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 IleSerGluGluLeuValGlnLygTyrSerAsnSerAlaLeuGly------His 95
                                                                                                                                                                                                                                                                                                                                                                        7 TyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeu
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460 TTACGTCAAGAATTAGAAGTGAAAAATGAACAAAGTTCCAATTTCCTATTATGATATTCAT
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                                                                                                                                                                                                                     1779
49
41
61
83
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Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
LENGTH: 1779
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133 TTCTGGAAACAGTGAAACGT---
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                                                                                                                                 TYPE: DNA
, ORGANISM: Enterococcus faecalis
US-09-134-000C-2072
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86.50
38:46%
20.94%
9.35%
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Best Local Similarity:
Query Match:
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5-08-956-171E-322 Sequence 322, Application US/08956171E

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APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
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||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: || ::: || ::: ||| ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORPUTER: NEARANDE FORM;

COMPUTER: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

OPERATING SYSTEM: MSDOS version 6.2

OPERATING SYSTEM: MSDOS version 6.2

OPTIANE ASCIT Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: January 5, 1996

APPLICATION NUMBER: 09/09,861

FILING DATE: January 5, 1997

ATTORNEY/AGENT INFORMATION:

NAME: MATA J. Hyman

NAME: MATA J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMUNICATION NUMBER: PB248P1

TELECOMUNICATION NUMBER: 96,789
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
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SEQUENCE DESCRIPTION: SEQ ID NO: 322:
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TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1302 base pairs
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SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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INFORMATION:
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Best Local Similarity:
Query Match:
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                                 -----ATTATCAGTGCG 319
                                                             100 IleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAla 119
                                                                                 320 ACAACTGAAGTATTTAAACCAATAATGTCATCGACACTAGTTACTATTATCGTCTTCTTA 379
                                                                                                                                                                                                                                                          ---TyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 322, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr 99
                                                                                                                                               |||::::::|||
380 CCACTTGTGTTTGTATCAGGTTCAGTAGGCGAAATGTTTAGACCTTTTGCATTGGCTATT
                                                                                                                                                                                          134 GlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle-----
                                                                                                                                                                                                                440 GCATTTAGTTTAGTTTAGTGTCATTAGTGTCAATTACACTCGTTCCAGCGTTGGCAGCT
                                                                                                                                                                                                                                                                                        500 ACACTATTTAAAAAAGGCGTTAAACGTCGTAATAAACAACATCAAGAAGGATTAGGTGTT
                                                                                                                         120 ValleuMetTrpValPheThrTyrValGlyAlaLeuPheAsn----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                 560 GTTAGTACAACTTATAAAAAGTATTA 586
                                                                                                                                                                                                                                                                                                                        166 AlaAsnLysSerValLysABpAlaMet 174
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                               290 CTAAAAGGTGAAAATTTA-----
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REGISTRATION NUMBER: 30,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 322:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
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41.80%
22.22%
9.30%
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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TOPOLOGY:
US-08-781-986A-322
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Streptococcus pneumoniae Polynucleotides and Sequences 391
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128 CCGTTATCACTTCTTATGGCCGCTTATTGCTCTGAAATTGAGTGATGTTTCATTGAATATA 187
                                                                                                                                                                                                                                                                                                                                              245 GTTGTTGAA------ATATTTATCGACGCTTAACAGATTCAGAAGAACAA 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------TyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500 ACACTATTTAAAAAGGGGTTAAACGTCGTAATAAACAACATCAAGAAGGATTAGGTGTT 559
                                                                                                                                                                                                                                                                                     --- AlaLeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValileGln 59
                                                                                                                                                                                                                                                                                                                                                                                                    60 AlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr 99
                                                   2 ValvalAspieuLeuTyrTrpArgAspileLysLysThrGlyVal---ValPheGlyAla
                                                                                                                                                                  21 SerieuPheleuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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US-09-830-972-2_COPY_975_1163 (1-189) x US-08-781-986A-322 (1-1302)
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: MSDOS version 6.2
SOFTWARE: ASCII Text
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Patent No. 6420135
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pr
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
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APPLICATION NUMBER: US/08/961,527
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REGISTRATION NUMBER: 36,373
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Sequence 1, Application US/08916421B
Parent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
ITILE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco.
Parent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------TCAATTGTATCTATACCAATGTCAATATTA 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HisValAsnSerThrileLysGluLeuArgArgLeuPhe-----LeuValAspAsp 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 PheSerIleProValIle-----TyrGluArgHisGlnValGlnIleAspHisTyr 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GluValAlaIleSerGluGluLeuValGlnLysTyrSer----AsnSerAlaLeuGly 94
                                                                                                                                                                                                                                                                                                                                                                                                     ValvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 ThralaTyrileAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly
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43
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62
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Mismatches:
Indels:
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Matches:
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO SEG ID NOS: 5674
LENGTH: 3156
                                                                                                                                     ; TYPE: DNA; CRANISM: Staphylococcus epidermidis US-09-134-001C-2168
                                                                                                                                                                                                                                                                                                                                                                   US-09-830-972-2_COPY_975_1163 (1-189)
                                                                                                                                                                                                                                0.459
85.50
42.05%
22.05%
9.24%
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Best Local Similarity:
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Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPERMIDES FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 -----LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGl 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSe 76
                                                                                                                                                                                                                                                                                                                                                                                                                           11 ilelyslysThrGlyValValPhe------GlyAlaSerLeuPheleuLeu
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53
34
65
33
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Mismatches:
Indels:
                                                                                                                                                                                                                                                      Length:
Matches:
 REFERENCE/DOCKET NUMBER: PB34
TELECOMONICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 6735 base pairs
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3398 TACAACGATTAAA 3410
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                                                                                                                                                                                                                                                  1.33
86.00
47.03%
28.65%
9.30%
                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-134-001C-2168
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PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22.
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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LOCATION: (103998)...(103998)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (163385)...(163385)
OTHER: INFORMATION: n equals a, t, c,
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                                                                                                                                     TYPE: DNA
ORGANISM: Methanococcus jannaschii
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OTHER INFORMATION: n equals a, t,
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t,
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LOCATION: (234220)...(234220)
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t,
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THER INFORMATION: n equals a, t, AME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a, t
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TYPE: DNA
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OCATION: (1349473)...(1349473)
THER INFORMATION: n equals a, t, c, or g ö c, or ö or or ö ö c, or ö ö ö AME/KET: misc feature LOCATION: (1084830) ...(1084830) THER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a, t, AME/KEY: misc feature LOCATION: (1119881)..(1119881) THER INFORMATION: n equals a, t, NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (741684). (741684) NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
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TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanocoe
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NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeu 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LysLysThrGlyValValPhe 18
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Conservative:
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Sequence 1, Application US/09692570

Patent No. 6797466

GENERAL INFORMATION:

APPLICANT: Bult et al.
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                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1603734). (1603734)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1637998). (1637998)
OTHER INFORMATION: n equals a, t,
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                  NAME/KEY: misc feature
LOCATION: (1470091) ..(1470091)
OTHER INFORMATION: n equals a,
                                                               NAME/KEY: misc feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a,
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LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a,
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Best Local Similarity:
Query Match:
DB:
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PATENT NO. 6797466
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275C1
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 2003-01-14
PRIOR FILING DATE: 1996-08-22
PRIOR FILING DATE: 1996-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
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LOCATION: (28257)..(28258)
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LOCATION: (84812)..(84812)
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LOCATION: (98239)..(98239)
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals
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INFORMATION: n equals
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals
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LOCATION: (84808)..(84808)
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LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals
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LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t,
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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COCATION: (1130881)..(1130881)
THER INFORMATION: n equals a,
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a,
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a,
                                                  NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals
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LOCATION: (871519)..(871619)
OTHER INFORMATION: n equals
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals
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RESULT 52
US-09-328-352-740
Sequence 740, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF TILLE TERETRENCE: GTC99-03PA
CURRENT APPLICATION UNMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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334 ACGCAACAACAAGTGTCTGGGGGATTTTACTGATCATCGCCATTGCCATTGCGAGAGAA
                                                                                           GlyHisValAsnSerThrIleLysGluLeuArg
                                                                                                                               105 ArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpVal
                                                                                                                                                                                          PheThrTyrValGlyAlaLeu-PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 SerGluGlu-----LeuvalGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSer
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Mismatches:
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Matches:
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US-09-328-352-740
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             88 TyrSerAsnSerAlaLeu---
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR PLING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
                           772112
                                                                                                                                   -----GTTAAAAGTAATATAAAGGAAGTT 772208
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                                                                                                                  LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeu 103
                                                                                                                                                                                                                                       119 AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 138
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                           772053 GCATTGTTCATTCCATCTATTTTATATGAAAATAAAATÄGAAACTCTTGAGAATAACATT
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Ile------BlnAlaIleGlnLysSerAspGluGlyHis
                                                         -----LeuGluSerGluValAlaIleSerGluGlu
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ATGGAAATCATTGCCTGCTATTAATTGTTCAGATGATCTATTGGATGAACAAAGGT
                                                                            ---ArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPhe
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772314 ATGTTAGCAAGAATTATGATT 772334
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Best Local Similarity:
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US-09-543-681A-2003
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Pred. No.:
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107 PheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr 126
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APPLICANT: Krüger, Hartwig
APPLICANT: Sch"der, Hartwig
APPLICANT: Sch"der, Hartwig
APPLICANT: Sch"der, Hartwig
APPLICANT: Sch"der, Gekar
APPLICANT: Sch"der, Gekar
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT APPLICATION NUMBER: DE 19931454.3
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-09
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PLICATION NUMBER: DE 19932128.0
LING DATE: 1999-07-09
PLICATION NUMBER: DE 19932180.9
LING DATE: 1999-07-09
PLICATION NUMBER: DE 19932180.5
LING DATE: 1999-07-09
PLICATION NUMBER: DE 19932182.5
LING DATE: 1999-07-09
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R FILING DATE: 1999-07-09
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APPLICATION NUMBER: DE 19933005.0
FILING DATE: 1999-07-14
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FILING DATE: 1999-07-14
APPLICATION NUMBER: DE 19940764.9
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FILING DATE: 1999-07-09
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FILING DATE: 1999-08-27
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1158 CAAATTGGT 1166
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US-09-602-787A-301
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275 CGTGAATTGGTGGGGTGCTGCTGGAAATACGGCCTCGTTGGGCGTGACTGTC 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlaLeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 TrpArgAspIleLysLys------ThrGlyVal-----ValPheGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-830-972-2_COPY_975_1163 (1-189) x US-09-602-787A-301 (1-1500)
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Matches:
Conservative:
Mismatches:
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PLING DATE: 1999-08-27
PRIOR PLING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR PRILING DATE: 1999-08-31
PRIOR PRILING DATE: 1999-08-31
PRIOR PLING DATE: 1999-09-03
PRIOR PLING DATE: 1999-09-03
PRIOR PLING DATE: 1999-09-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (101)...(1477)
; OTHER INFORMATION: RXN00456
US-09-602-787A-301
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40.38%
26.28%
9.03%
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Best Local Similarity:
Query Match:
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403 TCTGCCTACATGAACGCCCTCTACATCAGT-----GTAATTAAGGACGACCTGCAT 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSer
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                                                                                                GENOME THERAPEUTICS CORPORATION
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                  SOFTWARE: <URRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...1275
SEQUENCE DESCRIPTION: SEQ ID NO: 2599:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                     THERAPEUTICS
                                                                                                                100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1275 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2599:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                            STATE: Massachusetts
                                                          SEQUENCES: 5206
                                                      NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME
                                                                                                                                                                                                                     COMPUTER READABLE FORM
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47.40%
24.68%
8.92%
                                                                                                                    STREET: 100 Be
CITY: Waltham
                                                                                                                                                                             COUNTRY: USA
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Best Local Similarity:
Query Match:
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                                           Sequence 1302, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATH00-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT APPLICATION NUMBER: US 09/107,433

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 1302
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415 GATGCCATGGGGATTCAGGCAGTCTCTGATGAGGGTTGTCCGT--------456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AspLeuValAspSerieuLysPheAlaValLeuMetTrpValPheThr---TyrValGly 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ilelystysThrGlyValValPheGlyAlaSerteuPheLeuLeuLeuSerLeuThrVal 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x US-09-583-110-1302 (1-1233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   571 CATACCTTGTATGAGGTTGAAAAAGAATTGAAATGTCACAT 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 ProValIleTyrGlu---ArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn A Doucette-Stamm and David Bush
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6800744
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-830-972-2_COPY_975_1163 (1-189)
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82.50
47.40%
24.68%
8.92%
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
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Sequence 938, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT PAPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NOS: 3840
                                                                                                                                                                                                                                                                                                                                                                                                   9738 TITICATIAGITICAGICATIATGATIGICATCATCAACCICATCTCTGACACCCTIGAGC 9797
                                                                                                                                                                                                                                                                                                                          9900 ---ATTGTCGCCAATCTGGCTGGCTGGCTATTCTTATCAATGTTATAAGTATTCAAACTATT 9956
                                                                                                                                                                                                                         91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
                                                                                                                                                                                                                                                                                                    111 AspleuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr --- TyrValGly 129
                                                                                                                                                                                                                                                                                                                                                                               130 AlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIle--- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 TTACGCTGGATTTTTCATCAGCAAATGCTGGGCCAGTCGATGCAATTTTATCAAGATGAA 414
                                                                                                                                                  71 ArgalaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
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                                                                                                                                                                        9804 TCTGCCTACATGAAGGCCCTCTACATCAGT-----GTAATTAAGGACGACCTGCAT
                                                                         51 PheArglleTyrLysGlyVallleGlnAlaIleGlnLysSerAspGluGlyHisProPhe
PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 AlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 IleValSerValThrAlaTyrIleAlaLeuAlaLeuLeu---SerValThrIleSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 ArglleTyrLysGlyVallleGlnAlalleGlnLysSerAspGluGlyHisProPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TTCTCTGGCCGTGTGTCAGCC----AAGGTGATGCAAACCGCTTTAGCGGTGCGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-972-2_COPY_975_1163 (1-189) x US-09-540-236-938 (1-1845)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10014 CATACCTTGTATGAGGTTGAAAAAAAATTGAAATTGAAATGTCACAT 10055
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Matches:
Conservative:
Mismatches:
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22.01%
8.86%
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; ORGANISM: M.catarrhalis
US-09-540-236-938
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9678 ATTGCCAAAATCCAAAATCCTGCTCTACGCTATTTTGACAGTATTTCTCGTCTTGTCGCCC 9737
                                                                                                                                                                                     SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
                                                                                        111 AspleuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr---TyrValGly 129
                                                                                                                          499 ---ATIGICGCCAATCIGGCGCGCATTCCTTATCAATGTTATAAGTATTCAAACTATT 555
                                                                                                                                                                  130 AlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIle--- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 IleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrVal 30
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                                                                                                                                                                                                                                         149 ProValIleTyrGlu---ArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                                                                                                                 11887
38
35
50
31
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                        Sequence 146, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
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REGISTRATION UNMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34:
TELECOMMUNICATION INFORMATION:
TELEPAK: (301) 309-8504
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 11887 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
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82.50
47.40%
24.68%
8.92%
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity:
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112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrVal----- 128

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110880 CCCTTGTGTTTATCCCCAGTTCTTTGCACAACTTGTGGCACGCAGATTAATCATAGAAA 110939
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                                                                                                                                                                                                                                                                                                              POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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110664 GTCATGTGGTCCTGCTAACTGCATTAATTTGTCTGTATTTCATTCCGCATCTACAAAATG 110723
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                                       IleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGln 158
                                                                                                                                              159 IleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIle 177
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                                                                          144906 GCGGTTTCGGCTTTATTGGTATTTGCCACGCCTTCAGCGTACCAGTCGGATACAG
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Mismatches:
Indels:
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Patent No. 681239
GENERAL INFORMATION:
JAPPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GI
TITLE OF INVENTION: WITH HUMAN DISEASE, METI
TITLE RAPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELLOR DATE: 2000-04-14
PRIOR PELLOR DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-06
PRIOR PILING DATE: 2000-06
PRIOR PILING DATE: 2000-09
PRIOR PILING DATE: 2000-09
PRIOR PILING DATE: 2000-09
PRIOR PILING DATE: 2000-09
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PRIOR PILING DATE: 2000-09
SUMUBER OF SEQ ID NOS: 207012
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Matches:
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Best Local Similarity:
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LENGTH: 462589
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  526 decirintraecredearreaceceaeracreacegecerrrerarresarrira 585
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                                                                                                                                                                               586 GCGGTTTCGGCTTTATTGGTATTTGTATTGCCACGCCTTCAGCGTACCAGTCGGATACAG 645
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APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT PELLING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60,140,121
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SOPTWARE:
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                                                                                                                                                                                                                      159 IleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIle 177
                                                                                                                                                                                                                                                           646 GCGCAT---GCTCGTGCTTTGATGACAGGTCGAATTACCGATGCTTATGCTAATATC 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte template ID No. 6632636 41
; PUBLICATION INFORMATION:
US-09-596-002-41
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Matches:
Conservative:
Mismatches:
Indels:
                                                           129 GlyAlaLeuPheAsnGlyLeu----
                                                                                                                                                                                                                                                                                                                     US-09-596-002-41; Sequence 41, Application US/09596002; Patent No. 6612636
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ORGANISM: Moraxella catarrhalis
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Best Local Similarity:
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SEQ ID NO 41
LENGTH: 26923
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GENERAL INFORMATION:

APPLICANT: Keith Meinstock et al

APPLICANT: Keith Meinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA:

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/094,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NOS: 28208
                                                                                                                                                     124396 TTATTGAATAAATTAATGGTCCCATTTTTTTCCTAGCTCCACTGTGGAAGTCTCAGAT 124455
                                                                                                                  -----ThrLeuLeulleLeuAlaLeulleSerLeuPheSerIlePro 149
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                                                                          124456 TCCCAAGGATGTGTGTGTGCAGATAGGTTCCATGTGGCCCAGGGCTCTTGTTCAGTTTA
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Mismatches:
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196 TTAATCAAA-----
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Best Local Similarity:
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REPERBENCE: CL001307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR PELLING DATE: 2000-04-14
PRIOR PILLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-09-08
NUMBER: 60/231,498
PRIOR PILLING DATE: 2000-09-08
NUMBER: 05 207012
SEQ ID NO 12412
LEMETH: 476044
                                                                                                      111000 TCCCAAGGATGTGGTTGTGCAGATAGGTTCCATGTGGCCAGGGCTCTTGTTCAGTTTA 111059
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                                                                          ---ThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIlePro
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Query Match:
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; ORGANISM: Human
US-09-949-016-12412
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161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMet-
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: ZHENG, Jing
TITLE OF INVENTION: A MAMMALIAN PRESTIN
FILE REFERENCE: 0290-3701
CURRENT APPLICATION NUMBER: US/09/785,381
CURRENT FILING DATE: 2001-02-16
PRIOR PLLING DATE: 2000-02-18
                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09785381
Patent No. 6602992
GENERAL INFORMATION:
APPLICANT:
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                                                 -----ATTTCTGCTGAATTTGTTATC-----AATAAAGCTGTTGGTAAA 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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                                                                                                     173 AlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
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Matches:
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Mismatches:
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PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
SUMBER OF SEQ ID NOS: 7
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Patent No. 6632935
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Best Local Similarity:
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LENGTH: 640681
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1251 GTTGGATTTTCAGTGACGATCTCCCTGGCCAAAACCTTGGCAAATAAGCATGGCTACCAG 1310
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1134 CATGAGTCCTACAGTGTGGATGTCGTTGGAACACTTCCTCTGGGGCTACTTCCTCCGGCC 1193
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----- 174
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                                                                                        -AlaLysileGlnAlaLysileProGlyLeuLysArgLysAla
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2690 GGTTCTATTTTAAACATATTT 2669
                                                                              ; Sequence 2, Application US/09785381; Patent No. 6602992; GENERAL INFORMATION:
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                                               RESULT 65
US-09-785-381-2
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; Sequence 1, Application US/09762724
; Patent No. 6664053
; GENERAL INFORMATION:
    APPLICANT: KOVACS, et al.
; TITLE OF INVENTION: Identification of a region of the major surface
; TITLE OF INVENTION: 191vcpprotein (MSG) gene of human Pneumocystis carinii
FILE REPERENCE: 4239-58054
; CURRENT APPLICATION NUMBER: US/09/762,724
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US99/18750
; PRIOR PELLING DATE: 1999-08-17
; PRIOR FILING DATE: 1999-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 26
; SOSTWARE: Patentin Ver. 2.0
                     1473 TIGGICATATIAGCCACCGGATICCICITIGAGICGTIACCCCAGGCTGICCTITCCGCC 1532
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1653 GGCTTGGACTACGGACTGATTACCGCCGTGATCATTGCTCTGCTCACAGTGATTTAT--- 1709
                                                                                          1710 -----AGAACACAGAGTCCAAGCTACAAAGTCCTGGGCGCAGCTCCCTGACACGGATGTG 1763
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                                                                                                                            ---MetTrpValPheThrTyrValGlyAlaLeuPheAsn 133
                                                                                                                                                                                      GlyLeuThrLeuLeulleLeuAlaLeulleSerLeuPheSerIleProValIleTyrGlu 153
                                                                                                                                                                                                                                                    154 ArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAla 173
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                                                                                                                                              ------ValPheGlyAlaSerLeuPheLeuLeuLeuSer
                                                                                                                                                                                                                                                                                                                                                 1764 TACATTGACATAGATGCATATGAGGAGGTGAAAGAAATTCCTGGAATAAAA 1814
                                                                                                                                                                                                                                                                                                                 174 MetAlaLyslleGlnAla------LyslleProGlyLeuLys 185
104 ArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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Mismatches:
Indels:
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38.24%
8.76%
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; LOCATION: (1)..(3042)
US-09-762-724-1
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Best Local Similarity:
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US-09-762-724-1/c
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LENGTH: 3042
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1376 ---GGATCTCTTCCAGACCTTCTCCATTTCC---TGCTCCTTGTTTGTT 1429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 GlnLysTyrSer----AsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 ArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-972-2_COPY_975_1163 (1-189) x US-09-785-381-2 (1-4113)
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|1328 GTTGATGGCAATCAGGAGCTCATCGCTTTGGGGATATGCAACTCCATC-
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84
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Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: DALLOS, Peter
APPLICANT: ZHENG, Jing
APPLICANT: AMADISON, Laird
APPLICANT: MADISON, Laird
TITLE OF INVENTION: A MAMMALIAN PRESTIN
FILE REFERENCE: 0290-37U1
CURRENT APPLICATION NUMBER: US/09/785,381
CURRENT APPLICATION NUMBER: US 60/183,461
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 2
SEQ ID NO 2
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---ATTTCA 17992
                                                                                                                                                                              18053 TCATATAGTCAAGTACAAATAATTTGGGTGATATGTCTGGTTATATTGAAGAGGTTTTA 18112
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Thereof, and Uses Thereof
                                                            LeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArg----
                                                                                                 1993 CTTTCAATTTTAGCTACATTAATTACTTTTTTCTTTGCCTTTCTAAAGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LeuTyrTrp-----ArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe
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                                                                                                                                                                                                                       -----IleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAsp
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17942 ACAACCTCAGTATTAATATTTTTTATTAAGCCCAGTTATTGCACTT
                                                                                                                                          -----HisGlnValGln------
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APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
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Matches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3 1/2 inch diskett
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/476,102
FILING DATE: UNN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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REFERENCE/DOCKET NUMBER: PB
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ADDRESSEE: Human Genome
STREET: 9410 Key West Av
                                                                                                                                                                                                                                                                                                                      US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-972-2_COPY_975_1163 (1-189)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 301-309-8439 INFORMATION FOR SEQ ID NO: 1:
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STRANDEDNESS: double
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8.76$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rockville
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
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                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08545528D
Patent No. 653773
GENERAL INFORMATION:
APPLICANT: Fraser et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment Patent No. 6537773
FITTLE OF INVENTION: Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....TCATTAATTTACCCAACAAATTTA 17653
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                                                                              1670 GGCTTGGACTACGGACTGATTACTGCTGTGATCATTGCTCTGCTGACTGTGÄTTTÄC--- 1726
                                                                                                                                                           1727 -----AGAACCCAGAGTCCGAGCTACAAGGTCCTGGGAGCTCCCTGACACCGATGTA 1780
  1610 AGAACCAGCAAAATAGAGCTGACCATCTGGCTTACCACCTTTGTGTCTCCTCCTGTTCCTG 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                    154 ArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAla 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
                                       134 GlyLeuThrLeuLeulleLeuAlaLeulleSerLeuPheSerIleProValIleTyrGlu
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1781 TACATTGACATAGAGGAGAGGTGAAAGAAATTCCTGGAATAAAA 1831
                                                                                                                                                                                                  -----LysileProGlyLeuLys 185
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Matches:
Conservative:
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Indels:
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CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SEQ ID NOS: 1
SEQ ID NOS: 1
SEQ ID NOS: 1
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81.00
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US-08-545-528D-1
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37676 CTTATTIGGATITITACAAACGCTAGCCATCACTCAGTCGTCTTTAGTTTIGGCATTTTT 37735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38093 AAAACACAGTATTTATCAGAAAATCTTGATAACCCCGATCAAGGTATTCAACAAGATGTG 38152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                    PRICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SerGluGluLeuValGlnLys
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                         inch diskette
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                   MEDIUM TYPE: 3 1/2 inch disket:
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                          NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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  COMPUTER READABLE FORM:
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33.71
22.85
8.76
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Best Local Similarity:
Query Match:
DB:
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38213 ATGATCTTTACATTTTTGTTATGGGGATTAGCCGGTCCAATGATAGTGCTTGGTGTA 38272
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Thereof, and Uses Thereof
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                                                                               ------ArgAlaTyrLeuGluSerGluValAlaIle---
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CORRESSONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
                                                                                                                                                                                                                                              GlnLysSerAspGluGlyHisProPhe-----
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Mark D. Adams
Owen White
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Patent No. 6528289
GENERAL INFORMATION:
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  LeuLeuLeuSerLeuThr
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US-09-643-990A-1
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FOR DIAGN
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Patent No. 680074204
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NOCLEIC ACID AND AMINO ACID
THEO PERPENDICES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                      442 AGTTTTATATTAACTATATTTCCATCTATTCTTTATGGTACAGTTGATAATCATGTACTG
                                                                                                                                                                                                                                                                                                                             -----AsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProVal
                                                    -----ATTTCT
                                                                                                                                                           -----AsnSerThrIleLysGluLeu-----
               GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                    562 ITATTIGACACAAGTACTTTAATGAAGAGAGAATATTTTTCTT-----
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                              397 AGCAAGGTGTCTCAATCT---CCTTGGATAAAATATTTAGAG
                                                                                      GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: cUnknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTC-011
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REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (781)893-827
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US-09-107-433-2215
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                                                                                                                                          155 HisGlnValGlnIleAspHisTyr-LeuGlyLeuAlaAsnLysSerValLysAspAlaMe 174
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                                                                                                                                                                                                                LeuThrLeuLeulleLeuAlaLeulleSerLeuPheSerIleProValIleTyrGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
ATITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relat:
IIILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-830-972-2_COPY_975_1163 (1-189) x US-09-583-110-2219 (1-759)
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Matches:
Conservative:
Mismatches:
Indels:
97 AsnSerThrlleLysGluLeuArgArgLeuPhe--
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CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2219
                                                                   115 SerLeuLysPheAlaValLeuMetTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2219, Application US/09583110 Patent No. 6699703
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                                                                                                                                                                                                                                                                                                                                                             174 tAlaLysileGlnAlaLys 180
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80.50
38.73%
24.02%
8.70%
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Best Local Similarity:
Query Match:
DB:
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28
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PRIOR APPLICATION DATA: APPLICATION NUMBER: none
                                                                       ADDRESSEE: FUNL P.O. BOX
STREET: Washington Way
CITY: Richland
STATE: Washington
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.932
80.50
41.24%
20.34%
8.70%
                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                     FILING DATE: n/a INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
           CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Z
ADDRESSEE: Intellect:
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1797 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
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STRANDEDNESS: do
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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Best Local Similarity:
                                                            ADDRESSEE:
                                                                                                                                                     99352
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Patent No. 5925522
GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
                                                                                                                                                                                                                                                                                                                                                                                         621
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                                                                                                                                                                                                                                                                                                                          292 TITITGACTIATACCGTATIAATAAGTGTITITIATCCTAGAGITAGCAATCTITCATITA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 ATTGGGGAAGATTTTGCTACTAAATTGACTAACGAATATAAGAAAATTAGTCAGTTTAGA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 AGCAAGGTGTCTCAATCT---CCTTGGATAAAATATTTAGAG-------ATTTCT 456
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                                                                                                                                                                                                                                                                                                      SerValValAspLeu---LeuTyrTrpArgAspIleLysLysThrGlyValValPheGly 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly-------HisVal--- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 ACTCTTATCTTTTGATAAAATTTGTGCAGATACCACGATAAAATTTTTATTCATCAGA
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                                                                                                                                                                                                                                                                          US-09-830-972-2_COPY_975_1163 (1-189) x US-09-107-433-2215 (1-774)
                                                                                                                                                                  774
49
30
62
63
                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatchés:
Indels:
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                                            ORGANISM: Streptococcus pneumoniae
                                                               ) NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...774
; SEQUENCE DESCRIPTION: SEQ ID NO: 2215:
US-09-107-433-2215
                                                                                                                                                                 0.24
80.50
38.73%
24.02%
8.70%
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733 ATCAAAGAAAAG 744
HYPOTHETICAL: NO
              ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                    Alignment Scores:
                                                          FEATURE
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487 TGGAATGAGTTTCAGAAAATTAAACCCGTTTTATTAAACTCGATCTTTCAACGTATAGCC 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    567 ACTAATGAGTTAATGAACAAACAAAGAAGACAGAAGAACAGGAATATTTTATCTCA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -------GlyHisValAsnSerThrileLysGluLeuArgArg 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 TrpArgAspileLysLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGTTAATACATCAAATGAACAGTCGTATCTTÄÄCCTGAAGATÄAAGGAAATTÄAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the coding nucleotides of SEQ ID
NO:28 correspond to nucleotides 22630 through
24426 of SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-28 (1-1797)
                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
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Intellectual Property
Battelle Memorial Inst
PNNL P.O. Box 999
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Sequence 9, Application US/08853659A

Patent No. 522552

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: BATTELLE Memorial Institute
ADDRESSEE: PAUL P. O. Box 999
                                                                                                                                                      94 ----------GlyHisValAsnSerThrIleLysGluLeuArgArg 105
                                                                                                                                                                                                   106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
                                                                                                                                                                                                                                                                      57 ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                 7622 GAAGTTTTCTTATCTATTAAAATGATCCATACCTTAAATAATCAAGGTTTACTTTTTGAT
                                                                                                                                                                                                                                                                                                                                                        137 Leu-----LeuileLeuAlaLeuileSerLeuPheSerileProValile
                                                                  GluvalAlalleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: Unknown CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: nonf FILING DATE: n/a
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4
80.50
41.24%
20.34%
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APPLICATION NUMBER: US
FILING DATE: Unknown
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nucleotide
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richland
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Wa
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                                                                                                                                                                                                                 APPLICANT: Wong, K.K.; Saffer, J.D.

TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: OF A

TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||||||::: ::: ::: 907 GCCTITITITATGETAATCAAGGTGATGTTACTACTGGCGCAATTGTTTCATCTGTCATT 966
 -GlyAlaLeuPheAsnGlyLeuThr 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 TrpArgAspileLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:2
                                                                                       137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x US-08-853-659A-6 (1-8967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:6 corresponds to nucleotides 15735 through 24701 of
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette 3.50", 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
FILING DATE: UNKnown
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                     Intellectual Property Servi
Battelle Memorial Institute
PNNL P.O. Box 999
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                                                                                                                                                                  6, Application US/08853659A
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STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-830-972-2_COPY_975_1163 (1-189)
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Paul W. Zimmerman
124 ValPheThrTyrVal-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette 3.:
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
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80.50
41.24%
20.34%
8.70%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       Washington Way
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Washington
COUNTRY: U.S.A.
ZIP: 99352
                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                  US-08-853-659A-6
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CITY: Ri
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                                                                                                                                                                                  Patent No.
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APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSE: Paul W. Zimmerman
ADDRESSE: Datelle Memorial Institute
ADDRESSE: PNUL P.O. Box 999
STREET: Washington Way
CITY: Richland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::::::
7742 AUCUAUCAAUCUAUAUUGGGGAGUAUGUAUCUAUUACCCAAAUAACUAUUAUGGUAAUA 7801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7382 UGGAAUGAGUUUCAGAAAAUUAAACCCGUUUUAUUAAACUCGAUCUUUCAACGUAUAGCC 7441
                                                                                                                                                                                                                                                                                                                                                                                                   8 TrpArgAspileLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
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                                                                                                                                                                                                                                                  US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-64 (1-8967)
                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XT/AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 67, Application US/08853659A
Patent No. 5925522
GENERAL INFORMATION:
  single stranded
                                                                                                     12.4
80.50
41.24%
20.34%
8.70%
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                     linear
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Best Local Similarity:
Query Match:
DB:
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STRANDEDNESS:
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                            7 TOPOLOGI:
US-08-853-659A-64
                                                                                  Alignment Scores:
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Patent No. 5925522
GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
                                                        1586 İĞGAATGAGTTTCAGAAAATTAAACCCĞİİTTATTAAACİCĞATCİİİCAACGTATAGCC 1527
                                                                                                                                    1526 GATATTCCAATATTTATTATTTCTCATTGTTATATATGTAAATTTAGGTCTGGTTGTT 1467
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                                                                                                                                                                                   -----LeuSerValThrileSerPheArgileTyrLysGly 56
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                 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu
                                                                                                 27 SerteuThrValPheSerileValSerValThrAlaTyrIleAlaLeuAlaLeu----
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MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage COMPUTER: IBM PC/XT/AT.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. BOX 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word Processor (WordPerfect 5.1)
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APPLICATION NUMBER: US/08/853,659A
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INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 8967 bases
TYPE: nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC/XT/AT OPERATING SYSTEM: MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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STATE: Washington
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US-08-853-659A-64
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| GGGTTAATACATCAAATGAACAGTCGTATCTTAACCTGAAGATAAGGAAATTAAATCTT
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                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XT/AT
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
              Paul W. Zimmerman
Intellectual Property Servid
Battelle Memorial Institute
PNNL P.O. Box 999
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double stranded
                                                                                                                                                                                                                                                                                                                              FILING DATE: Unknown CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: none APPLICATION NUMBER: none FILING DATE: n/a INFORMATION POR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                        ADDRESSEE: PNNL P.O. BC
STREET: Washington Way
CITY: Richland
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20.34%
8.70%
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CORRESPONDENCE ADDRESS:
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                                                                                                                                    STATE: Washington COUNTRY: U.S.A.
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Best Local Similarity:
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TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
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Conservative:
Mismatches:
Indels:
              SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
FILING DATE: Unknown
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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Patent No. 5925522
GENERAL INFORMATION:
                                                                                                                                                                                                                                                    ; STRANDEDNESS: single stranded; TOPOLOGY: linear US-08-853-659A-67
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OPERATING SYSTEM: MS-DOS
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80.50
41.24%
20.34%
8.70%
                                                                                                                                                         FILING DATE: n/a
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   LENGTH: 8967 bases
TYPE: nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.D.
APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL W. Zimmerman
ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PINL P.O. Box 999
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                                                                                                          -- GlyHisValAgnSerThrileLysGluLeuArgArg 105
                                                                                 106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
                                                                                                                                                              --GlyAlaLeuPheAsnGlyLeuThr 136
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Conservative:
Mismatches:
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OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
                                                                                                                                                                                                                                                                                                                                                               ; Sequence 60, Application US/08853659A
; Patent No. 5925522
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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STATE: Washington
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Best Local Similarity:
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STRANDEDNESS:
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                                                                                                                                                         APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
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x US-08-853-659A-3 (1-24701)
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Matches:
Conservative:
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MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
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SOFTWARE: Word Processor (WordPerfect 5.1)
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Battelle Memorial Institute
PNNL P.O. Box 999
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                                                                               US-08-853-659A-3/c
; Sequence 3, Application US/08853659A
; Patent No. 5925522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 24701 bases
TYPE: nucleotide
STRANDEDNESS: double stranded
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                Paul W. Zimmerman
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APPLICATION NUMBER: US/08/FILING DATE: Unknown
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
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STATE: Washington
COUNTRY: U.S.A.
                                                                                                                                         GENERAL INFORMATION:
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ZIP: 99352
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1226 ATCTATCAATCTATATTGGGGAGTATGTCATCTATTACCCAAATAACTATTATGGTAATA 1167
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1466 ATTGTACCTATTACCATGTTTATCGTCTATTATTATTATTACCTCGTTAACCACCATTAT 1407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
                                                                                                                                                                                                                                                                                                                                              57 ValileGinAlaileGinLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
                                                                                                          8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu
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                                                                           US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-61 (1-24701)
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APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR PRILICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
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Mismatches:
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Gaps:
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Indels:
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Matches:
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US-09-2A7-373B-47/C
Sequence 47, Application US/09247373B
Patent No. 6168954
GENERAL INFORMATION:
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Best Local Similarity:
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TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                           23236 AUUGUACCUAUUACCAUGUUUAUCGUCUCUAUUAUUAUUAUCCCUCGUUAACCACCAUUAU 23295
                                                                                                                                  23296 ACUAAUGAGUUAAUGAACAAACAAAAGAAGGACAGAAGAACAGGAAUAUUUUAUCUCA 23355
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23416 UGGGUUAAUACAUCAAAUGAACAGUCGUAUCUUAACCUGAAGAUAAGGAAAUUAAAUCUU 23475
                                                                                                                                                                                                                                                                                                                                                      23536 GCCUUUUUAUGGUAAUCAAGGGUGAUGUUACUACUGGGGGAAUUGUUUCAUCUGUCAUU 23595
                                                                                                                                                                                                                                                                                                                            106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
                                                                                                                                                                          93
                     -----LeuSerValThrIleSerPheArgIleTyrLysGly 56
                                                                                                                                                                        77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu-----
                                                                                                                                                                                                                                                   --- GlyHisValAsnSerThrIleLysGluLeuArgArg
                                                                                                                                                                                                                                                                                                                                                                                                     ----GlyAlaLeuPheAsnGlyLeuThr
                                                                                              ValileGlnAlalleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 Leu-----LeulleLeuAlaLeulleSerLeuPheSerlleProValile 151
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
FILLING DATE: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Servi(
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: *PNNL P.O. BOX 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5-08-853-659A-61/c
Sequence 61, Application US/08853659A
Patent No. 5925522
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     124 ValPheThrTyrVal------
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STRANDEDNESS: single stranded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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80.50
41.24%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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U.S.A.
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CITY: Richland
STATE: Washingto
COUNTRY: U.S.A.
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99352
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Length:
Matches:
Conservative:
Mismatches:
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Patent No. 5880262
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola
TITLE OF INVENTION: No. 5880262e1 Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                          Indels:
                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                         US-09-830-972-2_COPY_975_1163 (1-189)
                                                                                                                          0.97
80.00
43.89%
25.00%
8.65%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 709 Swedeland
CITY: King of Prussia
                  TYPE: nucleic acid
STRANDEDNESS: single
 LENGTH: 1666 base
                                               linear
                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                               TOPOLOGY:
                                                                                                           Alignment Scores:
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                                                                             US-08-848-932-1
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                  -----CAAAAGCGAGCAAGAGCTCTTTGATGAGGATGGCAAGGTAAC 260
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                                                                                                                                                                                                                                                                                                                                       130 AlaLeu------PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSer--- 144
                                                                                                                                                                                                                                                                                                                                                                                                                  172 ACCTTCTTGTGAACCGGGTTCAACTGGAGAAGGAGATTGCTCTTGTTGAAGATATCTTCT 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 TCAATATACTCATACTCTATTCCCTTCAGTTTCAAAGCCCACTCAACCCTTTTACCAAAT
21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                           41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                        61 IleGlnLysSerAspGluGlyHisPro---PheArgAlaTyrLeuGluSerGluValAla
                                                                                                                                                                                                                                                                                                                     110 AspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGly
                                                                               ||| ::: |||
379 GCCTTTTCCTGTTCTTCCCCGCTGGTAGACATTGCTACC-----
                                                                                                                                                                                                                                                                                    259 AATGGATACTGCTTCCATGTTTCATCAATGTATTCAAGGATG
                                                                                                                                                                                       80 IleSerGluGluLeuValGlnLygTyr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Wallis, Nicola
TITLE OF INVENTION: No. 5766878el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PastSEQ for Windows Version 2.0 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,932
FILING DATE: 01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 TyrLeuGlyLeuAlaAsnLys 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9609125.1
FILING DATE: 01-MAX-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GGACTCACCCAAAAG 38
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Patent No. 5766878
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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95 HisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp-----AspLeu 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIleFroValIleTyr 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ATTTTATCGGTATCAGTCAGCAGGCTTTGAAATTGGATAGA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 GluSerGluValAlalleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly 94
                                                                                                32 ATCTTTTGCACGATGTCGAAAAACAGAAATCGAATTT------GTCTTTTATTG
                                                                                                                                                                                                                                                                                                                                                               -----ValileGinAlaileGinLysSerAspGluGlyHisProPheArgAlaTyrLeu
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                                                  LeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeu
                                                                                                                                                      LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla------
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US-09-134-001C-118/c

Sequence 118, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:
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79.00
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79.00
45.71%
22.86%
8.54%
                                                                                                                                                                 NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 93
                                                                                                                                                                                                                                    ORGANISM: M.catarrhalis
                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
      US-09-540-236-93/c
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                                                                                                                                                                                                                                                     US-09-540-236-93
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                                                                                                                                                                                                                        TYPE: DNA
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DB:
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DB:
                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,180
FILING DATE:
CLASSIFFCATION:
PRIOR APPLICATION NUMBER: 08/848,932
FILING DATE: 01-WAY-1997
APPLICATION NUMBER: 9609125.1
FILING DATE: 01-WAY-1996
ATTOMACY AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 931474
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
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                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:

LENGTH: 1666 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: mRNA
US-09-008-180-1
                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
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43.89%
25.00%
8.65%
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Best Local Similarity:
Query Match:
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Sequence 93, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
PAPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACLD AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA.
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-007
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
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TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-08-14

NUMBER: OF SEQ ID NOS: 5674

LENGTH: 777
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"Sequence 11439, Application US/09252991A
Sequence 11439, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENCE: 107196.136
CURRENT APPLICATION WHERE: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 GGCGCGGTGTTCCGCAAG------CTGATCGACTGGCCGCTTCTCCCGCTCC 514
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 AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Matches:
Conservative:
Mismatches:
                FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11432
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79.00
41.32%
23.95%
8.54%
   TITLE OF INVENTION:
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION:
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE POR INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ. ID NOS: 3840
SEQ. ID NO 99
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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707 TTATACTCATTTGAATTAGTGAAATCTTCACTTTTTTTAATAATAATAAAATTATCTATT 648
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383 TTTGTGATA-----ATTAATATCATAAAGTTTATCAATCTTTTAATAGCACTTACA 333
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Patent No. 6673910
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US-09-252-991A-11432
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Pred. No.:
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US-09-540-236-99
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Sequence 4170, Application US/09710279

Sequence 4170, Application US/09710279

GENERAL INFORMATION:

APPLICANT: KIMMERLY.

TITLE OF INVENTION: STAPHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

TITLE OF INVENTION: STAPHYLOCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: P0348009

CURRENT APPLICATION NUMBER: US/09/710,279

FRICH APPLICATION NUMBER: 00/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SEQ ID NO 4170

LENGTH: 2902
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                                                                                                                                                                                                                                                                                                  15 GlyvalvalPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleVal
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4170
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Mismatches:
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                                                                                                                                                                                                                                                             US-09-830-972-2_COPY_975_1163 (1-189)
                      ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11397
                                                                                                                   1.34
79.00
41.32%
23.95%
8.54%
                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-710-279-4170
                                                                                                     Alignment Scores:
    LENGTH: 1665
TYPE: DNA
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US-00-252-91A-11397
Sequence 11397, Application US/0925291A
Sequence 11397, Application US/0925291A
Sequence 11397, Application US/0925291A
Farent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: ARRUGINGS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1152 ATCGTCGCGCGGCGATCCCCTGCTCGGCACCCCCCCCAGCCGATGCTGGCGATCGTACTG 1093
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                                                                                                                                                                                                                                                                                                                                                                                                   GlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleVal
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Matches:
Conservative:
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                      60/094,190
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                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11439
LENGTH: 1500
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                                                                                                                                                                                                                                                                    SerPheArglleTyrLysGlyVallleGlnAlalleGlnLysSerAspGluGlyHisPro 69
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                                                                                                                                                                                                         30 ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIle 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GTTTCAGAAGAAAAAAAAAACACTTTTTA
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APPLICANT: FAUSTMAN, Denise L
TITLE OF INVENTION: TRANSPORT ASSOCIATED PROTEIN SPLICE VARIANTS
TITLE OF INVENTION: AND MODEL FOR IMMUNE DIVERSITY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
                                                                                                                   x US-09-710-279-4170 (1-2902)
              2902
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38
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
                                          Conservative:
Mismatches:
Indels:
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              Length:
Matches:
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Patent No. 6284879
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CITY: Cambridge
STATE: Massachusetts
COUNTRY: United States of Ameri
                                                                                                                 US-09-830-972-2_COPY_975_1163 (1-189)
                                        40.18%
22.83%
8.54%
              3.28
                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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ignment Scores:
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42
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                       i MOLECULE TYPE: other nucleic acid
j DESCRIPTION: synthetic DNA fragment
US-09-061-764A-18
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wincrosoft word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,764A
FILING DATE: April 16, 1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SANKHOH, LEON R
RESISTRATION NUMBER: 30,237
RESISTRATION NUMBER: MGH-002.0
TELECOMMUNICATION INFORMATION:
TELECHOME: 617-491-4343
                                                                      US/09/061,764A
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78.50
44.62%
22.58%
8.49%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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1162 GGGATCATGCTCTGGGGATCAGTGTCCTCACCATGGTCACCCTGATCACCCTGCCTCTG 1221
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                                                                                                                                                                                                                                                         99 ThrileLysGluLeuArgArgLeuPheleuValAspAspLeuValAspSerLeuLysPhe 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 IleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerVal 170
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                                                              119 AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu
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                                                                                                                                           79 AlaileSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSer
                             61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluVal--
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Sequence 1, Application US/09917254

Sequence 1, Application US/09917254

Sequence 1, Application US/09917254

GENERAL INFORMATION:

APPLICANT: Baak, Jan

TITLE OF INVENTION: Prognostic Classification of Breast Cancer

FILE REFERENCE: B0001/724 (JRV)

CURRENT APPLICATION NUMBER: US/09/917,254

CURRENT PILING DATE: 2001-07-27

PRIOR FILING DATE: 2000-07-28
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Matches:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2824
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ORGANISM: Homo Sapiens
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS: 1490
ADDRESSEE: INVTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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422
41
62
10
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APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Mismatches:
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Matches:
                                                                                                                                                                Sequence 1349, Application US/09016434 Patent No. 6500938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                             1069 CGGGAATCTCTGGCAAAG 1086
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CLASSIPICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-O
TELECOMMUNICATION INFORMATION:
  171 LysAspAlaMetAlaLys 176
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TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 134
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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TYPE: nucleic acid
STRANDEDNESS: singl
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IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-09-016-434-1349
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Oy 54 TyrLysGlyVallleGlnAlarleGlnLysSerAspGluGlyHisProPheArgAlaryr 73	Db 18459 TTTCAGGTATTATCAGGAAATATATGAAGTTGAGCCACTTTCTGCTTACACAGTACCGTCT 18518 Qy 116 LeuLyBPheAlaValLeuMetTrpValPheThrTyrVal 128 iii	Db 18579 GAAATGGGTCTCTTTACAGAATATCAACTATGTCCATTCTAAGTTATCCTTACCCTAC 18638 Qy 147 SerIleProVall1e 151 Db 18639 ACGCCACCGCTATA 18653	Sequence 1, Application US/10270878
	Qy 139	Qy 171 LysAspalaMetAlaLys 176 Db 1279 CGGGAATCTCTGGCAAG 1296 RESULT 93 HC-00-FGS. 10 10	Sequence 1, Application US/0958588

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	Alignment Scores: Pred. No.: Pred. No.: 78.00 Matches: 8.00 Percent Similarity: 38.10\$ Conservative: 34.3\$ Mismatches: 70 Ouery Match: 3

Db 277 GAGATGAATAAGCCGATTTTAAATGGCTTACTGCTTTTGCTATTGCGATTGCCATTGTA 336	Db 1929 Tropping AC	
	7777	at upototuous
<pre>Qy 54TyrLy8GlyVallleGlnAlalleGlnLy8SerAspGluGlyHisProPheArgAla 72 </pre>	Qy 66 GluGlyHisProPh Db 1276 GGAAGACAACT	GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85 :::
Qy 73 TyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92 Db 397 TTATTGGTGATTATGGCAAAGAATTGGTGCAGTATTAT 435	Qy 86 GlnLysTyrSerAenSerAlaLeuGl ::: Db 1330 GTGAAGATGGG	
Qy 93 LeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112	Qy	ValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
<pre>Qy 113 ValAspSerLeuLysPheAlaValLeu</pre>	Qy 112 LeuValAspSerLe Db 1435 CTGTGGAGGCAGGA	LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
Oy 125 PheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuAlaLeuIleSer 144	Oy 132 PheAsnGlyLeuTh	PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProval 150 ::: :::
Qy 145 LeuPheSerIle 148	Qy 151 IleTyrGluArgHi ::: Db 1555 GTTCGTTCACA	IleTyrGluargHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaasn
RESULT 97 US-09-795-927-6 S. Sequence 6, Application US/09795927	Qy 168LysSerValLy ::: ::: Db 1612 TATAGAAGCATCAA	LysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185 ::: TATAGAAGCATCAATGATTATCGGGAGATCATCACCATTCCTGGGGTGAAA 1662
GENERAL INFORMATION: APPLICANT: Walke, D. Wade APPLICANT: Walke, D. Wade APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Kieke, James A. APPLICANT: Kieke, James A. APPLICANT: Zambrowicz, Brian APPLICANT: Zambrowicz, Brian APPLICANT: Revelli, Jean-Pierre APPLICANT: Revelli, Jean-Pierre APPLICANT: Revelli, Jean-Pierre APPLICANT: Revelli, Jean-Pierre APPLICANT: Revelli, Jean-Pierre APPLICANT: Revelli, Jean-Pierre APPLICANT: LEX-0141-USA FILE REFERENCE: LEX-0141-USA CURRENT FILING DATE: 2001-02-28 PRIOR APPLICATION NUMBER: US 60/185,956 NUMBER OF SEQ ID NOS: 11 SOFTWARE: FastSEQ for Windows Version 4.0	RESULT 98 US-09-328-352-932 Sequence 932, Application US/09328352 Patent No. 6562958 GENERAL INFORMATION: APPLICANT: Gary L. Breton et al. TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: BAUMANNII FOR DIA FILE OF INVENTION: BAUMANNII FOR DIA CURRENT APPLICATION NUMBER: US/09/328 CURRENT PILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 SEQ ID NO 932 LENGTH: 3162 TYPE: DNA TYPE: DNA TYPE: DNA COGANISM: Acinetobacter baumannii US-09-328-352-932	et al. C ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER NNII FOR DIAGNOSTICS AND THERAPEUTICS 1. US/09/328,352 06-04
; SEQ ID NO 6 ; LENGTH: 2913 ; TYPE: DNA ; ORGANISM: homo sapiens US-09-795-927-6	Alignment Scores: 5.2 Pred. No.: 5.2 Score: 78.00 Percent Similarity: 39.51\$	Length: 3162 Matches: 34 Sonservative: 30
4.56 Length: 78.00 Matches:	dony or	nibilitationes: 54 Indels: 44 Gaps: 6 Gaps: 700, 170, 011, 011, 011, 011, 011, 011,
Percent Similarity: 42./1* Conservative: 3/ Best Local Similarity: 24.12* Mismatches: 68 Query Match: 8.43* Indels: 46 DB:	OS-09-830-9/2-2_COPY_9/5_II63 QY	Z_COPY_9/5_1163 (1-189) X US-09-328-35Z-93Z (1-316Z) LeuLeuTyrTrpArgAspIleLysLysTyrTrglyValValPhe
-09-830-972-2_COPY_975_1163 (1-189) x US-09-795-927-6 (1-2913) 21 SerLeuPheLeuLeuLeu	19 2794	
1102 AGCICCITICFGCTCAFAITTCTGGGGAAGAAGATTGCCAGFCTTCACAAFTACAGFGTC 11 34 ValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPhe 51	Qy 37 ThralaTyrIleal	ThralaTyrilealaLeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGly 56 :: ::: ::: CTAGGAACCATTATCCGGCATGATTATGCGTAACTCACTC
DD 1162 ARTICCAACCAGGATTTAATAGCCATCGGCCTTTGCAATGTCGTCATTTTTCAGA 1221 Qy 52ArgileTyrLysGlyValileGlnAlaileGlnLysSerAsp 65	Qy 57 ValileGlnAlail	VallleGlnAlalleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76 ::: .

1751 GGAAGACAACAGTTTGCATCTCTGGTAGGCGCAGGTGTGATGCTGCTCCTGATG 1804	86 GlnLysTyrSerAsnSerAlaLeuGlyHis	96ValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111	112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131	132 PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProVal 150	151 IleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsn 167 :::	168LysSerValLysAspalaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185 	453-702B ence 259 nt No. 6 NERAL IN APPLI TITLE NUMBE CORRE	3.5	OPERATION SIGNED PORTION OF PRESENCE OF CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-Dec-1999 CLASSIFICATION: «Unknown» PRIOR APPLICATION DATA: APPLICATION NATA: 60/110,955	ATTORNEY/AGENT INFORMATION: NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386 REFERENCE/DOCKET NUMBER: 960296.95017 TELECOMMUNICATION INFORMATION:	TELEFAX: (608) 251-9166 INFORMATION FOR SEQ ID NO: 259: SEQUENCE CHARACTERIZITICS:	TABLOIN: 1402 Date paris TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECTLE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 259:	-09-453-702B-259
a	\$ a	상 원	Sy da	ð 8	\$ A	B &	US-09-1		** ** ** ** ** ** ** ** ** ** ** ** **				-sn
Db 2905 ATTGATCAGATTGAACAAGACAGGCAGGCATCCA	Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96 ::: ::: Db 2944ACGTGGGAAGCAATTACTGGGAAGCAATT	Oy 97 AsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 116 ::::: ::: ::: ::: ::: ::: :::: ::: ::: ::: ::: ::: ::: ::: ::: :::: ::: ::: ::: :::: ::: :::: :::: :::: :::: :::: ::::: ::::: ::::: ::::: ::::::	Oy 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 136	Qy 137LeuLeulleLeuAlaLeulleSerLeuPheSerlleProVal 150	Qy 151 IleTyr 152 ::: Db 3124 TTGTAT 3129	RESULT 99 US-09-795-927-8 ; Sequence 8, Application US/09795927	APPLICANT: Walke, D. Wade APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Wilke, James A. APPLICANT: Zambrowicz, Brian APPLICANT: Zambrowicz, Brian APPLICANT: Turner, C. Alexander Jr. TITLE OF INVENTION: No. 6531309el Human Transporter Proteins and Polymucleotides Enco TITLE OF INVENTION: Same FILE REPERBUCE: LEX-041-USA FILE REPERBUCE: LEX-041-USA CURRENT APPLICATION NUMBER: US/09/795,927 CURRENT FILING DATE: 2001-02-28 PRIOR APPLICATION NUMBER: US 60/185,956	; FALON FILING DAIR: 200-02-29; NUMBER OF SEQ ID NOS: 11; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 8; LENGTH: 3749; TYPE: DNA 9; ORGANISM: homo sapiens US-09-795-927-8	Alignment Scores: 6.84 Length: 3749 Pred. No.: 6.84 Length: 3749 Score: 78.00 Matches: 48 Percent Similarity: 42.71\$ Conservative: 37 Best Local Similarity: 24.12\$ Mismatches: 68 Query Match: 443\$ Indels: 10	US-09-830-972-2_COPY_975_1163 (1-189) x US-09-795-927-8 (1-3749) Qy 21 SerLeuPheLeuLeuLeuLeu	Qy 34 ValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPhe 51	Qy 52ArglleTyrLysGlyVallleGlnAlalleGlnLysSerAsp 65 Db 1697 TCTTGTGTGTTTTACTGGTGCTALTGCTAGGACTATTATCCAGGATAAATCTGGA 1750 Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlalleSerGluGluLeuVal 85	

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	1-189) x US-09-453-702B-259 (1-4162)	TTCTGGAGTCTTTCGCTAAAAACTGGCGGCGCTACGGCGGTATTATGCTGGCGTCACTG	-PheleuLeuLeuSerLeuThrValPheSer	GTGGCGAACGTGCTGGCGCTGGCGGCGATGATTTTCTCGATGCAGGTTTACGATCGGGTG ValSerValThrAlaTvrIleAlaLeuAlaLeuLeuSerValThrTleSerPheArctle	 GTTCCGGCGCAATCGTACCGACGCTATGGGTGCTF	TyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyr	TTCGCCGGGGTGATGGCGATCCTGTTTGAGTTCTGTATGCGCATGGTGCGTACGCAT	alG	CTATCTGATGTGATCGGAAAGCGGGCAGACCTG		<u>ĠĠŤĊ</u> ĂĬĠĊĠĊĨAĊĠĠĊĬĠAĀAAAAAAĠŢĠĊĠAĬĊĠĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸ	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSer	:::::	-LeuLysPheAlaValLeuMetTrpValPheThrTyrValGly	GCGGACCTGCCATTCTTCCTGCTGTTTGTCTTTATTTTGTGGATG-	AlaLeuPheAsnGlyLeuThrLeuLeuleulleLeuAlaLeuIleSerLeuPheSerIlePro		-ValileTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAl	 GGCCTGCTGGTGCAACGCCCGCTGGCGCGG	AlaLys 176	STACGC 2921	
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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- nucleic search, using frame_plus_p2n model
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ALIGNMENTS

Sequence 17, Application US/09893348 Patent No. US20020072493A1 GENERAL INFORMATION:

US-09-893-348-17

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APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: BESERVAN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSLEM, Glia
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USF
FILE REFERENCE: EIS-SCHWARTZ=2A
CURRENT APPLICATION NUMBER: US/09/893,348
PRIOR APPLICATION NUMBER: US 09/314,161
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Percent Similarity:
Best Local Similarity:
        INFORMATION
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-07-21
PRIOR PILING DATE: 1998-07-21
PRIOR PILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 4684
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                                                                                                                                                                                 TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                               FEATURE:
NAME/KEY: CDS
LOCATION: (253)..(3744)
OTHER INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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US-10-810-653-17
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APPLICANT: COMEN, ITULE REPERENCE.

APPLICANT: COMEN, ITULE R.

APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
TITLE OF INVENTION: ACTIVATE2 D.-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US:
TITLE OF INVENTION: ACTIVATE 120
TITLE OF INVENTION: UNMBER: US/10/810,653
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: US/99/893,348
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
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Conservative:
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APPLICANT: BISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.
APPLICANT: BESERMAN, Pierre
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LOCATION: (253)..(3744)
OTHER INFORMATION:
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Alignment Scores:
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                                                                                                                 Sequence 165, Application US/10205194

Publication No. US20030134301A1

GENERAL INPORMATION:

APPLICANT: Warner-Lambert Company

APPLICANT: Dixon, Alistair

APPLICANT: Dixon, Alistair

APPLICANT: Pinnock, Robert

TILE BEFERENCE: WL.A-018201

CURRENT PILNG DATE: 5200-07-24

FILE REPERENCE: WL.A-018354.0

FRIOR APPLICATION NUMBER: GB 0118354.0

FRIOR APPLICATION NUMBER: GB 0118354.0

FRIOR APPLICATION VOWER: 2001-07-27

NUMBER OF SEQ ID NOS: 177

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 165

LENGTH: 2782
     1271 GCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 1330
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Matches:
Conservative:
Mismatches:
Indels:
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                                                    181 IleProGlyLeuLysArgLysAlaAsp 189
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Best Local Similarity:
                                                                                                RESULT 3
US-10-205-194-165
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US-10-956-157-9764

Sequence 9764, Application US/10956157

Sequence 9764, Application US/20950118625A1

Sequence 9764, Application US/20950118625A1

Sequence 9764, Application US/20950118625A1

Sequence 9764, Application US/20950118625A1

Sequence 9764, Application US/2095011862A1

Sequence 9764, William APPLICANT: Wounts, William NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITTILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REPERENCE: 031896-04300 (AM 101081)

CURRENT APPLICATION WUMBER: US/10/956,157

CURRENT APPLICATION WUMBER: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SEQ ID NO 9764

LENGTH: 600
                                                        91 AGCCTATTCCTGCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATT 150
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211 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
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CORGANISM: Homo sapiens
US-10-956-157-9764
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Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITT.
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 4529
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                                                                                                                                   Sequence 4529, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
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; ORGANISM: HOMO
US-10-956-157-4529
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APPLICANT: Wounts, William
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APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-110-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
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                                     511 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA
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US-10-956-157-9763
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Best Local Similarity:
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US-10-956-157-9763
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LENGTH: 1400
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                   GENERAL INCORMALIONICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANT: PRINJHA, RABINDER KUMAR
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30165-C1
CURRENT PILING DATE: 2001-02-21
PRIOR PPLICATION NUMBER: U.K. 9916898.1
PRIOR PILING DATE: 1999-07-19
PRIOR PLILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: U.K. 9916024.5
PRIOR APPLICATION NUMBER: U.K. 991698.1
PRIOR APLICATION NUMBER: U.K. 991698.1
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3579
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                                     ; Sequence 1, Application US/09789386; Patent No. US20020010324A1; GENERAL INFORMATION:
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908.00
98.94%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                                                                                  APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTEDARTHRITS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT PAPLICANTION WUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 4528
LENGTH: 3478
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Matches:
Conservative:
Mismatches:
Indels:
IleProGlyLeuLysArgLysAlaAsp 189
                                                                                      ; Sequence 4528, Application US/10956157; Publication No. US20050118625A1; GENERAL INFORMATION:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Homo
US-10-956-157-4528
                                                                       US-10-956-157-4528
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Pred. No.:
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                                          21 SerLeupheLeuLeuLeuSerLeuThrValPheSerlleValSerValThrAlaTyrIle
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                    AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp
                                                                                                              HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys
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Mismatches:
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Matches:
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Sequence 212, Application US/10267502

Publication No. US20040071700A1

GENERAL INFORMATION:
APPLICANT: Kim, Jaesecb
APPLICANT: Kim, Jaesecb
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERRINCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27

NUMBER OF SEQ ID NOS: 439
SOFTWARE: Patentin version 3.2

SEQ ID NO 212

LENGTH: 3579
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Best Local Similarity:
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3550 ATCCCTGGATTGAAGCGCAAAGCTGAA 3576
                                                                                          Sequence 22, Application US/09893348 Patent No. US20020072493A1 Patent No. US20020072493A1 APPLICANT: EISENBACH-SCHWARTZ, Michal
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ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (1)..(3579)
OTHER INFORMATION:
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Publication No. US20040132096A1
GENERAL INPORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: ASSAY
FILE REFERENCE: P80966 GCW
CURRENT APPLICATION NUMBER: US/10/466,258
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 8
SEQ ID NO 8
                                                                                       3550 ATCCCTGGATTGAAGCGCAAAGCTGAA 3576
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ORGANISM: Homo sapiens
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US-10-466-258-8
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Publication No. US20040121341a1
GENERAL INFORMATION:
APPLICANT: FILBIN, MARIE T.
APPLICANT: CAO, ZIXUAN
TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION FILE REFERENCE: CUNY/003
CURRENT APPLICATION NUMBER: US/10/327,213
CURRENT PILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 43
SOFTMARE: Patentin Ver. 2.1
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Conservative:
Mismatches:
Indels:
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98.94%
97.35%
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Best Local Similarity:
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Sequence 5, Application US/09758140

Sequence 5, Application US/09758140

Batent No. US20020012965A1

GENERAL INFORMATION:

APPLICANT: Stittmatter, Stephen M.

TITLE OF INVENTION: NO. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth

FILE REFERENCE: 44574-5073-US

CURRENT APPLICATION NUMBER: US/09/758,140

CURRENT PILING DATE: 2001-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5.
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                                                                                                                                                            Sequence 22, Application US/10810653
Publication No. US20040253218A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: BESENBACH-SCHWARTZ, Michal
APPLICANT: BESENBACH, Pierre
APPLICANT: MOALEM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USF
FILE REFERENCE: EIS-SCHWARTZ=2A
FILE REFERENCE: EIS-SCHWARTZ=2A
FILE REFERENCE: EIS-SCHWARTZ=2A
FILE REFERENCE: EIS-SCHWARTZ=2A
FILE REFERENCE: EIS-SCHWARTZ=2A
FILE REFERENCE: EIS-SCHWARTZ=2A
FILE REFERENCE: EIS-SCHWARTZ=2A
FILE REFERENCE: EIS-SCHWARTZ=2A
FILE REFERENCE: EIS-SCHWARTZ=2A
FRIOR PLILING DATE: 2004-03-29
FRIOR FILING DATE: 1998-12-22
FRIOR PLILING DATE: 1998-12-22
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-31
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; OTHER INFORMATION:
US-10-810-653-22
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  3204 AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATT 3263
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APPLICANT: "Year." Matalie C.
APPLICANT: Twine, Natalie C.
APPLICANT: Twine, Natalie C.
APPLICANT: Trepicchio, Milliam L.
APPLICANT: Slonim, Donna K.
APPLICANT: Slonim, Donna K.
APPLICANT: Storim, Donna K.
APPLICANT: Storim, Donna K.
APPLICANT: Storim, Donna K.
APPLICANT: Storim, Donna K.
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APPLICANT: Storim, Donna K.
APPLICANT: Storim, Donna K.
APPLICANT: Storim, Donna K.
CURRENT FILING DATE: 2003-11-21
PRIOR PAPLICATION NUMBER: US 60/459, 782
PRIOR PAPLICATION NUMBER: US 60/427, 982
PRIOR FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 4904
SOFTWARE: Patentin version 3.2
LENGTH: 4053
                                                                           SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle
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Publication No. US20040110221A1
GENERAL INFORMATION:
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LOCATION: (135)..(3710)
OTHER INFORMATION: Human DNA encoding for No. US20020077295Alo protein (KIAA0886,
OTHER INFORMATION: Accession No. US20020077295Al AB020693)
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A PAPLICANT: STRITTMATTER, STEPHEN M.

TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REPERENCE: COT7 CIP US
CURRENT PILING DATE: 2001-110-06
CURRENT PILING DATE: 2001-10-06
PRIOR PILING DATE: 2001-01-12
PRIOR PILING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 2000-00-29
PRIOR PLING DATE: 2000-00-29
PRIOR PLING DATE: 2000-05-26
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                       3211 AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATT
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                                                                                                             3271 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
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Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Ralos, Michael D.
APPLICANT: Persing, David H.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: APPLICANT: APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: APPLICANTON: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF PANCREATIC CAN, FILE REFERENCE: 21012.566
CURRENT PILING DATE: 2002-01-30
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 4632
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CORGANISM: Homo sapiens
US-10-060-036-53
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Best Local Similarity:
Query Match:
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APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: UCLERC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4532
LENGTH: 4623
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                                                                                                                                     41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
3144 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTGGTGCC
                                                       SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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Publication No. US20050118625A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-956-157-4532
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3220 ATAAAAGAATTGAGGCGTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCA 3279
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                                                                                                            3100 GCTATCCAGAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCC 3159
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                           3040 ATTGCCTTGCCTCTCTGTGACTATCAGCTTTAGGATATATAAGGTGTGTGATCCAA
                                                                                                                                                    80 IleSerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThr
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                                                                           60 AlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla
   40 IleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COMPUTRY: U.S.
COMPUTRY: U.S.
ZIPLE: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORRENT SYSTEM: DOS
SOSTWARE: FactSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/228,13A
FILING DATE: L2-Sep-2003
APPLICATION NUMBER: US/09/228,213A
FILING DATE: CUNKNOWN>
FILING DATE: CUNKNOWN>
FILING DATE: CUNKNOWN>
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
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TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
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                                                                         AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                   3211 AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATT
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Matches:
Conservative:
Mismatches:
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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
ITILE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT PILIGN DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Patentin version 3.2
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ORGANISM: Mus musculus
US-10-267-502-214
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Best Local Similarity:
Query Match:
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US-10-267-502-214
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                                                                                                                                                                                                                                                                                                                                                                                 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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Fatent No. US20020010324A1
GENERAL INFORMATION:
APPLICANT: MICHALOVICH, DAVID
APPLICANT: PRINJHA, RABINDER KUMAR
ITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30165-C1
CURRENT APPLICATION NUMBER: US/09/789,386
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: U.K. 9916898.1
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LENGTH: 799 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
                                                                                                       SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                        2.98e-100
904.00
98.94%
97.34%
                                                                              LIBRARY: <Unknown>
CLONE: Consensus
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Best Local Similarity:
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US-09-789-386-5
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MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
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PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: U.K. 9816024.5
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTER for Windows Version 3.0
SEQ ID NO 5
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Sequence 156, Application US/10175523

Publication No. US20030096264A1

GENERAL INFORMATION:

APPLICANT: Brockman, Jeffrey

APPLICANT: Evans, David

APPLICANT: Klimczak, Leszek

APPLICANT: Laeng, Pascal
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98.94$
97.34$
                                                                                                                                                                TYPE: DNA ORGANISM: HOMO SAPIENS
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                                                                                                                                               LENGTH: 1122
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RESULT 23
US-10-956-157-4527

Sequence 4527, Application US/10956157

Sequence 4527, Application US/10956157

Sequence 4527, Application No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: HUMAN OSTECARTRRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTRRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTRRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: UNBER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

LENGTH: 1609
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; ORGANISM: HOMO
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    ### PRIDICANT: Relain, Prithi | PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS) | TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS) | TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS) | FILE REPERBENCE: 3225/10/795-US3 | CURRENT APPLICATION NUMBER: US 60/299,151 | PRIOR PELICATION NUMBER: US 60/299,151 | PRIOR PELICATION NUMBER: US 60/317,828 | PRIOR PELICATION NUMBER: US 60/317,828 | PRIOR APPLICATION NUMBER: US 60/313,047 | PRIOR PELICATION NUMBER: US 60/313,047 | PRIOR PELING DATE: 2001-09-25 | PRIOR PELING DATE: 2001-11-14 | PRIOR PELING DATE: 2001-01-11-14 | PRIOR PELING DATE: 2002-01-18 | PRIOR PELING DATE: 2002-01-18 | PRIOR PELING DATE: 2002-01-18 | PRIOR PELING DATE: 2002-03-04 | NUMBER OF SEQ ID NOS: 197 | SOUTWARE: Patentin version 3.1 | SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF SEQ ID NO 156 | LENGTH: 1160 | NUMBER OF 
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904.00
98.94%
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Palfreyman, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-175-523-156
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Best Local Similarity:
Query Match:
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Pred. No.:
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S-09-765-205-5
Sequence 5, Application US/09765205
Sequence 5, Application US/09765205
Sequence 5, Application US/09765205
Sequence 5, Application
GENERAL INFORMATION:
APPLICANT: Cao, Li
TILLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REPERENCE: 1458.004/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001-01-17
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183
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Matches:
Conservative:
Mismatches:
Indels:
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5-10-347-669-5
Sequence 5, Application US/10347669
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: human
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LENGTH: 1610
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Pred. No.:
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Publication No. US20050084850A1
GENERAL INFORMATION:
APPLICANT: Cao, Li
TITLE OF INVENTOR: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 1458.004/200130.449
CURRENT APPLICATION UNMBRE: US/10/347,669
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/212,440
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-830-972-2_COPY_975_1163 (1-189) x US-10-347-669-5 (1-1610)
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GENERAL INFORMATION: APPLICANT: Aure, Thomas M
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904.00
98.94%
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Best Local Similarity:
                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: human
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US-10-439-388-62
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Sequence 4530, Application US/10956157
Publication No. US20050118625A1
Publication No. US20050118625A1
AEMERALION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
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            AND HUMAN PROTEASES
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Matches:
Conservative:
Mismatches:
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                        FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
LENGTH: 1785
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904.00
98.94%
97.34%
                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-956-157-1705
            TITLE OF INVENTION:
                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                Percent Similarity:
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US-10-956-157-4530
                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                    TYPE: DNA
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US-10-956-157-1705
; Sequence 1705, Application US/10956157
; Sequence 1705, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Wounts, William
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
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                         Autoimmune Disease
                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
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Matches:
APPLICANT: Olsen, Nancy J
TITLE OF INVENTION: Method for Predicting Aut
FILE REPERENCE: 1242/66
CURRENT APPLICATION NUMBER: US/10/439,388
CURRENT FILING DATE: 2003-05-16
PRIOR PLING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.2
SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                       Gaps:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                                                                                                                                                                LENGTH: 1785
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ORGANISM: Homo
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Matches:
Conservative:
Mismatches:
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Sequence 3, Application US/10466258
Sequence 3, Application No. US20040132096A1
GENERAL INFORMATION:
APPLICANT: GLAKO GROUP LIMITED
TITLE OF INVENTION: ASSAY
FILE REFERENCE: P80966 GCW
CURRENT APPLICATION UNDBER: US/10/466,258
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SERVINGENT: 2052
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CURRENT FILING DATE: 2004-10-04 NUMBER OF SEQ ID NOS: 319805 SOFTWARE: Patentin version 3.2 SEQ ID NO 4530 LENGTH: 2050
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904.00
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                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-956-157-4530
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Best Local Similarity:
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US-10-956-157-4531

Sequence 4531, Application US/10956157

Sequence 4531, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITHTILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT APPLICATION NUMBER: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 4531

LENGTH: 2226
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Matches:
Conservative:
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Indels:
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904.00
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FEATURE:

NAME/KEY: CDS

; LOCATION: (67)..(1188)

US-10-466-258-3
                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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us-09-830-972-2_copy_975_1163.rnpb

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; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-54
                                                          Alignment Scores:
Pred. No.:
Score:
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US-10-060-036-54
; Sequence 54, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Relso, Michael D.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Jang, Yudiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; SOFTWARE: PRESENCE FASCO for Windows Version 4.0
                                                                                                                                          US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-4531 (1-2226)
                                                         2226
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                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                       1.49e-99
904.00
98.94%
97.34%
             sapiens
                                                                               Percent Similarity:
Best Local Similarity:
 ; TYPE: DNA
; ORGANISM: HOMO
US-10-956-157-4531
                                              Alignment Scores:
Pred. No.:
Score:
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RESULT 32

US-10-220-891-22

Sequence 22, Application US/10220891

Sedience 22, Application No. US20030207286A1

Subjication No. US20030207286A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWARA, AKIRA

TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS

TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS

TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS

TITLE OF INVENTION: ROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS

TILE REFERENCE: 7388-7345

CURRENT APPLICATION NUMBER: US/10/220,891

CURRENT FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 108
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  2235
1183
3
0
0
Length:
Matches:
Conservative:
Mismatches:
Indels:
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1.5e-99
904.00
98.94%
97.34%
                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Alignment Scores:
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LENGTH: 994
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US-09-978-360A-110

Sequence 110, Application US/09978360A

Sequence 110, Application US/09978360A

SENERAL INFORMATION:

APPLICANT: Edwards, Jean-Baptiste Dumas Milne

APPLICANT: Bouqueleret, Lydie

APPLICANT: Bouqueleret, Lydie

APPLICANT: Jobert, Severin

APPLICANT: Complementary DNA's Encoding Proteins with Signal Peptides

TILE OF INVENITON: Complementary DNA's Encoding Proteins with Signal Peptides

CURRENT FILING DATE: 201-10-15

CURRENT FILING DATE: 1997-11-13
                                                                                                                                                                                                                                                                                                                                                                                                1185
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                                                                                                                                                                                                                     US-09-830-972-2_COPY_975_1163 (1-189) x US-10-220-891-22 (1-1980)
                                                                                                                                              Conservative:
Mismatches:
Indels:
Gaps:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 22
LENGTH: 1980
                                                                                                                 6.7e-99
898.00
98.41%
96.30%
                                          TYPE: DNA
CRGANISM: Homo sapiens
US-10-220-891-22
                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                     Alignment Scores:
Pred. No.:
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68 GTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 127
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PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-02-09
PRIOR PELION NUMBER: US 60/074,121
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR PILING DATE: 1998-08-10
PRIOR PILING DATE: 1998-08-10
PRIOR PILING DATE: 1998-10-10
PRIOR PILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR PILING DATE: 1998-11-13
PRIOR PILING DATE: 1998-11-13
PRIOR PILING DATE: 1998-12-17
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Mismatches:
Indels:
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NAME/KEY: sig_peptide
LOCATION: 35..160
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 8.6
OTHER INFORMATION: seq ASLFLLLSLTVFS/IV
FEATURE:
NAME/KEY: polya signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 979..994
US-09-978-360A-110
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NAME/KEY: CDS
LOCATION: 35..631
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Query Match: 96.32% Indels: 1 DB: 18 Gaps: 0	US-09-830-972-2_COPY_975_1163 (1-189) x US-10-641-643-382 (1-2610) Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValValPheGlyAlaSer 21		1371 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACAATTGC	Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArg11eTyrLysG1yValIleG1nAla11 61 	61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81	Db 1491 CCAGAAATCAGATGAAGGCCACCCAFTCAGGGCATATCTGGAAGTTGCFATATC 1550 Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrileLy 101	1551 TGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAA	Oy 101 sGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLe 121	Qy 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAgnGlyLeuThrLeuLeuIleLeuAl 141	141 aleulleSerLeuPheSerIleProVallleTvrGluhrqHisGlnValGlnIleAspHi 161	1731 TCTCAFTTCACTCTTCAGTGTTACTTATTATGAACGGCATCAGGCACAGATAGAT	Qy 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIl 181	Db 1791 TTATCTAGGACTTGCAAATAAGAATGTTAAAGGTGCTATGGCTAAAATCCAAGCAAAAAT 1850	181 eProGlyLeuLysArgLysAlaAsp		RESULT 35 US-10-466-258-10 . Camianna 10 amiliarion IIC/10466258	Gequence 10, Application 00, Application 00, Application No. US20040132096A1	; APPLICANT: GLAXO GROUP LIMITED ; TITLE OF INVENTION: ASSAY	; FILE REFERENCE: P80966 GCW ; CURRENT APPLICATION NUMBER: US/10/466,258	CORRENT FILLING DAILS: 2003-07-15 ; NUMBER OF SEQ IN NOS: 13 3	1	TYPE: DNA TYPE: DNA CRGANISM: Homo Bapiens		US-10-466-258-10	8.28e-95 864.00 ty: 97.88% arity: 96.30%	93.41% Indels: 19 Gaps:
Db 368 GAACTCAGGCGCCTCTTTTTTTTTTTTTTTTTTTTTTTT	Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141	Oy 142 LeulleSerLeuPheSerlleProVall1eProVall1eProFlukrgHisGlnValGln1leAspHis 161 Db 488 CTCATTCACTCTTCACTGTTACTATTTATAACGGCATCAGGCACAGATAGACCAT 547	162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle	Db 548 TATCTAGTACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC 607 Qy 182 ProGlyLeuLysAlgasp 189	Db 608 CTIGATITGAAGCGCAAAGCTGAA 631	RESULT 34 2-10-641-643-382 ; Sequence 382, Application US/10641643 ; Publication No. US20040077003A1	; GENERAL INFORMATION: ; APPLICANT: Cocks, Benjamin G.	Susan G. Stuart Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL	NUMBER OF SEQUENCES: 1508 CORRESPONDENCE ADDRESS: ADDRESCEF: TACYTE DIABMACETTICALS INC	ER DRIVE	STATE: CALIFORNIA COUNTRY: USA	COMPUTER READER FORM:	COMPUTER: FLORDY GIBS COMPATER: PARTIES COMPANIES DO COMPANIES	SOFTWARE: Word Derfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:	; APPLICATION NUMBER: US/10/641,643 ; FILING DATE: 14-Aug-2003	; CLASSIFICATION: <unknown> ; PRIOR APPLICATION DATA:</unknown>	FILING DATE: <pre>cubricom> company Agent INFORMATION</pre>	7,071	REFERENCE/DOCKET NUMBER: PA-0001 US TELECOMMUNICATION INFORMATION:	TELEFANCE: (650) 845-4166 TELEFAX: 0500 845-4166	JARACTERIST	; TYPE: nucleic acid; STRANDEDNESS: single	TOPOLOGY: linear	CLONE: 1508778 SEQUENCE DESCRIPTION: SEQ ID NO: 382 :	7.41e-98 Length: 891.00 Matches:	ercent Similarity: 98.41% est Local Similarity: 96.83%

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us-09-833-245A-349

sequence 349, Application US/09823245A

publication No. USZ0020039760A1

general information.

APPLICANT: Wong, Gordon G.

APPLICANT: Pechtel, Kind

APPLICANT: Resnick, Michael J.

APPLICANT: Resnick, Ramalakar.

APPLICANT: Resnick, Ramalakar.

APPLICANT: Resnick, Ramalakar.

APPLICANT: Graham, James R.

APPLICANT: Graham, James R.

APPLICANT: Graham, James R.

APPLICANT: Graham, James R.

PRICE REFERENCE: GIN 6401

CURRENT FILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 631

SOFTWARE: Patentin Ver. 2.0

SEMINICAL: FILING DATE: 2003-04-06

NUMBER OF SEQ ID NOS: 631

LENGTOWN 151
                         2 AAGAAGACTGGAGTGTTTGGTGCCAGCCTATTCCTGCTTTCATTGACAGTATTC
                                                                                            62 AGCATTGTGAGCGTAACAGCCTACCATTGCCCTGCTCTCTGTGACCATCAGCTTT
                                                                                                                                                52 ArgileTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg
                                                                          SerileValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPhe
LystysthrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPhe
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US-09-823-245A-349
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Pred. No.:
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US-10-956-157-9765
; Sequence 9765, Application US/10956157
; Sequence 9765, Application US/10956157
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
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; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; SOUTHWARE: PAPLICATION NUMBER: US/10/956,157
; SOUTHWARE: PALENTIN VERSION 3.2
; SOUTHWARE: PALENTIN VERSION 3.2
; SEQ ID NO 9765
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                                                                               308 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAAACAGCCTACATTGCC 367
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                                                                                                                               LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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                         US-09-830-972-2_COPY_975_1163 (1-189) x US-10-466-258-10 (1-1798)
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; ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/956.157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOCTWARE: PATENTIN VERSION 3.2
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TCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAGCTATCCAGAAATCAGAT 122
                                                                                   GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrlleLysGluLeuArgArg 105
                                                                                                      125
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                                                                                                                                                                                                      145
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                                           LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe
                                                                                                                                                                                                   ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeu
                                                                                                                                                                                                                                                                           423 GCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAATCCCTGGATTGAAG
                           GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal
                                                                                                                                                                        243 crerrerradireardarinagirearrereraagringeagrerreargregerarin
                                                                                                                                                                                                                                                              PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu
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; ORGANISM: Homo
US-10-956-157-9767
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Publication No. US20050118625A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Worth
APPLICANT: Wouts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTEOARTHATIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 9762
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                                                                  IleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArg
                                                                                   IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla
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             LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSer
                                                                                                                                                        ATATACAAGGGTGTGATCCAAGCTATCCAGAATCAGATGAAGGCCACCCATTCAGGGCA
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ORGANISM: Homo sapiens
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US-10-956-157-9762
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OTHER INFORMATION: Incyte ID No. US20030119009A1 092267CB1
                                                                                                                                                                                                                                Sequence 333, Application US/10084817
Sequence 333, Application US/10084817
Publication No. US20030119009A1
GENERAL INFORMATION:
APPLICANT: Shaan Stuart
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: ABOON M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
CURRENT APPLICANTON NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 365
SEQ ID NO 333
LENGTH: 1520
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-084-817-333
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Publication No. US20050118625A1
Fublication No. US20050118625A1
GENERAL INPORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, Worlescon Arguer 17TLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (Am 101081)
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NOS: 319805
SEQ ID NO 9766
LENGTH: 1400
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CRGANISM: Homo sapiens
US-10-956-157-9766
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US-10-956-157-9766
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Pred. No.:
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| GarnerAL Information:
| GarnerAL Information:
| TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer ITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer FILE REFERENCE: 689290-76
| FILE REFERENCE: 689290-76
| CURRENT PAPLICATION NUMBER: US/60/233,617
| PRIOR FILING DATE: 2000-09-18
| PRIOR FILING DATE: 2000-09-20
| PRIOR FILING DATE: 2000-09-20
| PRIOR FILING DATE: 2000-09-26
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  43 AlaLeuLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAlaIleGln
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Matches:
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Mismatches:
Indels:
Gaps:
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; Sequence 210, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
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84.49%
67.91%
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US-09-954-456-210
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Best Local Similarity:
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                                                                                                                                                                                   GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
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LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro
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                                                                    143 IleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHisTyr
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Matches:
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Mismatches:
Indels:
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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Kim, Jaeseob
TITLE OF INVENTION: Obesity Linked Genes
FILE REFRENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: PatentIn version 3.2
SEQ ID NO 213
LENGTH: 2331
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; ORGANISM: Homo sapiens
US-10-267-502-213
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Best Local Similarity:
Query Match:
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US-10-267-502-213
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2070 AAAACCGACGAAGGCCACCTTTCAAGGCCTACTTGGAGCTTGAGATCACCCTTTCTCAG 2129
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                                                                                                                                                                            83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
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; Sequence 386, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao Mao
; APPLICANT: Mao, Mao C.
; APPLICANT: Wan de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: User, Laura Dohanna
APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Van de Vijver, Marc J.
; PREMENT PETLION NUMBER: US/10/342,887
; CURRENT PILLOS DATE: 2003-01-18
; PRIOR PLILOS DATE: 2002-05-18
; PRIOR PLILOS DATE: 2002-05-14
; PRIOR PLILOS DATE: 2002-05-14
; PRIOR PLILOS DATE: 2002-05-14
; PRIOR PLILOS DATE: 2002-06-14
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                     LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu
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US-10-342-887-386
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 386, Application US/10172118
Publication No. US20030224374A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: He, Yudong
APPLICANT: Roberts, Chris
APPLICANT: Roberts, Chris
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
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DATABASE ENTRY DATE: 2001-06-18
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US-10-172-118-386
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LENGTH: 3202
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Sequence 3237, Application US/10843641A

Sequence 3237, Application US/10843641A

Bublication No. US20050064454A1

GENERAL INFORMATION:

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using

TITLE OF INVENTION: Signature Gene Sets

FILE REFERENCE: 689290-189

CURRENT APPLICATION NUMBER: US/10/843,641A

CURRENT FILING DATE: 2001-66-05

PRIOR FILING DATE: 2001-09-18

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

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PRIOR PLING DATE: 2001-09-28

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PRIOR PRIOR PLING DATE: 2001-10-03

PRIOR PLING DATE: 2001-10-03

PRIOR PLING DATE: 2001-10-03

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PRIOR PLING DATE: 2001-10-03

PRIOR PLING DATE: 2001-10-03

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                         1950 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGAGCGTCGTGGCCTACCTGGCCCTG 2009
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; Publication No. US20040253606A1
; Sequence 1480, Application US/20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aliaburg, Wendy M.
; APPLICANT: Clunk, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION Methods for Soft Tissue Sarcoma Modulators
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; WINDER APPLICATION NUMBER: 60/429,739
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 1480
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Publication No. US20030138803A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lee, Kevin
APPLICANT: Lee, Kevin
APPLICANT: Ee, Kevin
APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
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Conservative:
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679.00
84.49%
67.91%
73.41%
  SOFTWARE: Patentin version
SEQ ID NO 5926
LENGTH: 3305
                                                                                                     ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                               US-10-723-860-5926
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                                                                             TYPE: DNA
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Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: AA12, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators;
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators;
TITLE OF INVENTION: Methods 1023, 1040/723, 860
CURRENT APPLICATION NUMBER: US/10/723, 860
CURRENT FILING DATE: 2003-11-26
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
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SOFTWARE: PatentIn version 3.0 SEQ ID NO 3237
LENGTH: 3202
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679.00
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                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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US-10-723-860-5926
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Pred. No.:
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; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Mus m
US-10-267-502-215
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                                                              Alignment Scores:
  SEQ ID NO 215
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                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
TILE OF INVENTION: Obesity Linked Genes
TILE REPERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILLING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: PatentIn version 3.2
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                                                                                                              3.47e-72
678.00
84.49%
67.38%
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                                        TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
                                                                       ; OTHER INFORMATION: rS-Rex-s
US-10-205-219-94
         SOFTWARE: Patentin Ver. 2.
SEQ ID NO 94
LENGTH: 1502
 NOS:
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Percent Similarity:
Best Local Similarity:
Query Match:
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NUMBER OF SEQ ID
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US-10-267-502-215
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Sequence 8477 Application US/09960352
Sequence 8477 Application US/09960352
Sequence 8477 Application US/09960352
Sequence 8477 Application US/09960352
Setent No. US2002013133A1
GENERAL INFORMATION:
APPLICANT: Warren, Wagappan
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: MAINIAGAN, NAGABPAN
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILLE REFERENCE: 16511.006/37.21(10298)C
CURRENT APPLICATION NUMBER: US/0960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 8477
LENGTH: 422
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Best Local Similarity:
Query Match:
DB:
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205

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Sequence 11567, Application US/09960352

Batent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, NaGappan

APPLICANT: Byatt, John C.

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION NUMBER: US/09/960,352

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 11567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
                                                                                                                                                                                                                                                                                                        63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
                                                                                                206 CTGCTCTTCTCCCTGACCCAGTTCAGCGTTGTGAGCGTCGTCGCCTACCTGGCCCTG
                                                                                                                                                                                                                                      43 AlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValIleGlnAlaIleGln
                                                                                                                                                                                                                                                        266 GCTGCCCTCTCTGCCACCATCAGCTTCCGCATCTACAAGTCCGTTCTACAAGCTGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu
                                                                  US-09-830-972-2_COPY_975_1163 (1-189) x US-10-205-194-128 (1-1473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 50-BOVMS1-005-Q1-E1-E6
US-09-960-352-11567
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Best Local Similarity:
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Best Local Similarity:
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US-09-960-352-11567
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US-10-205-194-128
i Sequence 128, Application US/10205194
j Publication No. US20030134301A1
i GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
APPLICANT: Brooksbank, Robert
APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
APPLICANT: Pinnock, Robert
APPLICANT: Brookspank, Sobert
CURRENT APPLICANT: Udentification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 5200-07-24
PRIOR PILICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 177-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 ValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLys 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 AsnSerThr11eLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 AAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 LeuLeulleLeuAlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGln 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCCATATTTGGAATCT 121
                                                                                                                                                                                                                                                                                                                                                                                                                          122 GAAGTIGCTATATCTGAGGAGTIGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 GCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA 421
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                                                                                                                                                                                                                                                                                                                         ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 ThralaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly
                                                                                                                                                                                                                                                                          2 ACGGCCTACATTGCCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGT
                                                                                                                                                                                                                                                                                                                                                                                         77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal
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               ) ORGANISM: Bos taurus
) OTHER INFORMATION: Clone ID: 36-LIB34-048-01-E1-A8
US-09-960-352-8477
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Conservative:
Mismatches:
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SEQ ID NO 128
LENGTH: 1473
                                                                                                                             Percent Similarity:
Best Local Similarity:
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 TYPE: DNA ORGANISM:
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Query Match: 71.03% indels: DB: 9 Gaps:	0.0	qa —	259 ATCCTGGCTCTTCTCT
72-2_COPY_975_1163 (1-189)	x US-09-960-352-11567 (1-422)	8 1	
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle :::	erlleValSerValThrAlaTyrlle 40	8 & 	319 GTACAGAAGTCAGAAG 81 SerGluGluLeuValG
41 Ala		qa	379 rccrcagaagcrrrcc
64		<i>à</i> 1	101 LysGluLeuArgArgL
Oy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle		8 &	439 AAACTCATTATTCGCC
\$7T		දුය	
Qy 81 SerGluGluLeuValGlnLy8TyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	aleuGlyHisValAsnSerThrIle	ò	141 AlaLeulleSerLeuP
101 Lys	euValAspSerLeuLysPheAlaVal 120	<u>.</u>	559 GCTGAACTGCTCATTT 161 HisTyrLeuGlyLeuA
244		ි අ <u>ග</u>	
OY 121 DEWNETTPART PROPERTY OF THE PROPERTY OF	neAsnGlyLeuThrLeuLeuIleLeu 140 	ò	181 IleProGlyLeuLy
Oy 141 AlaLeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGhnIle	rGluarghisGlnValGlnIle 159 	DD RESULT 11S-10-1	679 55 06-698-
ods	of Treating Alzheimer's Disease	% & 15	Sequence 1945, Application UR Publication No. US2003010969 GENERAL INFORMATION: APPLICANT: Ruben et al. TITLE OF INVENTION: Colon an FILE REFERENCE: PA005P1 CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2002-6 PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: UP PRIOR APPLICATION NUMBER: UP PRIOR PILING DATE: 1999-09-09-09-09-09-09-09-09-09-09-09-09-
CORRENT FILING DATE: 2003-04-08 NUMBER OF SEQ ID NOS: 9 SEQ ID NO 1 LENGTH: 711 TYPE: DNA		Ø	PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-11-(NUMBER OF SEQ ID NOS: 8564 SOFTWARE: Patentin Ver. 3.0 IEQ ID NO 1945 LENGTH: 1330
US-10-408-967-1		; ; US-1	TYPE: DNA ORGANISM: Homo sapiens 10-106-698-1945
Pred. No.: 6.59e-66 Length: 622.50 Matches: 622.50 Matches: Percent Similarity: 81.05\$ Conservative: Best Local Similarity: 59.47\$ Mismatches: Query Match: 18 Indels: DB:	711 113 141 3: 15 1	Alignm Pred Score: Percen Best L	Alignment Scores: Pred. No.: Score: 622.50 Percent Similarity: 81.05% Best Local Similarity: 59.47% Query Match:
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-408-967-1	3-967-1 (1-711)	- 113-	US-09-830-972-2 COBV 975 1163
Oy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla :::		, , , ,	1 SerValValAspleule
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Db 199 ACGCTGATCATGCTTTCCCTGGCAGCTTTCAGTGTCAGTGTGGTTTTCTTACCTC	::::: TGTCATCAGTGTGTTTCTTACCTC 258	Š	
Qy 41 AlaLeuAlaLeuLeuSerValThrILeSerPheArgIleTyrLysGlyValIleGlnAla	GlleTyrLysGlyVallleGlnAla 60	~ <i>&</i>	41

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and Colon Cancer Associated Polynucleotides and Polypeptida
                              OGLUGIYHISProPheArgAlaTyrLeuGLUSerGLUValAla11e 80
                                                                                                                                                      LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
                                                                                                                                                                                                                  ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu11eLeu 140
                                                                                          GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                                                                                                                                                                                                                                             PheserileprovalileTyrGluArgHisGlnValGlnIleAsp 160
                                                                                                                                                                                                                                                                                                                                            AlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                             CATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTG 438
TCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 318
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Matches:
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Mismatches:
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US 60/157,137

US 60/163,280
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121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                                                                                                                                                                                                                                                                                                                      101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
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                                                                                                          225 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTTCTTACCTC 284
                                                                                                                                                                                                                                                            345 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 404
                                                                                                                                                                                                                                                                                                                81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
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645 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCCAATGTTGAAAAAGATCCAAGCAAAA 704
                                                                                                                                                                                                                                      61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
                                    41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                                                                  285 ATCCTGGCTCTTCTCTCTGTCACCTTCAGGATCTACAAGTCCGTCATCCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAsp
                                                                                         21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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CURRENT APPLICATION NUMBER: US/10/913,553
CURRENT FILING DATE: 2004-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 IleProGlyLeu---LysArgLysAlaAsp 189
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PRIOR APPLICATION NUMBER: US/09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
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Fechtel, Kim
Genetics Institute, Inc.
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US-10-913-553-19
Sequence 19, Application US/10913553
Publication No. US20050003491A1
GENERAL INFORMATION:
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Steininger II, Robert
Spaulding, Vikki
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APPLICANT: MCCOY, JOHN M.
BENLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
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Merberg, David
Treacy, Maurice
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; ORGANISM: Homo sapiens
US-10-913-553-19
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SEQ ID NO 19
LENGTH: 1656
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                                                                             141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
                   417 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 476
                                                                                                                                SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                                                                                                                                                                       LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
                                                                                                                                                                                                                                                                               121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIeLeu 140
                                                                                                                                                                                                                                                                                                                                                                                          717 GCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    777 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 836
                                                    61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaile 80
                                                                                                                                                                                                                           657 TTCATGIGGCIGATGACCTATGITGGTGCTGTTTTTAACGGAATCACCCTTCTAAITCTT
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APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILIG DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
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Conservative:
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Patent No. US20010039335A1
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Steininger II, Robert
Spaulding, Vikki
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LaVallie, Edward R.
Collins-Racie, Lisa
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Treacy, Maurice
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Clark, Hilary
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US-09-729-674-19
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LENGTH: 1656
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TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 1459.004/200130.449
CURRENT APPLICATION NUMBER: US/10/347,669
CURRENT FILING DATE: 2003-01-16
                                                                                  x US-09-765-205-25 (1-1668)
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777 CTCCCTGGAATCGCCAAAAAAAAAAAGGCAGAA 806
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PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-347-669-25; Application US/10347669; Publication No. US20050084850A1; GENERAL INFORMATION:
                                                                                  US-09-830-972-2_COPY_975_1163 (1-189)
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; ORGANISM: human
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Patent No. US20020034800A1
GENERAL INFORMATION:
APPLICANT: COO, Li
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 1458.004/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT PILING DATE: 2001-01-17
PRIOR PILING DATE: 1998-12-16
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SOFTWARE: FastSEQ for Windows Version 3.0
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Query Match: 67.30% Indels: 1 DB: 21 Gaps: 1 US-09-830-972-2_COPY_975_1163 (1-189) x US-10-347-669-25 (1-1668) Oy 1 ServalValAspLeuLeuTyrTrpAxgAspIleLysLysThxGlyValValPheGlyAla 20 Db 237 GCGGTGCACGATCTGATTTTCTGGAGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 296	Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40	357 ATCTGGCTCTTCTCTGTCACCATCAGGATCTACAAGTCGTCATCCAAGGCT 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle ::: :::	Oy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100	Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120	Qy 121 LeumetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIeLeu 140 ::	Qy . 141 AlaLeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAsp 160	Oy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180	Oy 181 IleproglyLeuLysargLysalaAsp 189 ::: :: :: Db 777 CTCCCTGGAATGGCCAAAAAGGCAGAA 806	RESULT 60 US-09-809-391-254 Sequence 254, Application US/09803391 Sequence 254, Application US/09803391 GENERAL INFORMATION: APPLICANT: Ruben et al. TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P2 CURRENT APPLICATION NUMBER: US/09/809,391 CURRENT FILING DATE: 2001-03-16 Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761 SEQ ID NO 254 LENGTH: 1766 TYPE: DNA CORGANISM: Homo sapiens US-09-809-391-254	. 440

8: 60/04 8: 60/04 8: 60/04 105-23 8: 60/04 8: 60/04 8: 60/04 8: 60/04 8: 60/04 8: 60/04 8: 60/04 8: 60/04 8: 60/04		1997-04-11 NUMBER: 60/043,568 1997-04-11 NUMBER: 60/043,314 1997-04-11 NUMBER: 60/043,511 1997-04-11 NUMBER: 60/043,671 1997-04-11 NUMBER: 60/043,674 1997-04-11 NUMBER: 60/043,674 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,313 NUMBER: 60/043,313 NUMBER: 60/043,914 NUMBER: 60/043,914 NUMBER: 60/043,914 NUMBER: 60/043,914 NUMBER: 60/043,914 NUMBER: 60/043,914 NUMBER: 60/043,914 NUMBER: 60/043,914 NUMBER: 60/048,914 NUMBER: 60/048,914 NUMBER: 60/048,914 NUMBER: 60/048,914 NUMBER: 60/056,886 NUMBER: 60/056,817 NUMBER: 60/056,817 NUMBER: 60/056,817
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PRIOR PELICATION NUMBER: 60/056, 893
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Mismatches:
Indels:
                                                                    Sequence 254, Application US/10164861
Publication No. US20030225248A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 186 Human Secreted proteins
TITLE OF INVENTION: 186 Human Secreted proteins
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
FRIOR APPLICATION NUMBER: PCT/US98/04493
FRIOR FILING DATE: 1998-09-08
NUMBER: OF SEQ ID NOS: 757
SOFTWARE: PatentIn Ver. 2.0
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       CTCCCTGGAATCGCCAAAAAAAGGCAGAA 856
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                          RESULT 62
US-10-164-861-254
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PRIOR APPLICATION NUMBER: 60/056,664
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR PELLING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,881
PRIOR PLING DATE: 1997-08-22
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PRIOR PELLING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,862
PRIOR APPLICATION NUMBER: 60/056,862
PRIOR APPLICATION NUMBER: 60/056,867
PRIOR PELLING DATE: 1997-08-22
PRIOR PELLING DATE: 1997-08-22
PRIOR PELLING DATE: 1997-06-06
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Sequence 980, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyesq, Inc.

APPLICANT: Tang, Y, Tom et al.

ITILE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-030

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SEQ ID NO 980

LENGTH: 1915
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; ORGANISM: Homo sapiens
US-10-276-774-980
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Best Local Similarity:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                       APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REPRENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM ox
NUMBER OF SEQ ID NOS: 761
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 255
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,672
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                        APPLICATION NUMBER: 60/047,582
                                                           PPLICATION NUMBER: 60/047,596
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ING DATE: 1997-04-11
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FILING DATE: 1997-06-06
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  682 GCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 741
                                                                           742 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 801
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TITLE REPERENCE: P2002P2
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CURRENT PILING DATE: 2001-03-16
PRIOR PELICATION NUMBER: 09/49,476
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Publication No. US20030175858A1
GENERAL INFORMATION:
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            PRIOR PRING DATE: 1997-08-22
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Length:
Matches:
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Percent Similarity: Best Local Similarity: Query Match:

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SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PSOLO2P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT PILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR PILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 255
LENGTH: 2664
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LOCATION: (2640)
OTHER INFORMATION: n equals a,t,g,
FEATURE:
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (2623)
OTHER INFORMATION: n
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PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 6867
LENGTH: 2768
                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                      NAME/KEY: misc feature
LOCATION: (2743)..(2747
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Best Local Similarity:
Query Match:
DB:
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Publication No. US20040253606A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Albert
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Slotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions (TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REPERENCE: 05882.0193.NPUS01
CURRENT PAPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
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Matches:
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81.05%
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                                                   NAME/KEY: SITE
LOCATION: (2662)
OTHER INFORMATION:
             LOCATION: (2652)
OTHER INFORMATION:
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  NAME/KEY: SITE
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Sequence 449, Application US/10108260A
PUBLICATION NO. US20040005560A1
GENERAL INFORMATION:
TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
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Mismatches:
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Publication No. US20040009154A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
FILE REPERENCE: 11613-56021
CURRENT PAPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
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NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 449
LENGTH: 3637
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Query Match:
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                                                            ; ORGANISM: Homo
US-10-108-260A-449
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Matches:
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Indels:
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1919 CTCCCTGGAATCGCCAAAAAAAGGCAGAA 1948
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Publication No. US20020039760A1
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukoca, Kamalakar
APPLICANT: Gulukoca, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                    US-09-830-972-2_COPY_975_1163 (1-189)
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SOFTWARE: Patentin version 3.1
SEQ ID NO 443
LENGTH: 3637
                                                                                                                                                                                              3.47e-64
617.50
80.53%
59.47%
66.76%
                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                 ; ORGANISM: Homo
US-10-159-563-443
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US-09-823-245A-510
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us-09-830-972-2_copy_975_1163.rnpb

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727 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS FILE REFERENCE: GIN 6401
CURRENT APPLICATION NUMBER: US/09/823,245A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/194,941
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver. 2.0
LENGTH: 1636
                                                                                                                                                                                                                                                                                                                         US-09-830-972-2_COPY_975_1163 (1-189) x US-09-823-245A-510 (1-1636)
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112
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Matches:
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787 CTCCCTGGAATCGCCAAAAAAAGGCAGAA 816
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; Sequence 5154, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nenghing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
                                                                                                                                                                                                                    4.87e-62
595.50
80.53%
58.95%
64.38%
                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                             US-09-823-245A-510
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Pred. No.:
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TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REFERENCE: 16511.006/37-21 (10298) C CURRENT APPLICATION NUMBER: US/09/960,352 CURRENT APPLICATION NUMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 15112 SEQ ID NO 5154 LENGTH: 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC ACID AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9092
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB34-043-Q1-E1-F5
US-09-960-352-5154
                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
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Matches:
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Patent No. US20020137139A1
GENERAL INFORMATION:
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563.00
99.15%
98.31%
60.86%
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US-09-960-352-9092
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2966 CIGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTTGTTCTTACCTCTCATC 3025
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                             LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr1leAla 41
                                                                                                                                                                                                   62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlalleSer
                                                                                                                LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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Publication No. US20040063131A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Au-Young, Janice
Goli, Surya K.
Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ValGlnIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/228,213A FILING DATE: «UNKNOWN» APPLICATION NUMBER: 08/700,607 FILING DATE: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/660,946
FILING DATE: 12-Sep-2003
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP.: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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Sequence 111, Application US/10302172

Publication No. US20040053250A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Polypeptides

FILE REFERRENCE: 803 LCNCP

TITLE OF INVENTION: Polypeptides

FILE REFERRENCE: 803 LCNCP

CURRENT APPLICATION NUMBER: US/10/302,172

CURRENT APPLICATION NUMBER: US 10/225,251

PRIOR PAPLICATION NUMBER: PCT US02/05095

PRIOR APPLICATION NUMBER: PCT US02/05095

PRIOR APPLICATION NUMBER: PCT US02/05095

PRIOR PLING DATE: 2001-03-05

PRIOR APPLICATION NUMBER: US 09/799,451

PRIOR APPLICATION NUMBER: US 09/799,451

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                                                                                                                                                                                                                       GlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuVal 113
                                                                                                                                                                                                                                                                                                            AspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsn 133
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                                                                                                                                                                                                                                              TTGGAATCTGAAGTTGCTATATCTGATGAGGTTGGTTCAGAAGTACAGCAATTCTGCTCTT
                                                                                                                                                                                                                                                                                                                                               GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT
                                                                                                                              LeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 ATGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAA 350
                                                                                    US-09-830-972-2_COPY_975_1163 (1-189) x US-09-960-352-9092 (1-423)
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Conservative:
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Gaps:
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Best Local Similarity:
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US-10-302-172-111
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                    Query Match:
DB:
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102
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Mismatches:
Indels:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs
TYPE: nucleic acid
STYPE: nucleic acid
STYPE: nucleic acid
STYPE: nucleic acid
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Matches:
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US-10-867-502-211
Sequence 211, Application US/10267502
; Publication No. US20040071700A1
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524.50
72.77%
53.40%
56.70%
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LIBRARY: THPINOB01
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Best Local Similarity:
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Matches:
Conservative:
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Indels:
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APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Patentin version 3.2
LENGTH: 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 102, Application US/09809391; Publication No. US20030049618A1; GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secret; FILE REFERENCE: PZ002P2
                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                         2.05e-53
520.00
74.59%
51.93%
56.22%
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US-09-809-391-102
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                                                                                                                                                   TYPE: DNA
ORGANISM: I
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DB:
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TELING DATE: 1998-09-08

R PELING DATE: 1998-09-08

R FILING DATE: 1998-03-08

R FILING DATE: 1998-03-07

R FILING DATE: 1997-03-07

R APPLICATION NUMBER: 60/040,333

R FILING DATE: 1997-03-07

R APPLICATION NUMBER: 60/038,621

R FILING DATE: 1997-03-07

R APPLICATION NUMBER: 60/040,626

R FILING DATE: 1997-03-07

R APPLICATION NUMBER: 60/040,334

R FILING DATE: 1997-03-07

R APPLICATION NUMBER: 60/040,336

R FILING DATE: 1997-03-07

R PILING DATE: 1997-03-07

R PELICATION NUMBER: 60/040,336

R FILING DATE: 1997-03-07

R PELICATION NUMBER: 60/040,163

R PILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R APPLICATION NUMBER: 60/047,584
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,500
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,587
R FILING DATE: 1997-05-23
R RAPLICATION NUMBER: 60/047,492
R FILING DATE: 1997-05-23
R RILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,612

R FILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,601
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APPLICATION NUMBER: 60/047,615
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,583
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,618
FILING DATE: 1997-05-23
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ILING DATE: 1997-05-23
PPLICATION NUMBER: 60/047,592
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-05-23
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,671
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APPLICATION NUMBER: 60/047,581
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                    CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 102
LENGTH: 794
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US-09-882-171-102

is Sequence 102, Application US/09882171

is Publication No. US20030175858A1

is GENERAL INFORMATION:

i APPLICANT: Ruben et al.

if TITLE OF INVENTION: 186 Human Secreted proteins

if PILE REFERENCE: PZ002P2

if CURRENT APPLICATION NUMBER: US/09/882,171

if CURRENT FILING DATE: 2001-06-18

if PRIOR PILING DATE: 2001-06-18
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Matches:
Conservative:
Mismatches:
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Gaps:
CURRENT APPLICATION NUMBER: US/09/809,391
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55.08%
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CORGANISM: Homo sapiens
US-09-809-391-102
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Query Match:
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PRIOR FILING DATE: 1997-04-11

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PRIOR APPLICATION NUMBER: 60/056, 819

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R APPLICATION NUMBER: 60/056,911

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R APPLICATION NUMBER: 60/056,636

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,874

R APPLICATION NUMBER: 60/056,910

R PILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,864

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,864

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APPLICATION NUMBER: 60/047,585
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APPLICATION NUMBER: 60/047,599
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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Matches:
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Best Local Similarity:
Query Match:
DB:
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LENGTH: 878
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                              spHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180
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                                                                                                                                                                               |||||| ::: ::::::|||||||::::||| TTGCTGATTGTCTATGAGAAGTACAAGACCCAGATTG
                                                  alleuWetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL
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TGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCC
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APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins;
FILE REFERENCE: PZ002P1

CURRENT APPLICATION NUMBER: US/10/164,861

CURRENT PILING DATE: 2002-06-10

PRIOR PPLICATION NUMBER: US/9/149,476

PRIOR FILING DATE: 1998-03-06

PRIOR FILING DATE: 1998-03-06

NUMBER OF SEQ ID NOS: 757

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 102

LENGTH: 794
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Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20030225248A1
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DB:
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; ORGANISM: HOMO
US-10-164-861-102
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US-10-164-861-102
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Pred. No.:
492
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                                                      US-10-264-237-163

Sequence 163, Application US/10264237

Sequence 163, Application US/10264237

PUBLICAGE 163, Application US/10264237

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: PA131P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

FRIOR PAPLICATION NUMBER: PCT/US01/16450

FRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR APPLICATION NUMBER: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: Patent IN Ver. 3.1

LENGTWARE: PATENTING DATE

LENGTWARE: PATENTION OF 13.1
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NAME/KEY:
LOCATION: (198]..(198)
OTHER INFORMATION: n equals a,t,g, 0)
FEATURE:
NAME/KEY: misc feature
LOCATION: (5667..(566)
OTHER INFORMATION: n equals a,t,g, 0)
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LOCATION: (632)..(632)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (579)..(579)
OTHER INFORMATION: n equals
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LOCATION: (586)...(586)
OTHER INFORMATION: n equals
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LOCATION: (590)..(590)
OTHER INFORMATION: n equals
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97.22%
53.30%
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ORGANISM: Homo sapiens
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                                                                                                                                                                  142 LeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                                          572 TGGGTCGCCCTTTTCCCTCTTCCAAAGCTTTTCGAAGTAAACAAGACTCAAATCGATGCT 631
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                                                                                                                                                                                                                                                           LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeu 103
                        GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                        US-09-830-972-2_COPY_975_1163 (1-189) x US-09-918-995-15830 (1-489)
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15830, Application US/09918995
; Sequence 15830, Application US/09918995
; Publication No. US2003007362341
; GENERAL INPORMATION:
APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR PILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTHARE: PSECSEQ for Windows Version 3.0
; SEQ ID NO 15830
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Matches:
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LOCATION: (1)...(489)
OTHER INFORMATION: n = A,T,C or
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62.76%
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Best Local Similarity:
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Sequence 3043, Application US/10723860

GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions of TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE. 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: 105/10/723,860
CURRENT FILING DATE: 2003-11-26
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: Incyte ID No: 7503970CB1
US-10-491-213-80
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70.33%
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                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
SOFTWARE: PERL Program
SEQ ID NO 80
LENGTH: 2017
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APPLICANT: RANGUMAR, JOSEPh P.; NGUYEN, DANIEL B.;
APPLICANT: RANGUMAR, JOSEPh P.; NGUYEN, DANIEL B.;
APPLICANT: RANGUMAR, JOSEPh P.; NGUYEN, Thomas W.;
APPLICANT: TANG, Y. Tom, TRAN, UPW. K.;
APPLICANT: TANG, Y. Tom, TRAN, UPW. K.;
APPLICANT: TANG, WARREN, Bridget A.; XU, Yuming;
APPLICANT: YAO, MONIQUE G.; YUE, Huibin;
APPLICANT: YO, MONIQUE G.; YUE, Huibin;
APPLICANT: YO, MONIQUE G.; YUE, Huibin;
APPLICANT: YO, MONIQUE G.; YUE, Huibin;
APPLICANT: YO, WORER: USOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REPERRNCE: PF-1213 USN
CURRENT APPLICATION NUMBER: US 60/326,389
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
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                                                                                 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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PRIOR FILING DATE: 2001-11-09
Remaining Frior Application data removed - See File Wrapper or PALM.
WUMBER OF SEQ ID NOS: 114
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-264-237-163 (1-668)
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APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
APPLICANT: BOROWSKY, Mark L.; CHAMLA, Narinder K.;
APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.;
APPLICANT: GANDHI, Ameena R.; GIRFIZEN, Kimberly J.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
APPLICANT: KABLE, Amy B.; KALAFUS, Daniel P.;
APPLICANT: KABLE, Amy B.; KALAFUS, Daniel P.;
APPLICANT: MAKGUIS, JOSEPH P.; NGUYEN, Danniel B.;
APPLICANT: RAMKUMAR, Jayalaxmi; RICHARDSON, Thomas W.;
APPLICANT: RAREHY, Stephanie K.; SWARNAKAR, Anita;
APPLICANT: TANG, Y. TOM; TRAN, Uyen K.;
APPLICANT: TANG, Y. TOM; TRAN, Yuing;
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; Sequence 80, Application US/10491213
; Publication No. US20050048490A1
; GENERAL INFORMATION:
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Sequence 51318
Sequence 51318 Application US/10424599
Sequence 51318 Application US/10424599
SUBJICATION OF US20040031072A1
SEQUENCE 51318 APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
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PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 7073
LENGTH: 3044
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US-10-723-860-7073
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Best Local Similarity:
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                                                                                                  TYPE: DNA
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UG-10-723-860-7073

UG-10-723-860-7073

Sequence 7073, Application US/10723860

Publication No. US20040255606A1

GENERAL INFORMATION:
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Clonik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUSG);
CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT FILING DATE: 2003-11-26
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Matches:
Conservative:
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Indels:
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PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 3043
LENGTH: 2190
                                                                                                                                                                              4.18e-47
475.00
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                                                                                              ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-723-860-3043
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Publication No. US20040013653A1

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

APPLICANT: ChondroGene Inc.

TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

TITLE OF INVENTION: 2002-09-12

FILE REFERENCE: 4231/2005

CURRENT FILING DATE: 2002-09-12

FRIOR PLICATION NUMBER: US 10/085,783

FRIOR FILING DATE: 2002-02-28

FRIOR FILING DATE: 2002-02-28

FRIOR FILING DATE: 2001-07-13

FRIOR FILING DATE: 2001-07-13

FRIOR FILING DATE: 2001-07-13

FRIOR FILING DATE: 2001-07-13
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Matches:
Conservative:
Mismatches:
Indels:
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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 51318
LENGTH: 613
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Best Local Similarity:
Query Match:
DB:
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US-10-242-535A-17576
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Sequence 17576, Application US/10085783A; Sequence 17576, Application US/10085783A; Publication No. US20040037841A1; Sequence 17576, Application No. US20040037841A1; Publication No. US20040037841A1; Septiment Information: Compositions and Methods Relatiing to Osteoarthritis APPLICANT: Liew, C.C.; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis File Reference: 4231/2002 202-02-28; CURRENT FILING DATE: 2001-07-13; PRIOR APPLICATION NUMBER: US 60/305,340; PRIOR PELING DATE: 2001-07-13; PRIOR PELING DATE: 2001-07-13; PRIOR PELING DATE: 2001-03-12; PRIOR PELING DATE: 2001-03-12; PRIOR PELING DATE: 2001-03-12; PRIOR PELING DATE: 2001-03-12; PRIOR PELING DATE: 2001-03-12; PRIOR PELING DATE: 2001-03-12; PRIOR PELING DATE: 2001-03-12; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING DATE: 2001-03-18; PRIOR PELING D
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PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17576
LENGTH: 566
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SOFTWARE: Patentin version
SEQ ID NO 17576
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US-10-085-783A-17576
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US-10-085-783A-17576
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US-10-764-420-1065
; Sequence 1065, Application US/10764420
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagapan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21 (10299)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2205
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                                                                                   GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr11eLysGluLeuArgArg
                                                                                                         1 CAGAAGCACAGTAATTCTGCTCTTGG-CATGTGAACTGCACGATAAAGGAACTCAGGCGC
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                                                                                                                                                    106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe
                                                          US-09-830-972-2_COPY_975_1163 (1-189) x US-10-085-783A-17576 (1-566)
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Clone ID: 10-LIB3058-011-01-K1-C5
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Matches:
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428.00
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93.27%
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Best Local Similarity:
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NAME/KEY: unsure
LOCATION: (309)
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US-09-960-352-2205
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Pred. No.:
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(53222)B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2009-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 152719
                                                                                                                                                                                                                                                                                                                                                                                                                                             705 TIGTIGICGTICGCATATAIGICACIGATIAGCGIAGCITGCTIAICTIGGCIAIGTICAIA 646
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: PZ039P1
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/130,991
                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_70862C.1 US-10-425-115-152719
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375.00
67.72%
43.04%
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Best Local Similarity:
                                                                                                                                          TYPE: DNA ORGANISM: Zea mays
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Pred. No.:
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US-10-050-704-93
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Publication No. US20050084872A1
GENERAL INFORMATION:
APPLICANT: Lum, Pek Yee
APPLICANT: Dai, Yejun
APPLICANT: Dai, Yejun
TITLE OF INVENTION: Methods For Determining Whether An Agent
TITLE OF INVENTION: Possesses A Defined Biological Activity
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Matches:
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CURRENT APPLICATION NUMBER: US/10/764,420
CURRENT APPLICATION NUMBER: US/10/764,420
FINCH APPLICATION NUMBER: US 60/442,797
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 3683
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1065
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Gaps:
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Sequence 152719, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: 267, 544, 623
OTHER INFORMATION: n = A,T,C or
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385.00
78.86%
60.16%
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Matches:
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Mismatches:
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Publication No. US20040152164A1
GENERAL INPORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: PEO3391
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT APPLICATION NUMBER: US/09/684,524
PRIOR APPLICATION NUMBER: DC7/US00/08979
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-6.06
PRIOR FILING DATE: 1909-04-06
PRIOR FILING DATE: 1909-04-06
PRIOR FILING DATE: 1909-04-06
PRIOR FILING DATE: 1909-04-06
PRIOR FILING DATE: 1909-04-06
PRIOR FILING DATE: 1909-04-06
NUMBER OF SEQ ID NOS: 344
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359.50
77.50%
54.17%
38.86%
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 93
LENGTH: 2454
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ORGANISM: Homo sapiens
FEATURE:
                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
                                                                                                            FEATURE:
NAME/KEY: SITE
LOCATION: (2317)
                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
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US-10-798-512-93
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LENGTH: 2454
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NAME/KEY: SITE

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131 LeupheAsnGlyLeuThrLeuLeulleLeuAlaLeuIleSerLeupheSerIleProVal 150 :::||||||||||::|||||:::
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                                                                                                                                                                                                                                                                                                                                             59 AGAGCCTACCTGGACGTAGACATTACTCTGTCCTCAGAAGCTTTCCATAATTACATGAAT
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NAME/KEY: unsure
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Sequence 3484, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

FILE REFERENCE: 44921-5028-W0

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                                                                         x US-10-798-512-93 (1-2454)
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Mismatches:
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; OTHER INFORMATION: n = a or c or g or
US-09-880-107-3484
                          or
; LOCATION: (2317)
; OTHER INFORMATION: n equals a,t,g,
US-10-798-512-93
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3484
LENGTH: 639
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Best Local Similarity:
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Best Local Similarity:
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                                                                                                     RESULT 96

US-10-427-741-9

Sequence 9, Application US/10427741

Publication No. US20040191291A1

GENERAL INFORMATION:
APPLICANT: Tohyama, Masaya
APPLICANT: Yamashita, Toshihide
TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
FILE REFRENCE: 5915-8023
CURRENT APPLICATION NUMBER: US/10/427,741

CURRENT FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-04-30
PRIOR PILICATION NUMBER: UP 2003-92923

PRIOR FILING DATE: 2003-03-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-830-972-2_COPY_975_1163 (1-189) x US-10-427-741-9 (1-60615)
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5532
LIBROTH: 497
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Matches:
Conservative:
Mismatches:
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                        62 GlnLysSerAspGluGlyHisProPheArg
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 25
SOFWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 60615
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Best Local Similarity:
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US-09-918-995-5532
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                         473 TAGGAGTGGGTCANAAGTCAAGAATCTGTCT------GGGCANGTGAACTG-AC 519
                                                                                                                                                  233 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 292
                                                                                                                                                                                                                                   293 crarrccrecrecrircarreacagrarrcagearrereagegraacagneracarrece 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/10633423
; Sequence 9, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; APPLICANT: Yamashita, Toshihide
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; CURRENT APPLICATION NUMBER: US/10/633,423
; CURRENT FILING DATE: 2003-07-11
; PRIOR PELLING DATE: 2003-07-11
; PRIOR PILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9;
                                                            US-09-830-972-2_COPY_975_1163 (1-189) x US-09-880-107-3484 (1-639)
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; ORGANISM: Mus musculus
US-10-633-423-9
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Pred. No.:
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US-10-633-423-9
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Query Match:
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NAME/KEY: unsure

COCATION: 25, 37, 57, 82, 119, 150, 174, 184, 202, 217, 225, 303, 332, 354, 100 and 25, 375, 429, 443, 490, 509, 523, 527, 547

COCATION: 375, 429, 443, 490, 509, 523, 527, 547

CTHER INFORMATION: unknown base
                                                                                                                                             265 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTNATCAGTGTTTCTTACTC 324
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              323 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGGGGTTTCTTACCTC
                                                           41 AlaLeuAlaLeuLeuServalThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                         61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlalle
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SerieuPheleuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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                                                                                           383 Arcciedercriciciererenciacearcaderreadanteracaagreegrearecaader
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APPLICANT: Baker Kevin P.
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TILE OF INVENTION: NOVEL POLYNUCLEOTIDES AND METHOD OF USE THEREOF
FILE REPERBNCE: P2751R1C1
CURRENT APPLICATION NUMBER: US/10/052,283
CURRENT PILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: PCT/US00/20006
PRIOR APPLICATION NUMBER: US 60/145,701
PRIOR PILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 564
SEQ ID NO 128
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Indels:
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Publication No. US20030064379A1
GENERAL INFORMATION:
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71.19%
54.24%
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ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
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US-10-052-283-128
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                                                                                                                                                                                                                                                                                                                                                                                      236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 GATCAGACCAAGTCAATTGTTGAAAGATCCAAGCAAAACCACCCTGGAATCGCCAAAAAA 356
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                                                                                                                                                                                                                                            237 GTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGATCACTATGTTGGCATCGCCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 401, Application US/10101510
Fublication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
TITLE OF INVENTION:
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
FRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: Patentin Ver. 2.1
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LOCATION: (1)...(497)
OTHER INFORMATION: n = A,T,C or
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357 AAGGCAGAA 365
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, ORGANISM: Homo sapiens
US-10-101-510-401
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Best Local Similarity:
                                                                                                            Percent Similarity:
Best Local Similarity:
   ; LOCATION: (1)...; OTHER INFORMATIUS-09-918-995-5532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 98
US-10-101-510-401
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LENGTH: 573
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DB:
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US-09-758-140-19

Sequence 19, Application US/09758140

Sequence 19, Application US/09758140

Sequence 19, Application US/0012965A1

Sequence 19, Application US20020012965A1

SETURENT Strittmatter, Stephen M.

TITLE OF INVERTION: NO. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth

FILE REPERENCE: 44574-5073-US

CURRENT APPLICATION NUMBER: US/09/758,140

CURRENT PILING DATE: 2001-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 19

LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (1). (198)
CTHEN INFORMATION: Full receptor binding region of No. US20020012965Alo gene
US-09-758-140-19
80 eSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr11 100
                          SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLygTyrSerAsn 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 PheArgileTyrLysGlyValileGlnAlaIleGlnLysSerAspGluGlyHisProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC
                                                                                100 elysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLys 117
                                                                                                             US-09-830-972-2_COPY_975_1163 (1-189) x US-09-758-140-19 (1-198)
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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CR56672 DKEZP469C
AL573494 AL573494
CR611869 Eul1.1eng
AF077050 Homo sapi
B1079496 602876306
AU297347 AU297347
CV030029 9024 Full
CN646472 LLLUMIGEN
CN64721 11CHUMIGEN
CN64721 11CHUMIGEN
AK034902 Mus muscu
B1611132 60214519
CK357937 AGENCOURT
AA986233 uC77312.9
CC735185 SILE04610
BM801698 AGENCOURT
BG56048 602393712
BG715173 602675631
BG36048 602393712
BG715173 AGENCOURT
CN865577 ILLUMIGEN
CD110203 AGENCOURT
BUG502291 AGENCOURT
BG36048 602393712
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CN865577 ILLUMIGEN
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National Institutes of Health, Mammalian Gene Collection (MGC)
Lunpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUBULABS 779 bp MRNA linear EST 01--
AGENCOURT 26749547 NIH MGC_255 Rattus norvegicus cDNA clone
TMAGE:1317070 5', mRNA sequence.
                    CK977984
CB162885
CK971318
CK971318
CD102817
BG697436
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AF077050
BI079496
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CB067821
CV030029
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AK034902
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CN482802
CO735185
BM801698
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CK357937
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VERSION
KEYWORDS
SOURCE
ORGANISM
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CO401465
LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-O=/Cqn2_1/USPTO_spool_pJUS09830972/runat_16062005_153945_19031/app_query.fasta_1.654
-O=/Cqn2_1/USPTO_spool_pJUS09830972/runat_16062005_153945_19031/app_query.fasta_1.654
-DB=ST_QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LLOOPEXT=0
-UNITG=bits -START=1 -END=-1 -MATRIX=blosmin62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIE=00000000
-USREW1505930972 @GGM 1 1 6628 @runat_16062005_153945_19031 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AY404972 Mus muscu
B1149602 602848410
B1157842 602923001
AU080127 AU080127
AU080133 AU080133
CF118424 f6543.21
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2812.411 Million cell updates/sec
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925
1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189
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                                                                                                                                           June 19, 2005, 06:25:42 ; Search time 2558 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                           - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34239544 seqs, 19032134700 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AY404972
BI1149602
BI157842
AU080133
CF118424
                                                                                                                                                                                                                                                                                                                                                            Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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/lab host="DH10B TODA"
/lab host="DH10B TODA"
/clone_lib="NIH MGC_251"
/clone_lib="NIH MGC_251"
/note="Organ: thymus, Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1: RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer
s-pGACTACTTCTMGATCCGAGCGGCGCCC(T)25-3' and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.6 kb. This primary
library is normalized (non-normalized primary library is
NIH MGC_250) and was constructed by Open Biosystems. Note:
this is a NIH_MGC library"
                                                                                            EST 25-AUG-2004
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                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                             CV077130 695 bp mRNA linear EST 25-7
AGENCOURT 31475102 NIH MGC 251 Rattus norvegicus cDNA clone
IMAGE:7388978 5', mRNA sequence.
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Conservative:
Mismatches:
Indels:

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    /organism="Rattus norvegicus"

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/db_xref="taxon:10116"
/clone="IMAGE:7388978"
                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                             CV077130.1 GI:51544161
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                                                                                                                                                                                                                                                          /lab host="Initiation"
/lab host="Initiation"
/clone lib="NIH MGC 255"
/clone lib="NIH MGC 255"
/note="Organ: brain/CNS; Vector: pExpress-1; Site_1:
ECORV; Site_2: Not1; RNA obtained from brain tissue of 8
wk old animal. Tissues were snap-frozen and kept at -80C
before RNA extraction and purification (Tri-reagent
method). cDNA was primed using oligo-dT primer:
5. pGACTACTTCTACATCGCGACGCCGCCC(T)25-3' and cloned into
the ECORV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This primary
library is a normalized (primary library is NIH MGC_254)
and was constructed by Express Genomics (FrederIck, MD).
Note: this is a NIH_MGC library"
                                                                                                                                                                                                          /tissue type="Brain - Pooled from several tissues from one or more_individuals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 AAAGAACTGAGGCGGCTTTTCTTTAGTTGATTTAGTTGATTCCCTGAAGTTTGCAGTG
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Matches:
Conservative:
Mismatches:
Indels:
                                                              /organism="Rattus norvegicus"
|mol_type="mRNA"
|bxref="taxon:10116"
|clone="IMAGE:7317070"
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/tissue type="Retinal Ganglion Cells"
/tissue type="Retinal Ganglion Cells"
/tissue type="Retinal Ganglion Cell"
/clone lib="Rat retinal ganglion cell"
/note="Organ: Eye; Vector: pDNR-LIB; Site_1: Sfil; Site_2: Sfil; The library was constructed from purified rat retinal ganglion cells. The Creator SMART CDNA Library method (Clontech) was used. EST analysis was performed on the unamplified, non-normalized, non-subtracted library."
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F26A06 048.abl.R Rat retinal ganglion cell Rattus norvegicus CDNA,
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                              TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Farkas, R.H., Qian, J., Goldberg, J.L., Quigley, H.A. and Zack, D.J.
Gene Expression Profiling of Highly Purified Rat Retinal Ganglion
                                          81
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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GluGluLeuValGlnLysTyrSerAanSerAlaLeuGlyHisValAsnSerThr11eLys
                                                                                                                GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA
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                                                                                                                                                                                                                                                                                       TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAAATC
                                         GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                    Unpublished (2003)
Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5330
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.
Location/Qualifiers
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/strain="Sprague-Dawley"
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Alignment Scores:

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Mus musculus RTM4 gene, VIRTUAL TRANSCRIPT, partial sequence, AY404972
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                                                                                                                                                                                                                                                                                                                         227 TIATTCCTGCTGCTGTCTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 286
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Mus musculus
Mus musculus
Mus musculus
Muscayota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Fertlera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
791
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Conservative:
Mismatches:
Indels:
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AUTHORS
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BI149602.1
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KEYWORDS
SOURCE
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TITLE
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602848410F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5011899 5',
mRNA sequence.
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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 GAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA
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DEFINITION

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. B. 1 (bases 1 to 679)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 01
High quality sequence stop: 708.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Mam3"

//note="Organ: mammary; vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI: Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
Library amples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                                                                                                                                                                                                                                            BI157842 1702_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5062944 5',
                    456
                                                  161
                                                                                                                                          576
                                                                                                             181
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NHF-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaser 21
                                                                                                        LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis
                                                                  708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:5062944"
|tissue type="tumor, gross tissue"
|dev_stage="10 months"
|lab_host="DH108"
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Matches:
Conservative:
Mismatches:
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
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Query Match:
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TITLE
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COMMENT
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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E (Dases 1 to 794)
E 1 (Dases 1 to 794)
E Habhimoto, K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A., Suzuki, Y., Sasaki, M. and Sugano, S.
Esolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method
Unpublished (1999)
Conteact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama --chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp/yoken/genbank/.
Location/Qualifiers
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57, mnAA sequence.
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                            179 TIGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 238
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                                                                                        LeuAlaLeuLeuSerValThrileSerPheArglleTyrLysGlyValIleGlnAlaile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 LeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHis
22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                   GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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/mol_type="mRNA"
/strain="C57BL"
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/clone="MNCb-5261"
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/lab_host="TOP10"
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/clone lib="Sugano mouse brain mncb"
/clone lib="Sugano mouse brain mncb"
/note="Organ: brain; Vector: pME185-FL3; 1st strand cDNA
was primed with an oligo(dT) primer
ATGTGGCCTTTTTTTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a Drail adaptor [TGTTGGCCTACTGG], digested and
cloned into distinct DrailI sites of the pME185-FL3. XhoI
sites just outside the DrailI sites of the pME185-FL3. XhoI
sites just outside the DrailI sites can be used to isolate
the cDNA insert. Size selection was performed to exclude
fragments <1.5 kb. Library was constructed by Sugano et
al.(University of Tokyo, Institute of Medical Science).
Custom primer used for sequencing: 5' end primer
[CGACCTGCCTGCAGCACA]"

[GGACCTGCAGCACACA]"
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 799)
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                                                                         Hashimoto, K., Kueuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A., Suzuki, Y., Sasaki, M. and Sugano, S.
Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method
Unpublished (1999)
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
National Institute of Infectious Diseases
Sal, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp/yoken/genbank/.
Location/Qualifiers
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Mismatches:
Indels:
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="MNCb-5268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="female"
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Best Local Similarity:
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Pred. No.:
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                                                                                   AUTHORS
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/note="Organ: brain; Vector: pME18S-FL3; lst strand cDNA was primed with an oligo(dT) primer argumed with an oligo(dT) primer argumed with an oligo(dT) primer argumed with an oligo(dT) primer argumed construction and primer arguments. Total adaptor [TGTGGCCTACTGG], digested and cloned into distinct DrailI sites of the pME18S-FL3. XhoI sites just outside the DrailI sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments al.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing: S' end primer [CTTCTGCTCTAAAAGCTGG], 3' end primer [CGACCTGCAGCACA]"
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AU080133 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-5268
AU080133.1 GI:6084887
BEST.
Mus musculus (house mouse)
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AY404970 600 bp DNA linear GSS 16-DEC-2003
Homo sapiens RTN4 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                     92 TTATTCCTGCTCTCACTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 151
                                                                                                                                                                                                                                                         82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Ford,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrica,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                         212 CAGAAATCTGATGAAGGACACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT
                                                                                                                                                                                                                                                                                  332 GAACTCAGACGCCTCTTCTTAGTTGATTAGTTTGTTTCTCTGAAGTTTGCAGTGTTG
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1 (Dases 1 to 598)
Adelson, D.L., Cam, G.R., DeSilva, U. and Franklin, I.R.
Gene expression in sheep skin and wool (hair)
Genomics 83 (1), 95-105 (2003)
Contact: Adelson, David L.
CSIRO Livestock Industries
To Cardon, Robert Cardon, St. Lucia QLD 4067, Australia
Tel: +61 7 3214 2700
Fax: +61 7 3214 2000
                                                                                                         MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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organism="Ovis aries"
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Location/Qualifiers
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'strain="Merino"
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1. .600 /organism="Homo sapiens"

source

ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

x CF118424 (1-598)

US-09-830-972-2_COPY_975_1163 (1-189)

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FEATURES

Location/Qualifiers

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/Lissue type="normal endometrium, late proliferative phase, cycle day 13"
| Lab host="DHIOB (T1-resistant)" |
| /clone lib="NICHD HS Ut1" |
| /note="Organ: uterus; Vector: pCMV-SPORT6.1.ccdb (ReeGen, Invitrogen Corporation); Site_1: Not1; Site_2: EcoRV; Cloned unidirectionally from microquantity amounts of mRNA from normal endometrial tissue (late proliferative phase, cycle day 13). Average insert size 1.9 kb. Library constructed by ResGen (Invitrogen Corporation)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 318
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                                                      CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution information can linfowing through the I.M.G.E. Consortium/LLNL at: infowing clulingov Plate: LLAM13163 row: G column: 23 Seq primer: MI3RP1 reverse primer (ABI).
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| Organism="Homo sapiens"
| Mol_type="mRNA"
| db xref="texon:9606"
| clone="IMAGE:5937070"
             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov CDNA Library Preparation:
                                                                                                                                                                                                                                                                                               /sex="female"
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1 (bases 1 to 650)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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Mismatches:
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fas: 650 473 7760
Email: rbrandenberger@geron.com
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Location/Qualifiers
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Geron Corporation
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Broduction of EST from cDNA libraries derived from immunologically activated bovine gut
Unpublished (2004)
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Animal and Natural Resources Institute
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fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia ostertagi was initiated at 15 weeks
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4109431 BARC 9BOV Bos taurus cDNA clone 9BOV37_106 5', mRNA
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Fax: +82-42-860-4470
Email: yongsung@mail.kribb.re.kr
Plate: 41 row: F column: 04
High quality sequence stop: 682.
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1 (bases 1 to 682)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and YKim,Y.J.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        654
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Matches:
Conservative:
Mismatches:
Indels:
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101 317

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Homo sapiens (numan)

Homo sapiens (numan)

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Cararhini; Hominidae; Homo.

I (bases 1 to 743)

Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mational Linstitutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bisoscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stope 617.

High quality sequence stope 617.
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Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                               318 GAACTCAGACGCCTCTTCTTAGTTGATGTTTGGTTCATTCTCTGAAGTTTGCAGTGTTG 377
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                                                198 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT
                                                                                                                           GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
                                                                                                                                                                   122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis
      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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IMAGE:30373271 5', mRNA sequence.
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Site_2: NotI; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasums
                                                             CK971318 712 bp mRNA linear EST 16-MAR-2004 4087182 BARC 9BOV Bos taurus CDNA clone 9BOV3_407 5', mRNA
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bosinae; Bosinae; Bosinae; Bosinae; D. 1. (bases 1 to 712)
Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosas, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically activated bovine gut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt " -trim_fasta. Vector identified by cross match using options -minmatch 12 -minscore 12 plate: 3 row: 10 column: 07 Seg primer: CCGACTCACGATCTAAAACG High quality sequence stop: 712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2004)
Contact: Tad S. Sonstegard
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Adg. 200 Rma.A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
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Conservative:
Mismatches:
Indels:
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/strain="Holstein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tads@anri.barc.usda.gov
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                                                                                                                                                                                   CK971318.1 GI:45489292
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ProGlyLeuLysArgLysAlaAsp 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrieuGlyleuAlaAsniysSerValiysAspAlaMetAlaLysIleGlnAlaLysIle 181
insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Liaboratories (Palo Alto, CA). Note: this is a NIH_MGC Library"
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                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                  451 GAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                                                                                                                                                                    151 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGTTTTGTGCCAGC
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Matches:
Conservative:
Mismatches:
Indels:
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602660523F1 NCI_CGAP_Skn3 Homo s
mNA sequence.
BG697436 131:13963656
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904.00
98.94%
97.34%
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Homo sapiens (human)
Homo sapiens
                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                   Scores:
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
   Tissue Procurement: James Cleaver, M.D.
   CDNA Library Preparation: Life Technologies, Inc.
   CDNA Library Preparation: Life Technologies, Inc.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
   Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov
   Plate: LLAM10700 row: m column: 05
   High quality sequence stop: 756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
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Matches:
Conservative:
Mismatches:
Indels:
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BG570231 843 bp mRNA linear EST 10-APR-2001
602590632F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717662 5',
mRNA sequence.
BG570231
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 843)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
   Tissue Proturement: CLONTECH Laboratories, Inc.
   CDNA Library Preparation: CLONTECH Laboratories, Inc.
   CDNA Library Preparation: CLONTECH Laboratories, Inc.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Incyte Genomics, Inc.
   Clone distribution: MGC clone distribution information can be
   found through the I.M.A.G.E. Consortium/LLNL at:
   http://mage.llnl.gov
   Plate: LLCM1567 row: o column: 07
   High quality sequence stop: 801.
                                                                                                        GAACTCAGGCGCCTCTTCTTAGTTGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                                                                                                                                        516 AIGIGGGAITITACCTAIGTGGGGCCTTGTTTAAIGGTCTGACACTACTGAITTTGGCT
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                       GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                                                 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                  GlubeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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JOURNAL
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, P. 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRY sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
                                                                            AL533461 ALMO Sapiens ADULT BRAIN Homo Sapiens CDNA clone CSDDN004YJ08 5-PRIME, mRNA Sequence.
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                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 788)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Vall-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:31260542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence belongs to sequence cluster 1423.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODNO04DE04QPl&c=1423.r.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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Gaps:
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572 CCTGGATTGAAGCGCAAAGCTGAA 695
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                                                                                                                                                             AL533461.3 GI:45708351
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904.00
98.94%
97.34%
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B49 bp mRNA linear EST 23-SEB-2004

DKFZp469C2134 rl 469 (synonym: pkidl) Pongo pygmaeus cDNA clone

DKFZp469C2134 5', mRNA sequence.
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This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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Ottenwaelder, B. Obermaier, B., Deutschenbaur, S., Schaipp, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
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Deutschenbaur,S., et al.)
Unpublished (2004)
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitogen.
                                                                                                                                                                                                                                                                                                                                                                                                                    CR611869 1540 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DN004YJ08 of Adult brain of Homo sapiens
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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                                                 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/tissue type="Adult brain"
/plasmid="pCMVSPORT_6"
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/db_xref="taxon:9606"
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HTC; CNSLT_CDNA.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                       Contact: Genoscope Contre National de Sequencage Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
AL->73494 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA
clone CSODIO51YB11 3-PRIME, mRNA sequence.
AL573494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31294840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO5ICA06NP1&c=1423.r.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI051YB11"
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/protein_id="AAD27783.1"
/db_xref="cf1:4689148"
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SYTAYTALALSVTISFFIYTKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA
IGHNWCTIKELRRLELUDDLVDSLKPAVLMWYFTYVGALFNGITLLILALISLFSVFV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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                                                                                   GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai Institute
Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II,
Shanghai 200025, P.R. China
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="pituitary"
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BIO79496 781 bp mRNA linear EST 20-JUN-2001
602876306F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5008248 5',
mRNA sequence.
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Mus musculus
Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 781)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
1785
1183
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                                           Conservative:
Mismatches:
Indels:
  Length:
Matches:
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1.41e-100
904.00
98.94%
97.34%
                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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EST 08-MAY-2003

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Pan troglodytes verus
Pan troglodytes verus
Bukaryota, Metazoa Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa Chordata, Craniata, Vertebrata, Euteleostomi,
1 (bases 1 to 730)
Sakate, R., Osada, M., Hida, M., Sugano, S., Hayasaka, I., Shimohira, N.,
Yanagi, S., Suto, Y., Hashimoto, K. and Hirai, M.
Analysis of 5'-end sequences of Chimpanzee CDNAs
Genome Res. 13 (5), 1022-1026 (2003)
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                   AU297347 female adult cerebrum, full-length enriched chimpanzee cDNA library Pan troglodytes verus cDNA clone PorA0834 5' similar to human RefSeg mRNA NM_007008, mRNA sequence.
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chimpanzee cDNA library"
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Department of Integrated Biosciences
The University of Tokyo, Graduate School of Frontier Sciences
5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan
Tel: 81-4-7136-3688
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Bmail: mhirai@k.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                         AU297347.1 GI:29531646
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901.00
98.94%
96.81%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
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Pred. No.:
                                                                                                                             EST.
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DB:
                     LOCUS .
DEFINITION
                                                                                                                                                           ORGANISM
                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
PUBMED
COMMENT
       AU297347
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: /LiAM11052 row: k column: 01
High quality sequence stop: 773.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                  781
185
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                          /db_xref="taxon:10090"
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903.00
98.40%
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Best Local Similarity:
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CV030029 670 bp mRNA linear EST 20-AUG-2004 9024 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC014366, mRNA sequence.
                                                                                                                                                                                                               TIGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 gaacrcaggggccrcrrcrragrrgargarrragrrgarrcrcrgaagrrigcagrgrig 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics
                                                                                                                                                                                                                                                                                                         22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 670)
                                                                                                                                                                                                                                                                                                                                                                                             42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                  Length:
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Conservative:
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                                                                                                           Indels:
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Dana Farber Cancer Institute
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97.08%
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Best Local Similarity:
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/tissue_type="Purified pancreatic islet"
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Noti; Site_2: XhoI; cDNA made by oligo-dT priming-
Size-selected on agarose gel. Average insert size -lkb. 5'
XhoI site was destroyed after directional cloning.
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Buclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Melton, D. Brown, J. Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wyle, T., Martin, J., Blistain, A., Schmitt, A., Thetsing, B., Ritter, B., Ronko, I., Bennett, J., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium

Unpublished (2000)

Other Ests: ig3asoc.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                               CB067821 634 bp mRNA linear EST 21-JAN-2003 iq38a06.yl HR85 islet Homo sapiens cDNA clone IMAGE: 5' similar to TR: Q9Y293 Q9Y293 FOOCEN-S. [1] ;, mRNA sequence.
                         141
                                                               581
                                                                                                                               TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                           LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                                                                                         642 TATCTAGGACTIGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCGAAAATC 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 634)

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Fax: 617-495-8557
Email: dmelton@blohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
                      MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                               522 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 160.
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CB067821.1 GI:27812341
EST.
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Homo sapiens
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CB067821
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121

61

513 181

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JLLUMIGEN MCQ_26335 Katze MMBR Macaca mulatta cDNA clone IBIUW:8548 5' similar to Bases 129 to 958 highly similar to human RTN4 (Hs.436349), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stremdate
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MMBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
Kit (actalog #20040) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Macaca.

1 (bases 1 to 960)

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)

Contact: C. Magness
Illumigen Biosciences Inc.
                                                                162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
                                                                                      2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400
Fax: 2063780408
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cmagnesseillumigen.com
Sequenced on 2004.03.09, 743 Q20 bases.
PCR PRimers
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Matches:
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/organism="Macaca mulatta"
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10sert Length: 960 Std Error: 0.
Plate: CLO00173 row: H column: J
Seg_primer: CCCTCACTAAAGGGAACAAA
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/clone="IBIUW:8548"
                                                                                                                                              182 ProGlyLeuLysArgLysAlaAsp 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-830-972-2_COPY_975_1163 (1-189)
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97.08%
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Best Local Similarity:
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1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
EAX: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as PCR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATGCC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLygGlyValIleGlnAlaIle 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAGCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db xref="taxon:9606"
/tissue type="mixed"
/clone lib="Full Length cDNA from the Mammalian Gene
                                                                                                                                                                                 FORWARD: ATGGACGGTCAGAAAAATTGG
BACKWARD: CATTCAGCTTTCAGCTTCAGACCTTCAATC
Insert Length: 670 Std Brror: 66.00
Plate: 11045 row: 02 column: B
Seg primer: ACTGCCGTCGTTTTACAACGTCGTCAAACC
High quality sequence start: 101
High quality sequence stop: 669
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182
3
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Matches:
Conservative:
Mismatches:
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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898.00
98.40%
96.81%
97.08%
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Query Match:
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CN647521 1031 bp mRNA linear EST 13-MAY-2004 ILLUMIGEN MCQ_28658 Katze_MMBR Macaca mulatta cDNA clone IBIUW:7529 5' similar to Bases 129 to 1018 highly similar to human RTN4 (Hs.436349), mRNA sequence.
CN647521.1 GI:47160964
                           /gex="female"
/dev stage="adult"
/lab_host="E. coli SOLR"
/clone lib="Katze MMBR"
/note="Organ: braIn; Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-CDNA Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit (Catalog #200450)"
                                                                                                                                                                                                                                                                                                                                                          195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
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181
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Mismatches:
Indels:
                                                                                                                                                                                               Length:
Matches:
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Macaca mulatta
                'clone="IBIUW:11396"
                                                                                                                                                                                                                                                                                                   US-09-830-972-2_COPY_975_1163 (1-189)
                                                                                                                                                                                             3.33e-100
898.00
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Best Local Similarity:
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308
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                                                                                                                                                                                                                                        GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                                            61
                                                                                                                      81
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Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                249 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTATC
                                                            LeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValileGlnAlaile
                                                                                                                   GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                    429 GAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAGTTTGCAGTGTTGCAGTGTTG
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                                                                                                                                                                                                         369 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Mag
Large-scale Rhesus Macaque cDNA Sequencing
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.04.03.731 Q20 bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGGGAATTGGGTA
Insert Length: 983 Std Brror: 0.00
Plate: CL000275 row: C column: 03
Seg primer: CCCTCACTAAAGGGAACAAAA
POLYA=No.
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Macaca mulatta
Bukaryota; Metazoa; Chordata; (
Mammalia; Butheria; Primates; (
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 ProGlyLeuLysArgLysAlaAsp 189
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/strain="Indian"
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CN803408
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COMMENT
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
927/923
10349636
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                                                                                                                                                                                                  CCTGGATTGAAGCGCAAAGCTGAA 692
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Functional annotation of
                                                                   <del>:</del>
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/lab_host="E. coli SOLR"
/clone lib="Katze MMBR"
/clone="Organ: brain, Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit [catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTATC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutherita, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Macaca.

1 (bases 1 to 1031)

Katze, M.G. Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Large-scale Rhesus Macaque CDNA Sequencing
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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                                                                                                       Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
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Matches:
Conservative:
Mismatches:
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Email: cmagness@illumigen.com
Sequenced on 2004.03.24. 773 Q20 bases.
PCR PRimers
FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CCCTATAAAGGGGAATAGGTA
Insert Length: 1031 Std Brror: 0.00
Plate: CL000187 row: G column: 05
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA=No.
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forganism="Macaca mulatta"
mol_type="mRNA"
strain="Indian"
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clone="IBIUW:7529"
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898.00
98.94*
96.28*
97.08*
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Best Local Similarity:
Query Match:
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AK034902

Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library. Clone:9430059L06 product:RETICULON 4 (NEWENTE OUTGROWTH INHIBITOR), (NOGO PROTEIN) norvegicus], full insert sequence.

AK034902.1 GI:26084268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3533)
Adachi,J., Aizawa, K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayatsu,N., Hiramotto,K., Hiraoka,T., Hirzozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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                                                                                                                                                                                                                                                                                                                                                             668
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                               162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
                                                                                                                       LeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis
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BI691132 990 bp mRNA linear EST 18-SEP-2001 603314519F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5354477 5',
                           1100 Argreachartractracerrecrecerrerrearecrireacerreacherrearranger 1159
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                                                                                               MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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NIH-MGC http://mgc.nci.nih.gov/.
       GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLy8PheAlaValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Rolert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

http://image.llnl.gov

Plate: LiAM11901 row: e column: 06

High quality sequence stop: 758.
                                                                                                                                                                                            142 LeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHis
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Gaps:
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KEYWORDS
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AUTHORS
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Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nahai, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Direct Submission

L. Submitted (16-Jul-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-reseggsc.riken.jp, Tel:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev gage="12 days embryo"
1. .5dev Eage="12 days embryo"
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                                                                                                                                                                                                                                                                                                                                                                                 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          920 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 979
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/d_one="Indg8:7105316"
/tissue_type="heart, pooled"
/lab_hote="Huart, pooled"
/lab_hote="Huart, pooled"
/lab_hote="Huart Bronn"
/clone lib="NHH MGC 233"
/clone lib="NHH MGC 233"
/note="Organ: heart; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from pooled heart tissue from any of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
5-pGACTAGTTCTAGACGCGCGCCCCC(7)25-3' and cloned into the EcoRV/Not1 sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2 kb. This primary library is not normalized (normalized primary library is NIH MGC 234) and was constructed by Express Genomics (FrederIck, MD). Note: this is a NIH_MGC library."
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                                                           _type="mRNA"
xref="taxon:10116"
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: capabbe-rémail.nih.gov

Tissue Procurement: Howard Jacobs

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMA1964 row: g column: 16

High quality sequence stop: 685.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                     ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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                                           EST 28-MAY-1998
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                                   AA986233 1near EST 28-uc73g12.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1431334 5' similar to TR:Q16801 Q16801 NEUROENDOCRINE-SPECIFIC PROTEIN C. ;, mRNA sequence.
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Seq primer: primer name ambiguous
High quality sequence stop: 489.
Location/Qualifiers
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Mismatches:
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Matches:
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/mol_type="mRNA"
/strain="C57BL"
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/clone="IMAGE:1431334"
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Best Local Similarity:
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No.:
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RESULT 34
AA986233
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JOURNAL
COMMENT
                                                                                                                             ACCESSION
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KEYWORDS
SOURCE
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CN482802 592 bp mRNA linear EST 26-APR-2004 hw24h12.yl Human primary human ocular pericytes. Unamplified (hw) Homo sapiens cDNA clone hw24h12 5', mRNA sequence.
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215 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 274
                                                                                                                                                                                                                                                                                                                      275 TIGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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/dev_stage="Adult"
/lab_bost="EWDH108"
/clone_lib="Human primary human ocular pericytes.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Section on Molecular Structure and Function
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(3131, N14, Betheeda, MD 20892-2740, USA
Tel: 301 402 3452
Pax: 301 496 0078
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Plate: 24 row: h column: 12
Seg primer: M13RP1 reverse primer (ABI).
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="hw24h12"
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            ORGANISM
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        /norge="Organ: Bye, Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5.-pGATAGTTAGATGGGGCGC(T)15-3'). cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
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CO735185 GI:50822455
EST.
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                                                                                                                                                                                                                                                                                                                               ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
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Matches:
Conservative:
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Indels:
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Unamplified (hw)"
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97.31%
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                                                                                                                                                                                                               hibernation
                                             Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
Spermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_gtage="embryonic"
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/clone lib="squirrel embryo library 1"
/note="vector: pFLC; Site 1: SalI GTCGAG; Site 2: BamHI
GGATCC; Normalized and subtracted cDNA library prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGTGTAAACAGCCTACATTGCC
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                                                                                                          1 (bases 1 to 805)
Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
Rogers, J. and Cossins, A.R.
Microarray analysis of transcriptional changes during hibernat
in the golden mantled ground squirrel, Spermophilus lateralis
Unpublished (2004)
                                                                                                                                                                                                                                                                         Unpublisher Accord.
Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Liverpool
School of Biological Sciences, The Biosciences Building, Crow
Street, Liverpool, United Kingdom, L69 72B
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been triamed from this EST.
Plate: 10 row: o column: 12
Plate: 10 row: o column: 12
Req primer: pflc T7 (5'-AATACGACTCACTATAGGG-3')
High quality sequence stop: 805.
Spermophilus lateralis (golden-mantled ground squirrel)
Spermophilus lateralis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Spermophilus lateralis"
/mol_type="mRNA"
/db_xref="taxon:76772"
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Conservative:
Mismatches:
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DUZJOV48 11near EST 21-FEB-2001
602393712F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4505499 5',
mRNA sequence.
                                              CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 185
                                                                                                                                              186 rigeccerecrecrerereacearcaecriragararacaaegererearecaaecrare 245
                                                                                                                                                                                                                                 246 cagaaarcagargaaggccacccarrcaggccararcragaarcraaagrrgcrarararcr 305
                                                                                                                                                                                                                                                                         GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                    306 gaggagrīnggrīncagaagracagraarīncigcrcrīnggrcargrgaacrgcagaraaag 365
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria,
I (bases I to 74)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10379 row: g column: 04

High quality sequence stop: 745.
                                                                                                      LeualaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACTACTGATTTGGCT
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                      LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                         GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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/clone_lib="NIH_MGC_94"
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AUTHORS
TITLE
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BG296048
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/mol_type="mRNA"

/mol_type="mRNA"

/mol_type="mRNA"

/dob_xref="taxon:9606"

/clone="ImMGE:5558493"

/tissue_type="duodenal adenocarcinoma, cell line"

/lab_hogt="DHIOB (phage-resistant)"

/clone=lib="NHH MGC 88"

/note="Organ: small_intestine, Vector: pCMV-SPORT6;

Site_1: NOtI; Site_2: Sall; Cloned unidirectionally;

oligo-dr primed. Average insert size 1.767 kb. Library

enriched for full-length clones and constructed by Life
Technologies. Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                       bp mRNA linear EST 05-MAR-2002
Homo sapiens cDNA clone IMAGE:5558493
                                          599
                                                                                                                                                                                                               719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMA12281 row: i column: 22

High quality sequence start: 25

High quality sequence stop: 579.
                                                                                                                             629
                                                                                    LeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                     TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 958)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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                                                                                                             CTGATTTCACTCTTCAGTGTTCCTGTTATTTACGAACGGCATCAGGCACAAAATAGATCAC
                                                                                                                                                                                                660 TATCTAGGACTTGCATATAAGAATGTTAAAGATGCTATGGCTAAAATTCCAAGCAAAAATT
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                       182 ProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                                                                                                                720 CCTGGATTGAAGCGCAAAGCTGAA 743
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5', mRNA sequence.
BM801698
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96.28%
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Homo sapiens
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AUTHORS
TITLE
JOURNAL
COMMENT
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BM801698
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KEYWORDS
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Shiraki

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GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | LeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
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Contact: Robert Strausberg, Pn.D.

Email: Gapbb- **Cmaal.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDMA Library Preparation: Michael J. Brownstein (NHGRI), Shirak

CDMA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiAMH0685 row: n column: 08

High quality sequence stop: 757.

Location/Qualifiers
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4798279"
/tissue_type="hypothalamus"
/lab_host="NHIOB"
/clone_lib="NHIOB"
/note="Organ: brain; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.69e-99
891.00
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                                                                                                                                                                                                                                                                                                                                                  TTATTCCTGCTGCTGCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 244
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                                                                                                                                                                                                                                                                                                                                                                                                              CAGAAATCAGATGAAGGCCACCCATTCAGGCATATTTGGAATCTGAAGTTGCCATATCA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluLeuArgArgLeuPheLeuValAspAspieuValAspSerLeuLysPheAlaValLeu 121
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                                                                                                                                                                                                                                                                                                   GITGITGACCICCIGIACIGGAGAGACAITAAGAAGACIGGAGIGGIGITIGGIGCCAGC 184
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1 (bases 1 to 757)
11H-MG http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                  ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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ILLUMIGEN_MCO_36873 Katze_MMBR Macaca mulatta cDNA clone
IBIUW.12670 5' similar to Bases 138 to 1022 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
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                                               364 TIGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 423
                                                                                                                                                                                              GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Macaca.

1 (bases 1 to 1042)

Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.

Large-scale Rhesus Macaque cDNA Sequencing

Unpublished (2003)

Contact: C. Magness

Illumigen Biosciences Inc.
                      LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                   424 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGCTATATCT
                                                                                                                                                                                                                           MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAla
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                                                                                                          GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cmagness@illumigen.com
Sequenced on 2004.05.12. 633 Q20 bases.
PCR PRimers
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BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 1042 Std Error: C
Plate: CL000243 row: C column: C
Seg primer: CCCTCACTAAAGGGAACAAA
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/clone="IBIUW:12670"
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/strain="Indian"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN805577.1 GI:47701553
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/note="Organ: ovary; Vector: poTB7; Site_1: EcoRI; Site_2:
/note="Organ: ovary; Vector: poTB7; Site_1: EcoRI; Site_2: Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                         BUB45601 924 bp mRNA linear EST 16-OCT-2002 AGENCOURT 10414454 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:6579264 5', mRNA sequence.
659 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (basea I to 924)

II (Basea I to 924)

III-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                      TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Phttp://image.llhl.gov
Plate: LLCM2782 row: e column: 24
High quality sequence stop: 696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
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Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue. Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:6579264"
                                                                                                                          182 ProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                     719 CCTGGATTGAAGCGCAAAGCTGAA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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ઠે 셤 ઠે (MGC)

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/tissue type="pre-clamptic placenta"
/lab_host="pre-clamptic placenta"
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/clone lib="NHH MGC 148"
/clone lib="NHH MGC 148"
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directionally cloned using primer
S'-TTTTTTTTTTTTTTTTTTTTTY, size_selected for average insert
size_2:3 kb and normalized to ROT 5. This is a primary
library enriched for full-lenght clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
                                                                                                  Brownstein (NHGRI) with help
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                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with h
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
(LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM347 row: p column: 18
High quality sequence stop: 630.
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      of Health, Mammalian Gene Collection
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:30331865"
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96.30%
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AGENCOURT 13994940 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30331865 5', mRNA sequence.
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Site_2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit [catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 871)
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ILLUMIGEN MCQ_38898 Katze_MMBR Macaca mulatta cDNA clone IBIUW:16203 5° similar to Bases 112 to 991 highly similar to human RTN4 (Hs.436349), mRNA sequence.
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                    276 TIGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 335
                                                                                                      336 CAGAAATCAGAAGGACGACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 395
                                                                                                                                                          GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr11eLys 101
                                                                                                                                                                                   396 GAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 455
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1 (bases 1 to 1013)

Katze,M.G. Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L. Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)

Contact: C. Magness

Illumigen Biosciences Inc.

2203 Alixport Way S, Suite 450, Seattle, WA 98134, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 2063/80408
Fax: 2063/80408
Fax: 2063/80408
Fax: Canagness@illumigen.com
Sequenced on 2004.05.13. 609 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Michael Katze Lab at University of Washington DNA Sequencing:
http://www.macaque.org
PCR PRimers
                                                                               81
61
                                                                               GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 1013 Std Brror: 0.00
Plate: CL000160 row: G column: 08
Seg primer: CCCTCACTAAAGGGAACAAAA
POLYA-Yes.
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/organism="Macaca mulatta"
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Macaca mulatta
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/strain="Indian"
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                                       999
                                                                                                   667 TATCTAGGACTTGCAAATAAGAATGTTAAAGGTGCTATGGCTAAAATCCAAGCNAAAATC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14040 row: h column: 15
High quality sequence stop: 627.
                                                                               TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 921)
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/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 94"
/clone_logan: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                  LeulleSerLeuPheSerIleProvalIleTyrGluArgHisGlnValGlnIleAspHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BUS03291.1 GI:22809480
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6490526"
                                                                                                                                                          ProGlyLeu-LysArgLysAlaAsp 189
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CCTGGAATGAAGCGCAAAGCTGAA 751
                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
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Magness, C.L.

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USA

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/dev_stage="adult"
/lab_host="E. col; SOLR"
/lab_host="E. col; SOLR"
/clone_lib="Katze MMBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
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   Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                            WA 98134,
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                                                , Iadonato, Sequencing
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                         2203 Airport Way S, Suite 450, Seattle, Tel: 2063780400
Fax: 2063780408
                                                                                                                                                                     Email: cmagnes@illumigen.com
Sequenced on 2004.05.14. 594 Q20 bases.
PCR PRIMERS
FORWARD: CCCTCACTAAAGGGAATTGGGTA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 1018 Std Error: 0.00
Plate: CL000272 row: E column: 10
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA=No.
                                                                                                                                                                                          Q20 bases
                                                                                                                                                                                                                                                                                                                                             /organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
                 Cercopithecinae; Macaca.

1 (bases I to 1018)

Katze, M.G., Thomas, M., Korth, M., I
Large-scale Rhesus Macaque cDNA Se
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9544"
/clone="IBIUW:16016"
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="female"
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                              /dev_stage="adult"
/lab host="E. col; SOLR"
/clone lib="Ktze MMBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-cDNA Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit (catalog #200450).
                                                                                                                                                                                                                                                                                                                             TyrLeuGlyLeuAlaAsnLysSer-ValLysAspAlaMetAlaLysIleGlnAlaLysIl 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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                                                                                                                                                                                                                                                                                                                                                                                            LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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Macaca mulatta
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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181
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                     1.41e-98
885.00
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95.77%
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Best Local Similarity:
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Pred. No.:
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BG740561 10.1_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778131 5',
                              GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 192
                                                                                                                         CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 252
                                                                                                                                                                                                                                             TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                          GluGluLeuValGlnLygTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLyg 101
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 758)
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Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIGS33 row: f column: 20
High quality sequence stop: 743.
Location/Qualifiers
                                                                                                                                                                                                           LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                           ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
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                                                                                        LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
/clone="IMAGE:4778131"
/lab_host="DH10B (T1 phage-resistant)"
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/note="Torgan of the placenta; Vector: pDNR-LIB (Clontech);
/note="Torgan of the placenta; Vector: pDNR-LIB (Clontech);
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/note as follows: S' adaptor sequence: S'-CACGGCCATTATGGCC-3'
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/note as follows: S'-CACGGCCATGGC-3'
/note as follows: S'-CACGGCCATGGC-3'
/note as follows: S'-CACGGCCATGGC-3'
/note as foll
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                                                                                                                                                                                                                                    685
                                                                                                                   625
                                                         LeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1636 row: g column: 06
High quality sequence stop: 742.
Location/Qualifiers
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11H-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                          162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla-LysIl
                                                                                                                                                                                                     626 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCCGAAAAT
   506 AIGTGGGTATTTACCTAIGTTGGTGCCTTGTTTAATGGTCTGACGCTACTGATTTTTGGCT
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BG623462.1 GI:13674833
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Alignment Scores:

ORIGIN

Pred. No.:

Query Match:

552

141

EST.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT REFERENCE AUTHORS

FEATURES

DEFINITION

RESULT 46 BG623462

372

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           Sequencing
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
  Large-scale Rhesus Macaque cDNA Sequenci
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle,
Tex: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.12.04. 735 Q20 bases.
FOR PRIMERS
FORRARD: CCTCACTAAAGGGAACAAA
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                                                                                                 Seattle,
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/clone="IBIUW:6014"
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/clone_lib="NCI_CGAP_Skn3"
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Site_l: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size l.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 1081)
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
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DEFINITION

RESULT 49 CO259245

8 셤 ð 셤 ACCESSION VERSION . KEYWORDS SOURCE ORGANISM

JOURNAL COMMENT

TITLE

REFERENCE AUTHORS

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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Eu (Dases 1 to 742)
Eu (Dases 1 to 742)
I (Dases 1 to 742)
I (Dayblished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11559 row: k column: 15
High quality sequence stop: 734.
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603083162F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222534 5',
mRNA sequence.
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                                                                                                      LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                         GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTCCGGTGCCAGC
                                                                                                                                                                                                                 LeuAlaLeuLeuSerValThrileSerPheArgIleTyrLysGlyValIleGlnAlaIle
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/organism="Homo sapiens"
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// Jesue L'Edutarion Neonatal"
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// Jeab_host="DH10B TonA"
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BARC 8BOV Bos taurus cDNA clone 8BOV_51K20 5', mRNA
                                                   181
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                                                                                                      695
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Baumann, K.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.
Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Contact: Richard G. Baumann
Bovine Functional Genomics Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
STyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIl
                                                                                                      636 TTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGGGAAAAT
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Gaps:
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                                                                                                                                                           eProGlyLeuLysArgLysAlaAsp 189
                                                                                                                                                                                     organism="Bos taurus"
/mol_type="mRNA"
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clone="8BOV_51K20"
bex="Female"
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Fax: 3015048744
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FEATURES

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ORIGIN

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Lundeberg.7.
Lundeberg.7.
Lundeberg.7.
EST analysis of brain and testis cDNA libraries from White leghorn and Red Jungle Fowl
Unpublished (2004)
Lontact: Peter Savolainen
Department of Biotechnology, KTH
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0)8 5537 8481
Fax: +46 (0)8 5537 835
Email: Peter Savolainen@biotech.kth.se
Seq primer: M13 reverse primer.
Seq primer: M13 reverse primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: brain; Vector: pSPORT-1; Site 1: Hind III; Site 2: EcoRI; The cDNA libraries were created with the Superscript Plasmid System (Invitrogen)."
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                                                     Arvestad, L., Andersson, L.
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/clone_lib="WLbrain"
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Archosauria; Aves; Neognathae; Galliformes;
Phasianinae; Gallus.
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Mismatches:
Indels:
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                                               Savolainen, P., Fitzsimmons, C.J.,
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/strain="White Leghorn"
/db_xref="taxon:9031"
/sex="female"
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            /clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCWV-SPORTS; Site_l: Not!, Site_2: ECORV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(ECORV site is destroyed upon cloning). Average insert
size l: S kb, insert size range l-2: S kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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CN219472
EXT. 91:46298814
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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'lab host="DH10B'
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eProGly-LeuLysArgLysAla 188
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E 1 (Dases 1 to 784)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Miklosel J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Miklosel J. Brownstein (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC Clone distribution information row Plate: LLAM10709 row: m column: 07

High quality sequence stop: 747.
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169 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 228
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Mismatches:
Indels:
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/organism="Homo sapiens"
/mol type="mRNN"
/db_xref="taxon:9606"
/clone="IRMAE:4814382"
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/lab_host="DH108"
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Matches:
                                                  182 ProGlyLeuLysArgLys 187
                                                                      717 CCTGGGCTGAAGCGCAAA 734
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butheriai; Eutheriai; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 817)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capaba-romantinh.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CLOne Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                817 bp mRNA linear EST 09-JUL-2003
UI-M-FX0-cck-n-21-0-UI.rl NIH BMAP_FX0 Mus musculus cDNA clone
LMAGE:6820918 5', mRNA sequence.
409 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 468
                                                                                                                                                                                349 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 408
                                                                                                                                                                                                                                                                               GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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/mol_type="mkNa"
/mol_type="mkNa"
/do_xref="twan:1000"
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/tissue_type="whole brain"
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/lab_host="bH108 (11 phage resistant)"
/clone lib="NHH BMAP RXO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 469 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTTCTGAAGTTTGCAGTGTTG
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Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with ECoR I adaptor, digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603397035F1 NIH_MGC_94 Mus musculus cDNA linear EST 11-OCT-2001

ENDIA sequence.

B1872386.1 GI:16046048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCATTATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCCATGGCCAAAATCCAAGGAA 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 laSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrI 40
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                                                                                                                                                                                                                                                                                                                                                                                                                      SerValValAspLeuLeu-TyrTrp-ArgAsplleLysLysThrGlyValValPheGlyA
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186
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Matches:
Conservative:
Mismatches:
Indels:
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872.00
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96.88%
94.27%
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Best Local Similarity:
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DEFINITION ACCESSION VERSION

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 857)
Millendia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Nith-MGC http://mgc.nci.nih.gov/.

Nith-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC. Clone distribution information can be http://image.llnl.gov
Plate: LLAM12021 row: f column: 09
High quality sequence stop: 754.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATTGAGGCGTCTCTTCTTAGTTGATTTAGTTCCCTGAAGTTTGCAGTGTTG 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Lissue_type="retina"
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/clone_lib="NHH_MGC_94"
/clone_log="NHH_MGC_94"
/note="Organ eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size_3:3 Mb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5400584"
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  Mus musculus (house mouse)
Mus musculus
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872.00
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                                                                                     REFERENCE
AUTHORS
TITLE
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요 ò 셤 ò 셤

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Consect: Kobert Straubergy, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: Tre I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0702 row: 1 column: 11
High quality sequence stop: 774.

High quality sequence stop: 774.
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                                                                                     GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 GAAGAGCTGATTCAGAAATACAGCAGTGTTGTGCTTGGTCACATCAATGGCACACAGCAAG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 774)

11 HMG Thtp://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                          42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                 234 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTAGTGTAGTTGTAGTTGTAGTGTGTTCT
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                                                      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
US-09-830-972-2_COPY_975_1163 (1-189) x CO504431 (1-647)
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Homo sapiens
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KEYWORDS
SOURCE
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/lab_host="DHs alpha"
/lab_host="DHs alpha"
/clone lib="chicken breast muscle - CB1"
/clone lib="chicken breast muscle - CB1"
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/clone lib="chicken breast muscle - CB1"
/clone lib="chicken breast muscle - CB1"
/clone library was constructed with the SuperScript Plasmid System with Gateway Technology kit (Invitrogen), following manufacture's protocols. Plasmid DNA was purified using a modified alkaline lysis method. Sequencing reactions were conducted using the DYBnamic Cycle Sequencing reactions were manufacturer's recommendations. Clones were sequenced by the 5' end with T7 primer. Sequencing reactions were highly conducted with and conducted sequenced by the 5' end with T7 primer. Sequencing reactions were highly conducted by the form with the conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted conducted c
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S Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B., Discovery of new genes expressed in the chicken breast muscle Unpublished (2004)

L Ontert: Helena J. Alves
Laboratory of Animal Biotecnology, Dep. of Animal Production ESALQ - University of Sao Paulo
Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4434
                                                                                                                                                                                                                                                                                                                                                                                    CO504431 647 bp mRNA linear EST 13-JUL-2004 GGEZCB1023A09.g chicken breast muscle - CB1 Gallus gallus cDNA clone GGEZCB1023A09, mRNA sequence.
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                                                                                                          Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br
PCR PRimers
BACKWARD: T7.
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Mismatches:
Indels:
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1. 647
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                                                                                                                                                                                                                      181 leProGlyLeu-LysArgLysAla 188
                                                                                                                                                                                                                                                                             670 receredarreda de ceca de 693
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Gallus gallus
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AUTHORS
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source

FEATURES

ORIGIN

Score:

cDNA clone SB02029A2B02.fl 5, mRNA sequence

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Alignment Scores:
Pred. No.:
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                            VERSION
KEYWORDS
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LOCUS CK305449
DEFINITION SB02029A2B02.fl normalized Keck-Tagu Library SB02 Taeniopygia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 GAGGAGNTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           649 ATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAA 708
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Indels:
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Matches:
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94.05%
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Best Local Similarity:
Query Match:
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Vector Trimming: Cross match from Washington University Genome Center PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script. This sequence is vector free and at least 200 bp in length. Funded by PHS grant # RO1 NSO45264, 'Songbird Neurogenomics Initiative.' PCR PRIMERS PORWARD: TATAACGACTCACTATAGGG(T7)
BACKWARD: ATTAACCACTCACTAAAGG(T3)
Insert Length: 736 Std Error: 0.00
Plate: SB02029Az row: B column: 02
Seq primer: TAATAGGACTCACTATAGGG (T7)
High quality sequence stop: 736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior Unpublished (2004)
Unpublished (2004)
University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 3668
Exa: 217 244 1648
Exa: 217 244 1648
Exa: 217 248 1648
Exail: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
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                                                                                 Taeniopygia guttata
Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
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                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 736)
Clayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M.,
Mello, C.V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.
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CK305449.1 GI:44815023
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Best Local Similarity:
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(1996), Genome Research 6(9): 7791-806. An identiying tag was added at the 3'during cDNA synthesis:
insertAAAAAAAAAAAAAAAAAAAAAGGCGA."
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Location/Qualifiers
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/organia="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
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E Strildinae; Taeniopygia.

E (Dayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M., Mello, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M., and Liu, L.

The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior

Unpublished (2004)

Contect: David F. Clayton
University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA

Tel: 217 244 3668
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                                             245 CTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCAATC
                                                                                              GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                  365 GAGGAGCTCATCCAGAAGTACAGCAACGTCGTGCTGGGCCAACGTGAAAGGACCGTCGG
                                                                                                                                                                                                                                                 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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                     LeuAlaLeuLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAlaIle
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SB02018A1G04.fl normalized Keck-Tagu Library SB02 Taeniopygia guttata cDNA clone SB02018A1G04.fl 5, mRNA sequence.
CK303615
EX703615.1 GI:44813189
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Base Calling/Quality Scores: PHRED from Washington University
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Insert Length: 765 Std Error: 0.00
Plate: SB0210BA1 row: G column: 04
Seg primer: TAATACGACTCACTAAAGG (T7)
High quality sequence stop: 765.
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                                                                                                                                                                                                                                              The Study of Genes, Brain, and Behavior
for Study of Genes, Brain, and Behavior
for Study of Genes, Brain, and Behavior
for Study of Genes, Brain, and Behavior
Contact: David F. Clayton
University of Illinois
BIOT CELE,, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 1648
Fax: 217 244 1648
Base Calling/Quality Scores: PHRED from Washington University
Genome Center.
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/note="Organ: brain; Vector: pBS II SK(+); Site_1:
ECORI(5' side of insert); Site_2: NotI (3' side_of
insert); The library was constructed and normalized as
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
(1996), Genome Research 6(9): 791-806. An identifying tag
was added at the 3'during cDNA synthesis:
                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves; Neognathae, Passeriformes; Estrildidae, Estrildidae, Estrildinae, Taeniopygia.

1 (bases 1 to 73)
Clayton, D. P., Arnold, A. P., Ball, G. F., Brenowitz, E., George, J. M., Mallo, C. V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.
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SB02042A1A11.fl normalized Keck-Tagu Library SB02 Taeniopygia
guttata cDNA clone SB02042A1A11.fl 5, mRNA sequence.
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(lab_host="DH108"
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Matches:
Conservative: 1
Mismatches: 7
Indels: 0
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/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="GB02042A1A11.f1"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: TAATACGACTACAGGG (T7)
BACKWARD: ATTACCTCACTAAAG (T3)
INSET Length: 793 Std Brror: 0.00
Plate: SB02042A1 row: A column: 11
Seq primer: TAATACGACTCACTATAGGG (T7)
High quality sequence stop: 793.
Location/Qualifiers
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Vector Trimming: Cross_match from Washington University Genome Center PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script. This sequence is vector free and at least 200 bp in length. Funded by PHS grant # RO1 NSO45264, 'Songbird Neurogenomics Initiative.'
                                                                                                                   268
                                                                                                                                                                                                                                              328
                                                                                                                                                                                                                                                                                                           101
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Contact: David F. Clayton
TTGTTCCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGTGTCACAGCCTACATTGCC 208
                                                             19
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Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
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Clayton, D. F., Arnold, A. P., Ball, G. F., Brenowitz, E., George, J. M.,
Mello, C. V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.
                                                                                          CTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCAATC
                                                                                                                                                                                                                    269 CAGAAGTCTGATGAGGCCACCCCTTCAGGCTTACCTGGACTCGGATGTGGCCGTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 ATGTGGTTTTTCACTTACGTTGGTGCCTTGTTCAATGGTCTGACATTACTGATCCTGGCT
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                                                                                                                                                                                                                                                                                                           GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
                                                                                                                                                                                                                                                                                                                                                                     329 GAGGAGCTCATCCAGAAGTACAGCAACGTCGTGCTGGCCACGTGAACGGCACCGTCCGG
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SB02022B2C10.fl normalized Keck-Tagu Library SB02 Taeniopygia
guttata cDNA clone SB02022B2C10.fl 5, mRNA sequence.
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Base Calling/Quality Scores: PHRED from Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 3668
Fax: 217 244 1648
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BACKWARD: ATTAACCCTCACTAAAG (T3)
INBERT Length: 852 Std Error: 0.00
Plate: SB02022B2 row: C column: 10
Seg primer: TAATACGACTCACTATAGGG (T7)
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o mRNA linear EST 12-JUL-2004
pkidl) Pongo pygmaeus cDNA clone
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/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 Grigirica cerecreta en de de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya del companya del companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya del companya de la companya de la companya del companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya del la companya de la companya de la companya del la companya del la companya del la companya del la companya de la companya de la companya del la companya del la companya del la companya del
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert clone from S. Wiemann
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemannadkfz-heidelberg.de; sequenced by Qiagen
(Hilden/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZP6949H132) is available at
the RZPD in Berlin. Dease contact the RZPD; Ressourcenzentrum,
Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY; Email:
clone@rzpd.de Further information about the clone and the
sequencing project is available at
http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                    Chordata, Craniata, Vertebrata, Euteleostomi,
Primates, Catarrhini, Hominidae, Pongo.
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1. (bases 1 to 68)
Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pongo,G., Han,M. and Wiemann,S.

Pongo pygmaeus mRNA (Bahr,A., Lauber,J., Mewes,H.W., et al.)
Unpublished (2004)
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Conservative:
Mismatches:

    . 683
    /organism="Pongo pygmaeus"
/mol_type="mRNA"
    /db_xref="taxon:9600"

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CR548792 683 bp
DKFZp469H1132_r1 469 (synonym: p
DKFZp469H1132 5', mRNA sequence.
                                                                                                                                                                                          Pongo pygmaeus (orangutan)
Pongo pygmaeus
                                                                                                                     CR548792.1 GI:50242416
EST.
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Best Local Similarity:
Query Match:
DB:
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
                                                                                                 ACCESSION
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                                                                                                                  // mol type="mRNA" | Mol type="mRNA" | Mol type="mRNA" | Mol xref="taxon:59729" | Ab xref="taxon:59729" | Ab xref="taxon:59729" | Abone="spotsatin" | Aev stage="late embryo, post-hatch days 1, 10, 20, 45, and adult (pooled)" | Abone="bhioba" | Abone="bhioba" | Abone="bhioba" | Abone="bhioba" | Abone="bridge" | Abone="cragan: brain; Vector: pBS II SK(+); Site 1: note="cragan: brain; Vector: pBS II SK(+); Site 1: ECORI(5' side of insert); Site 2: NotI (3' side of insert); The library was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research (6): 791-806. An identifying tag was added at the 3'during cDNA synthesis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 CAGAAGTCTGATGAGGGCCACCCCTTCAGGGCTTACCTGGACTCGGAATGTGGCCGTGTCG 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrLeuGlyLeuAlaAsnLysSerVallysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Matches:
Conservative:

    .852
    organism="Taeniopygia guttata"

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Indels:
Gaps:
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   ity sequence stop: E
Location/Qualifiers
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Eukaryotz, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1798)

2 Longe, 1 to 1798

2 Longe, C.J., Fu, G., Zhong, M., Zhao, M., Zhao, C.J., Fu, G., Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W., Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z. Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells

Genome Res. 10 (10), 1546-1560 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF125103 1798 bp mRNA linear HTC 22-MAY-2001
Homo sapiens neuroendocrine specific protein c homolog mRNA,
                                                                                                                                                                     72 GTTGTTGACCTCCTTTACTGGCGAGACATTAAGAAGACAGGAGTGGTGTTTGGTGCCAGC 131
                                                                                                                                                                                                                                          252 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGAAGTGTAGCTGTGTCT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
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2 (Dases 1 to 1798)
Ye, M., Zhang, Q., Zhou, J., Shen, Y., Guan, Z., Wu, X., Fan, H., Mao, H.,
Dai, M., Huang, Q., Chen, S. and Chen, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                  82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 ATGTGGGTGTTCACTTACGTTGGTGCCTTTAATGGTCTGACATTACTGATACTGGCT 491
                                                                                                                                                                                                                                                                                      LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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 171
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                                                                                                           x CO503803 (1-685)
                    Conservative:
Mismatches:
Indels:
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96.28%
90.96%
93.51%
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AF125103
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MEDLINE
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AUTHORS
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KEYWORDS
SOURCE
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SM Gallus gallus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

I (bases 1 to 685)

S Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B.,

Patricio, M., Ledur, M.C. and Coutinho, L.L.

Discovery of new genes expressed in the chicken breast muscle

Unpublished (2004)

Contact: Helena J. Alves

Laboratory of Animal Biotecnology, Dep. of Animal Production

ESALQ - University of Sao Paulo

Av. Padua Disas, 11, Piracicaba, SP, 13418-900, Brazil

Tel: 55 19 3429 4434
                                                                                                                                                                                                                                                                                                                                                       CO503803 685 bp mRNA linear EST 13-JUL-2004 GGEZCB1022G02.g chicken breast muscle - CB1 Gallus gallus cDNA clone GGEZCB1022G02, mRNA sequence.
                                                                                                                                           619
                                                                        559
                                       141
                                                                                                           161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosciences). The quality and clustering of the ESTs were analyzed using the softwares Phred/Cap3. Only EST sequences with Phred quality greater than 20 and at least 150 bp were considered for clustering."
                                                                                                                                                                          MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAla
                                                                                                                            GAACTCAGGCGCCTCTTCTTAGTTGATTTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                    LeulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gallus gallus"
/mol type="mRNA"
/db xref="taxon:9031"
/clone="GGEZCB1022G02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
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CO503803.1 GI:50273989
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CCT 682
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Pred. No.:
                                   122
                                                                    200
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LOCUS DEFINITION

RESULT 62 CO503803

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT

PEATURES

REFERENCE AUTHORS

19

41

551

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/cinde=invalsiato//o
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="Side=2: XhoI; CDNA made by oligo-dT priming.
Size=selected on agarose gel. Average insert size -lkb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
114-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                Allowers I. (Searce, M., Berstelli, J., Gradwohl, G., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium

In Unpublished (2000)

Other ESTS: in63405.x1

Conteact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                               BU950008 569 bp mRNA linear EST 21-OCT-2002 in63d05.yl HR85 islet Homo sapiens cDNA clone IMAGE:6126776 5' similar to TR:Q9X2X7 Q9X2X7 FOOCEN-M. [2] TR:O94962 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 TGGAGAGACATTAAGAAGATTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 TrpArgAspileLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSer
                                                                                                                                                                                                                                                                                                                                               Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (hinoue@im.wustl.edu)
Seg primer: -40RP from Gibco
High quality sequence stop: 488.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/clone="IMAGE:6126776"
  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 569)
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Homo sapiens
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           Humblished

(bases 1 to 1798)

Ye, M., Zhang, Q., Zhou, J., Shen, Y., Guan, Z., Wu, X., Fan, H., Mao, H.,
Dai, M., Huang, Q., Chen, S. and Chen, Z.

Direct Submission
Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
Shanghai 200025, P. R. China
Location/Qualifiers
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    neuroendocrine specific protein c homolog mRNA, complete cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCAAGTGAACTGCACGATAAAG 547
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215. -814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGAGATCCAAGGTATC
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/clone_lib="NIH_MGC_95"
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gallus cDNA clone ChEST539d19 5', mRNA
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Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoseuria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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B. (Dasses 1 to 731)

S. NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

L. Ordatic Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMITJ19 row: h column: 17

High quality sequence stop: 724.

Location/Qualifiers

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BI544917. GI:15432229
                                                                                                                                                                                                         | LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyr 127
                                                                                                                                                                                                                                                                                       312 TTAGTTGATGATTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGGTATTTACCTAT 371
                                                                                                                                                                                                                                                                                                                                ValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSer 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 IleProValileTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsn 167
                                                                                                                                                                                                                                                                                                                                                                                                             47
                                                                                     ThrileSerPheArglleTyrLysGlyVallleGlnAlalleGlnLysSerAspGluGly 67
                                                                                                                                               HisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLys 87
                             LeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerVal
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Homo sapiens
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/lab host="Mindle Inches" (T1-phage-resistant)"
/lab host="Mindle Inches" (T1-phage-resistant)"
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/clone_lib="NIH MGC_144"
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/note="Organ: Brain; Vector: pDNR-LIB; Site_1: Sfil
/ggccattatgggc; Site_2: Sfil (ggccgctcggc); cDNA made
by oligo-dT priming and directionally cloned. S' and 3'
adaptors were used in cloning as follows:
S'-AAGCAGTGGTATCAAGCAGAGGAGGACATACGGGCGGG-3' and
S'-AATCTAGAGGCGGAGGACATGGCTATACGGCGGG-3' and
S'-AATCTAGAGGCGGGGCGACATGGGTTACGGGGGG-3' and
S'-AATCTAGAGGCGGGGGCGACATGGGGGGGG-3' RUll-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.2-0.5
kb size fraction (chher fractions present in NIH MGC_143).
Library created in the laboratory of M. BrownsteIn (NIHM,
NIH). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BUB48611 BT 16-OCT-2002 AGENCOURT 10276498 NIH MGC_144 Mus musculus cDNA clone IMAGE:6596409 5', mRNA sequence.
                                                                                                                      575
                           515
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                                                                                                                                                                      LeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                                                                      635
                                                                                                                                                                                                                                                                   TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 813)
GAGCTGAGACGCCTCTTCCTCGTTGATGACTTGATTCTTCTGAAGTTTCCAGTTGATTGTG
                                                                                                  516 ATGIGGGGTTCACTTACGTTGGTGCCTTGTTTAATGGTCTGACATTACTGATACTGGTCTGGCT
                                                                         MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://imaqe.llnl.gov
Plate: LLCM2825 row: p column: 09
High quality sequence stop: 160.
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/constructed lighted to NotI adapters, diggsted with
/constructed lighted to NotI adapters, diggsted with
/constructed from cloned into the NotI and EcoRI
/constructed from custom modified MCS of the
/pBluescript (KS+) vector. The library was normalized in 2
/conds using conditions adapted from Soares et al., PNAS
/close light light a significantly longer
/connealing hybridization was used."
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr11eLys 101
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                                                                                                                                                                 Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
FOR DOX 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 0161280409
Fax: 0161280409
Email: Simon. Hubbard@umist.ac.uk.
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Contact: Simon Hubbard
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B. (bases 1 to 713)

B. NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1367 row: f column: 13

High quality sequence stops: 712.
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                                                                                                                                                                                                                                                                                                    LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                   279 TTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC
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CD511521 758 bp mRNA linear EST 06-JUN-2003
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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BI394814 16-AUG-2001 pgpln.pk009.15 Normalized Chicken Pituitary/Hypothalamus/Pineal Library Gallus gallus cDNA clone pgpln.pk009.15 5 aimilar to gi[590206 ref[NP 008939.1] reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sapiens] gi[13637055 ref[XP 002439.3] neuroendocrine-specific protein C like (foocen) [Homo sapiens] gi[AAD27783.1]AF077050_1 (AF077050) neuroendocrii, mRNA sequence.
  LeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMet-AlaLysIleGlnAlaLysIl 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                   628 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGGCTAAAAATCCAAAGCAAAA 687
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Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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| Porter, T. E. and Cogburn, L. A.
| ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA library USDA/IFRES Animal Genome Project
| Unpublished (2001) | Contact: Larry A. Cogburn | University of Delaware | Tel: 302-811-1335 | Tel: 302-831-12822 | Fax: 302-831-2822 | Fax: 302-831-2822 | Email: cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                                    GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                                        GluteuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheeda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratoriem (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLML at:
http://image.llnl.gov
Plate: NDCM193 row: n column: 17
High quality sequence stop: 614.
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/clone="forgan: Blood vessels - aorta, adaptor sequence:
5- ATTCTAGAGGCCATTATGGCC-30 and 3' adaptor sequence:
5- ATTCTAGAGGCCATGACATG-4T(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb
/clone observation of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the action of the actio
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                                                                                                                                           Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 CTATTCCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
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                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 758)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mismatches:
Indels:
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Matches:
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                               GI:31443239
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                                                                                     Homo sapiens (human)
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97.31%
95.70%
                                                                                                                    Homo sapiens
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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No
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AUTHORS
TITLE
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/dev stage="16 day embryo"
/lab_host="DH10B"
/lab_host="DH10B"
/clone_lib="CSEQCH124"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved on DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and BamHI sites [5/9gocgegtgeagcccggatccgaaaaaaaag]
[5/aattcttttttcggatccggaaccgcagaaaaaaaag]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla-LysIleGlnAlaLy 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 AlaLeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValileGlnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                          /mol_type="mRNA"
/Brzain=White Leghorn, Hisex"
/db xref="taxon:9031"
/clone="ChEST117m23"
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                                                              l. .1028
/organism="Gallus gallus"
 Fax: 01612360409
Email: Simon Hubbard@umist.ac.uk.
Location/Qualifiers
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Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1028)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU139629 1028 bp mRNA linear EST 25-NOV-2002 603134795F1 CSEQCHL24 Gallus gallus cDNA clone ChEST117m23 5', mRNA
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                                                                                                                                                                                                 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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                                                                                                                                                                                                                                                                                               TTGGCCCTGCTTTCTGTGACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCAATC
                                                                                                                                                                                                                                                                                                                                                                     231 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTAGCTGTGTCT
                                                                                                                         ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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   9900
Conservative:
Mismatches:
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                                                                                       US-09-830-972-2_COPY_975_1163 (1-189)
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                               377 Argresstartracctarstrestscristraarstractscristactactactartrasscr 436
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(Ercopithecinae; Macaca.

(Exaze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Liarge-scale Rheaus Macaque cDNA Sequencing
Unpublished (2003)

Contact: C. Magness

11lumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cmagness@illumigen.com
Sequenced on 2004.06.24. 532 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COS81452 960 bp mRNA linear EST 20-JUL-200
ILLUMIGEN MCO 47216 Katze MMLV Macaca mulatta cDNA clone
IBIUW:17799 5' similar to Bases 83 to 959 highly similar to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="adult"
/lab_host="Electromax DH10B"
/clone lib="Katze MMLV"
/note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
Site_2: BsrG I; Created from CloneMiner cDNA Library
Construction kit (catalog #18249-029)"
                                                                                   MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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BACKWARD: CACTATAGGGGAATTGGGTA
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/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTN4 (Hs.436349), mRNA sequence.
CO581452
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/clone="IBIUW:17799"
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Macaca mulatta
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (base 1 to 819)
S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM10021 row: f column: 12
High quality sequence stop: 647.
Location/Qualifiers
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/clone_lib="NHH MGC 86"
/note="Organ: bone; Vector: pcMV-SPORT6; Site_1: Not!;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.53 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
             61250548181 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4368011 5', BG109465
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/organism="Homo sapiens"
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Homo sapiens
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     http://image.llnl.gov
plate: LfCM131 row: g column:
High quality sequence stop: 708.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

L (base 1 to 905)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contect: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG400408 905 bp mRNA linear EST 12-MAR-2001
620464428F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592670 5',
MRNA sequence.
BG400408
                                                                                                                                                                                   AAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCGATATCTGAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAGGCGCCTCTTCTTAGTTGATGATGTTGTTGTTCTCTGAAGTTTGCAGTGTTGATG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAlaLeu
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                                                                                                                                                                                                                                                          LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
                                                                                                                                                                                                                                             AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
                                                                                                                                                                                                                                                                                                     LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
                                                                                                                             ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu
  960
175
6
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1
                                                                                                    US-09-830-972-2_COPY_975_1163 (1-189) x CO581452 (1-960)
Length:
Matches:
Conservative:
Mismatches:
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  1.59e-94
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96.28%
93.09%
92.11%
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Homo sapiens
                             Percent Similarity:
Best Local Similarity:
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212

21

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392 101

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452 121

512 141 572

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[Stratagene] vector to accommodate cDNA produced with the
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing Bsgl and
BanHI sites [5/ggccgcgtgcagccccggatccgaaaaaaaag]
[5'aattctttttcggatccggatcagcacggl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BU138907 759 bp mRNA linear EST 25-NOV-2002
603133909F1 CSEQCHL24 Gallus gallus cDNA clone ChEST115a3 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken CDNAs.

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                        GlubeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases 1 to 759)
                                  GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                                                                          463 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAGTTTTGCAGTGTTG
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Gallus gallus"
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Tel: 01612008930
Fax: 01612360409
Email: Simon-Hubbard@umist.ac.uk.
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                                                            BG427986 743 bp mRNA linear EST 14-MAR-2001
0025039851 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613876 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Context: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1864 row: j column: 21
High quality sequence stop: 716.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea I to 743)
NIH-MGC http://mgc.nci.nih.gov/.
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BG427986.1 GI:13334492
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/organism="Mus musculus"

/mol_type="mRNA"

/do_tref="txxxn:10000"

/clone="txxn:10000"

/tissue_type="Pooled thyroids from 5 mice"

/tissue_type="Pooled thyroids from 5 mice"

/tissue_type="Pooled thyroids from 5 mice"

/lab host="MIH MGC 230"

/clone= lib="NHH MGC 230"

/note="Organ: thyroid; Vector: pExpress-1; Site_1: NotI;

Site_2: NotI; RNA obtained from 5 normal wild-type mice
thyroid. cDNA was primed using oligo-dT primer:

5-pGACTAGTTCTAGATCGCAGCGCCCC(T) 25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection 1.4 kb
resulted in an average insert size of 1.2 kb. Normalized
version of this library is NIH MGC 189ibrary constructed
by Express Genomics (Frederick, MD). Note: this is a
NIH_MGC Library."
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cDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov a column: 13 http://image.llnl.gov a column: 13 High quality sequence stop: 680.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muzinae; Mus.
1 (bases 1 to 826)
11 (hases 1 to 826)
12 (hapto://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Shioko Kimura/Atsushi Yamada, (NCI,CCR)
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AGENCOURT_18667576 NIH MGC_230 Mus musculus cDNA clone IMAGE:30848940 5', mRNA sequence.
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TyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLys 171
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1 (basea I to 660)

1 (kasea I to 660)

1 (kasea, Vang, J. Rung, J. Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                AGGAAGACTGGAGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTC
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                                                       CD623553 660 bp mRNA linear 56088673JI FLP Homo sapiens CDNA, mRNA sequence. CD623553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol type="mRNA"
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: gfu@incyte.com.
Location/Qualifiers
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846.00
98.88%
96.63%
91.46%
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                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 659)
10, G. Wang, J. T., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/db_xeref="taxon:9606"
/clone lib="FLP"
/note="Vector: pDrive Cloning Vector"
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3160 Forter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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Homo sapiens
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CR755212 Rattus norvegicus muscle Sprague-Dawley Rattus norvegicus CR755212 CON CON CONA Clone GP0AAA15ZC09, mRNA sequence.
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Analysis of altered gene expression in rat soleus muscle atrophied
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/clone lib="Rattus norvegicus muscle Sprague-Dawley"
/note="Vector: pCRII-TOPD, Pietu G., Cros N., Leger J.J.,
Dechesne C.A. Substracted library from atrophied and
control soleus muscles Substraction was performed
according to Diatchenko et al. (Diatchenko L, Lau YF,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                       262 TTGGCCCTGCTCTGTGTGCCATCAGCTTTAGGATATACAAGGGTGTGTATCCAAGCTATC
                                                                                                                                                                                                                                                                           GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys
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                                        LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                        GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                      382 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACATAAAG
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Contact: Genoscope
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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Rattus norvegicus
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/note="Organ: placenta; Vector: placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta; Vector placenta;
                                                                                                                                                                                                                                                                                                                                                                                              BE733819 716 bp mRNA linear EST 15-SEP-2000 601569133F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843729 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Collection
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM539 row: a column: 10
High quality sequence stop: 716.
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                                                                                             TyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLys 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 716)
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Mismatches:
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/clone="IMAGE:3843729"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE733819.1 GI:10147721
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846.00
96.84%
95.26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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Best Local Similarity:
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DB:
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
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/done.lb="MRS5 islet"
//oloe="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Xho1; cDNA made by oligo-dr priming.
Size-selected on agarose gel. Average inser size ~1kb. 5'
Xho1 site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, Mn 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                  Endocrine Pandreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GTATTCAGCATTGTGAGCGTAACAGCGTACATTGCCTTGGCCCTGCTCTCTGTGACCATC 120
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Sacarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Thoising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                             MA 02138
Tel: 617-495-1812
Fax: 617-495-8825
Email: dmeltono@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSer
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                                                                                                                                                                          Unpublished (2000)
Other_ESTs: in67h09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:6127360"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                             (hinoue@im.wustl.edu)
Seg primer: -40RP from Gibco
High quality sequence stop: 471.
Location/Qualifiers
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Best Local Similarity:
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Campbell AP, Chenchik A, Mogadam F, Huang B, Lukyanov S, Lukyanov K, Gurakaya N, Sverdlov ED, Siebert PD.
Suppression subtractive hybridization: a method for regenerating differentially regulated or tissue-specific CDNA probes and libraries. Proc Natl Acad Sci U S A. 1996, 31 :6025-310) Rats were female Sprague Dawley between 200 and 220g. Soleus muscle atrophy was performed by 14 days of hindlimb suspension."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU949473 609 bp mRNA linear EST 21-OCT-2002 in67h09.yl HR85 islet Homo sapiens cDNA clone IMAGE:6127360 5' similar to TR:Q9Y2Y7 Q9Y2Y7 FOOCEN-M. [2] TR:O94962 ;, mRNA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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Matches:
Conservative:
Mismatches:
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110 AspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGly	Qy 170 VallysAbalaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArglysAlaAsp 189 Db 481 GTTAAAGATGCTATGGCTAAAATCCAAGCAAAATCCTGGATTGAAGCGCAAAGCTGAA 540 RESULT 83 CD000871 735 bp mRNA linear EST 01-MAY-2003 LOCUS DEFINITION AGENCOURT 13650322 NIH MGC 186 Homo sapiens cDNA clone ACCESSION CD000871.1 G1:30295402 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Chuman)	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 735) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL COMMENT Email: capabe remail.in, gov Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium(LLML) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov	High quality sequence stop: 530. Location/Qualifiers 1. 735 Location="Homo sapiens" //organism="Homo sapiens" //mol_type="mRNA" //db_xref="taxon:960s" //lone="INMAGE:30321390" //lone="INMAGE:30321390" //lone="Organ: Pooled-Skin; Vector: pDNR-LIB; Site 1: Sfil (spccattatggc); Site 2: Sfil (spccattatggc); Library is oligo-dT primed and directionally cloned. CDNA was prepared from a pooled samples of tissues from Skin, menings, duramatter, pia matter and choroid plexus. 5, and 3 adaptors were used in cloning as follows: 5,	adaptor sequence: 5'-CACGGCCATTATG-GT(30) Bn-3' equence: 5'-ATTCTAGAGGCCGACACAG-dT(30) Bn-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15.15 colonies contained inserts by PCR. This library was enriched for full.length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library" Alignment Scores: Pred. No.: 2.51e-93 Length: 735 Score: 841.00 Matches: 176 Percent Similarity: 97.27\$ Conservative: 2 Best Local Similarity: 96.17\$ Mismatches: 3

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CN791158 677 bp mRNA linear EST 26-MAY-2004
4125836 BARC 8BOV Bos taurus cDNA clone 8BOV_41013 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 3015048604
Fax: 3015048604
Fax: 301504874
Fax: 301504874
Fax: 301504874
Fax: 301504874
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
by cross using options -trim_alt ' -trim_fasts. Vector identified
by cross match using options -minmatch 12 -minscore 18
Plate: 4I row: 0 column: 13
Seq primer: CCTATTAGGTGACACTATAGGAAC
High quality sequence stop: 677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: Total Interior, Vector: pCMVSport6.1; Site 1: Not1; Site_2: EcoR1; Normalized cow cDNA intestinal library in pCMVsport6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Diodenum, Distal Ileum.
                                                                                                                                                                                                                 1 (bases 1 to 677)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                                                                                                                                                                                                                                                            Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                              BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
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dev stage="Lactating, Neonatal"
lab_host="DH10B TonA"
/clone_lib="BARC 8BOV"
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Matches:
Conservative:
Mismatches:
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/mol_type="mRNA"
/strain="Holstein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9913"
/clone="8BOV_41013"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                         Bovine Functional Genomics Lab
                                                                                                                                                                                                                                                                                                                                     Contact: Richard G. Baumann
                                                                                          GI:47687138
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Bos taurus
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                                                                                                                         /dev feage="22"
/lab_host="DH108"
/clone_lib="CSEQCHL13"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
EcoR1; Site_2: Not1; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with Not1 and EcoRI.
Ligate in double stranded adaptor containing Bsg1 and
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[5'aattcttttttccggatccggggctgcacgc]"
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Indels:
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               1. .915
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CR771568 684 bp mRNA linear EST 23-SEP-2004 DKFZp469C2337_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone DKFZp469C2337_5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                              316 TATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTAT 375
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                   GTTGTTGACCTCCATCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTAGTGCCAG
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Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pongo pygmaeus mRNA (Ottenwaelder, B., Obermaier, B., Deuteschenbaur, S., et al.)
Unpublished (2004)
Contact: MIPS
                                  1057
178
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                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                      2.68e-92
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92.71%
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/clone lib="Rattus norvegicus muscle Sprague-Dawley"
/clone lib="Rattus norvegicus muscle Sprague-Dawley"
/note="Vector: pCRII-TOPO; pietu G., Cros N., Leger J.J.,
Dechesne C.A. Substracted library from atrophied and
control soleus muscles Substraction was performed
according to Diatchenko et al. (Diatchenko L, Lau YF,
Campbell AP, Chenchik A, Mogadam F, Huang B, Lukyanov S,
Lukyanov K, Gurskaya N, Sverdlov ED, Siebert PD.
Suppression subtractive hybridization: a method for
generating differentially regulated or tissue-specific
CDNA probes and libraries. Proc Natl Acad Sci U S A. 1996;
93:6055-30; Rats were female Sprague Dawley between 200
and 220g. Soleus muscle atrophy was performed by 14 days
of hindlimb suspension."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR753971 10-57 bp mRNA linear EST 02-SEP-2004 CR753971 Rattus norvegicus muscle Sprague-Dawley Rattus norvegicus CR753971 CR753971
                                                                                                                                                                                   GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 515
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Cros, N., Tkatchenko, A.V., Pisani, D.F., Leclerc, L., Leger, J.J.,
Marini, J.F. and Dechesne, C.A.
Analysis of altered gene expression in rat soleus muscle atrophied
                     CAGAAATCTGATGAAGGCCACCCATTCAGGCCATATTTGGAATCTGAAGTTGCTATATCT 395
                                                                                                      GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                             MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                                                                                                                                                LeulleSerLeuPheSerIleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                     CTGATTTCACTCTTCAGTGTTCTGTTTATGAACGCCATCAGGCGCAAATAGATCAT 635
                                                                               GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrlleLys 101
  81
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
Zrue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Genoscope sequence ID : GPOAAA15ZC09CP1.

Location/Qualifiers

1.1057
                                                                                                                                                                                                                                                                                                                                                                                                             TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla 175
                                                                                                                                                                                                                                                                                                                                                                                                                                J. Cell. Biochem. 83 (3), 508-519 (2001)
21479502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
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CR753971
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1. 906
| organisms=Momo sapiens"
| wol_type="mRNA"
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                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 916)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
        602501030F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614679 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGGAGCGTAACAGCCTACATTGCC
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                                                                                                                                                                                                                                                                                                                                                                   Email: cgapDs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can bfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1366 row: I column: 08
High quality sequence stop: 730.
Location/Qualifiers
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Homo sapiens
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKPZ);
Bmail s.wiemanngekfz-heidelberg.de; sequenced by Medigenomix
(Martinsried/Germany) within the CDNA sequencing consortium of the
German Genome Project. This clone (DKPZp669C2337) is available at
the READ Deutsches Resourcentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469C2337
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="DKFZD669C2337"
/tissue_type="kidney"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/clone="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
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/mol_type="mRNA"
/db xref="taxon:9600"
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                                                                                                                                                                                                                                                                                                                                              Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.

(bases 1 to 961)

Boardman, P.E., Sana-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Compy.W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNAs.

Curr. Biol. 12 (22), 1965-1969 (2002)
                      MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                               LeulleSerLeuPheSerIleProVallleTyrGlu-ArgHisGlnValGlnIleAspHi 161
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                                                                 463 ATGIGGGTATTTACCTATGITGCTGCTTGTTTAATGGTCTGACACTACTGATTTTGGT-
        GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST1198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PO Box 88, Manchester, M60 1QD, UK
Tel: 016122008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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                                                                                                                                                                                                   641 CCCTGGATTGAAGCGCAAAGTGAAT 665
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BQ807975
NISC_kK12d10.yl NCI_CGAP_Brn72 Macaca mulatta cDNA clone
IMAGE:5331139 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 619)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: The I.M.A.G.E. Consortium/LLNL
CDNA Sequencing by: National Institutes of Health Intramural
   961
171
9
8
8
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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GI:50275382
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                                                                                                                                    /clome="IMAGE:5331139"
/tissue_type="hypothalamus"
/lab_host="DHIOB (phage-resistant)"
/clome lib="NRIO GGAP Brn72"
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/incte="Corgan: brain; Vectoring infractionally. Primer: Oligo dT.
Average insert size 2.2 kb. Constructed by Invitrogen.
Note: this is a NCI_GGAP Library."
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                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                  /organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
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829.00
98.84%
96.53%
89.62%
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Best Local Similarity:
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ACCESSION

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Gallus gallus (chicken)

Gallus gallus

Gallus gallus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

El (Dasses I to 669)

Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B.,

Patricio, M., Ledur, M.C. and Coutinho, L.L.

Discovery of new genes expressed in the chicken breast muscle

Unpublished (2004)

Laboratory of Animal Biotecnology, Dep. of Animal Production

ESALQ - University of Sao Paulo

Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil

Tel: 55 19 3429 4438

Fax: 55 19 3429 4285

Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br
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Conservative:
Mismatches:
Indels:
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/lab host="nplloB"
/lab host="nplloB"
/clone_lib="NIH_MGC_95"
/clone_lib="NIH_MGC_95"
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(Gregaj; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIWH/MGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI547877 614 bp mRNA linear EST 05-SEP-2001
601192073F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5263026 5',
                                                                                                                                                                                                                                                                                           rLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182
                    tTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLe 142
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                                                                        uheuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMe 122
                                                                                           GCTGAGACGCCTCTTCCTCGTTGATGACTTGGTTGATTCTCTGAAGTTTGCAGTGTTGAT 401
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 614)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov

Plate: LLAMI163 row: b column: 19

High quality sequence stop: 614.
                                                                                                                                                                   GTGGGTGTTCACTTACGTTGGTGCCTTGTTTAATGGTCTGACATTACTGATACTGGTCTTT
                                                                                                                                                                                                                                       GATTTCGCTGTTCAGTGTTCCTGTTATTTATGAGAGACATCAGGCCCAGATCGACCATTA
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uGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Homo sapiens"
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SOURCE
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AUTHORS
TITLE
JOURNAL
COMMENT
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LX/112/2

DKFZp469F2235 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKFZp469F2235 S', mRNA seguence.
                                                                                                                                                                                                                                                                                                                                                       GGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAA 186
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This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSer 115
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pongo.
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Further information about the clone and the sequencing project is
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                                                                                                                                                                                                                                                                                  GTGGTGTTTGGTGCCAGCCTATTCCTGCTTTTCATTGACAGTATTCAGCATTGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                      56 GlyvalileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 SerGluValAlalleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHis
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                                                                                                                                                                                                                                                                                                                                  ValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLys
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Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysileGlnhlaLysileProGlyLeuLysArgLysAlaAsp 189
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169
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Length:
Matches:
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Lebkowski, J and Stanton, L.W
   Fang, R.,
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828.00
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/organism="Pongo pygmaeus"

/organism="Pongo pygmaeus"

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/clone="DKF2p469F2235"

/clone type="kidney"

/dev atage="adius"

/lab_host="DH10B"

/clone lib="469 (synonym: pkid1)"

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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 708)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
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17000599934467 GRN_PRENEU Homo sapiens CDNA 5', mRNA sequence.
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at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
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Mismatches:
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CN429726.1 GI:47417320
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LOCUS
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1. .708
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/note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
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                              Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 708 Std Brror: 0.00.
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Matches:
Conservative:
Mismatches:
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603138816F1 CSEQCHL15 Gallus gallus cDNA clone ChEST12704 5', mRNA
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Boardman, P. B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATCTAGGACTTGCAAATAAGGAATGTTACAGATGCTAATGGTTAAAATCCAAAGGAAAAA 716
                              LeulleSerLeuPheSerlleProVallleTyrGluArgHisGlnValGlnIleAspHis 161
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
                                                                                                                                                                             GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                                                                                                                                                                                                                                       122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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                                                                                                                                           102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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PO Box 88, Manchester, M60 1QD, UK
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. 934
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Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 755)

E 1 (bases 1 to 755)

S NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCN1564 row; j column: 10

High quality sequence stop: 719.

Location/Qualifiers
                                                                BG568630 755 bp mRNA linear EST 10-APR-2001 602587637F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4716393 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10697 row: o column: 08
High quality sequence stop: 763.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

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I (Dapublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Michael J. Brownstein (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Locatin/Qualifiers

Locatin/Qualifiers
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6031895633F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261007 5',
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                 LeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeu
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AW230936 543 bp mRNA linear EST 10-DEC-1999 uo69£05.yl NCI CGAP Maml Mus musculus CDNA clone IMAGE:2647809 5' similar to TR:094962 KIAA0886 PROTEIN. ;, mRNA sequence. AW230936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/lab_host="minths"
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/clone lib="NCI_CGAP_Mam1"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 GTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Other ESTs: uo69f05.xl
Contact: Robert Strausherg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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/mol_type="mRNA"
/strain="FVB/N"
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High quality sequence stop: 437.
Location/Qualifiers
                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
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AV702687 ADB Homo sapiens cDNA clone ADBBBB01 5', mRNA sequence.
AV702687.1 GI:10719017
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1 (bases 1 to 719)

Peng Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, Z., and Han, Z.

Unpublished (2000)
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Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801912
Fax: 86-21-50801922
Fax: 86-21-50801922
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            aLeuIleSerLeuPheSer-IleProValIleTyrGluArgHisGlnValGlnIleAspH
                                                                                                                LeuPheLeuLeuLeuSerLeuThrValPheSer1leValSerValThrAlaTyr1leAla
                                                                                                                                                                  LeualaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle
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                                                            ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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                                     x BI548612 (1-815)
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 IleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerVal 170
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                                                                                                 /clone lib="ADB"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
KhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGATGCTATGGCTAANATCCAAGCAAAAATCCTTGGATTGAAGCGCANAGCTGAA 538
                                                                                                                                                                                                                                                                                                                                                             SeralaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp
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171
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                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
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/mol type="mskNa"
/db xref="taxon:9606"
/clone="ADBBBB01"
/tissue_type="Adrenal gland"
/dev stage="Adrenal gland"
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                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: June 19, 2005, 10:16:37 Job time : 2588 secs
                                                                                                                                                                                                                                                                                                                            US-09-830-972-2_COPY_975_1163 (1-189)
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821.00
96.67%
95.00%
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein

June 16, 2005, 12:31:51 ; Search time 170.11 Seconds Run on:

(without alignments)
2678.292 Million cell updates/sec

US-09-830-972-29 Title:

5923 1 MEDLDQSPLVSSSDSPPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched: 2105692

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04: Database :

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp1980s:* geneseqp2000s:*

geneseqp2003bs:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aay71311 Human neu	Human	Abp68600 Human pan	Human	Adp45551 Human Nog	Aay56967 Human MAG	Aab82349 Human NOG	Abg30938 Human Nog	Abb81078 Human neu	Adp67234 Human Nog	Adr13966 Human NOG	Ado08103 Human pol	Adk67502 Human RTN	Ado26400 Human tru	Aau33228 Novel hum	Abul1573 Human MDD	Aay95012 Human sec	Aay71310 Rat neuri	Abb81074 Rat neuro	Ado26399 Rat trunc	Adp45572 Rat NogoA	Aay71557 Rat Nogo	Adt89537 Mus muscu	Aay71384 Alternati	Ado08105 Mouse pol
	ID	AAY71311	AAU04591	ABP68600	ABR59667	ADP45551	AAY56967	AAB82349	ABG30938	ABB81078	ADP67234	ADR13966	AD008103	ADK67502	AD026400	AAU33228	ABU11573	AAY95012	AAY71310	ABB81074	AD026399	ADP45572	AAY71557	ADT89537	AAY71384	AD008105
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	Match	99.3	98.2	98.2	98.2	98.2	98.1	98.1	98.1	98.1	98.1	98.1	98.1	97.8	97.2	93.3	77.0	74.3	72.5	72.5	72.5	72.5	72.5	72.4	72.4	72.2
ć	Score	5882	5815	5815	5815	5815	5810	5810	5810	5810	5810	5810	5808	5794	5758	5526.5	4560	4400	4296.5	4296.5	4296.5	4296.5	4294.5	4289	4286.5	4277.5
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'note= "Region specifically described in claim 16"

99WO-US026160.

05-NOV-1999;

02-JUN-2000.

WO200031235-A2

Adp45553 Human NiG Aay71560 Rat Nogo Aaw58383 Human sec	Aab90682 Human BG1 Aay71562 Rat Nogo Ad026414 Rat trunc Aay1386 Rat Nogo		Ado26415 Rat trunc Aay71387 Rat Nogo Aay71394 Rat Nogo Aay71388 Rat Nogo	Aay71396 Rat Nogo Aay71389 Rat Nogo Aay71563 Rat Nogo Aay71392 Rat Nogo	A bo Huma
ADP45553 AAY71560 AAW58383	AAB90682 AAY71562 ADO26414 AAY71386	AAY71391 AAY71398 AAY71399	ADO26415 AAY71387 AAY71394 AAY71388	AAY71396 AAY71389 AAY71563 AAY71392	AAY5624 AAY56969
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ALIGNMENTS

RESULT 1

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Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antieense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening.
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/note= "Region specifically described in claim 16"
                                                                                                                                                                                                                                        Human neurite growth inhibitor Nogo.
                                 AAY71311 standard; protein; 1178 AA
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                                                                                                                                                                                                                                                                         The present sequence is a human Nogo protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The human Nogo sequence was derived by aligning human expressed sequence tags (ESTS) e.g. AA156616, AA313267, AA081783, AA167765, AA322918, AA092565, AA081525 and AA081840 with the rar Nogo sequence. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
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                                                                                                                                                                            roteins and nucleic acids useful for treating neoplastic disorders central nervous system and inducing regeneration of neurons.
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Pred. No. 9.3e-297;
0; Mismatches 3;
                                                                                                                                                                                                                                      Claim 11; Fig 13; 122pp; English.
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98US-0107446P
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Best Local Similarity 99.7
Matches 1175; Conservative
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                                     (SCHW/) SCHWAB
(CHEN/) CHEN M
06-NOV-1998;
                                                                                                 Schwab ME,
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                              EKDSESSNDDTSPPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE
                                                                                                                  KKIEBKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL
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26-SEP-2001 (first entry)

Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein; cranial trauma; cerebral trauma; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasis demyelination; encephalowyelitis; multifocal leukoencephalopathy; panencephalitis; Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy; Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; viral infection;

Homo sapiens

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The sequence is the human Nogo protein, a 250kDa myelin-associated axon nogo protein, their nucleic acide, vectors expressing them and antibodies against them, to isolate acide, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral frommas, spinal cord injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasis demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bigmami disease, pontine myelinolysis, adernoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease
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quence is specifically claimed"
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sequence is specifically claimed"
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claimed"
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Pred. No. 2.8e-293;
4; Mismatches 13;
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1064. 1088
/label= Pep2
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1084. .1108
//nobel= Pep4
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1095. .1119
//nore- Pep5
                                                  "This sequence is
                                                                                                                                           /note= "Receptor binding
sequence is specifically
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            Location/Qualifiers
1054. .1119
'label= Lumenal_ext'
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26-MAY-2000; 2000US-0207366P.
29-SEP-2000; 2000US-0236378P.
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|abel= Pep3
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                                                                .055. .1094
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                                                                                          SSGA-----VVXXXXXXIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polymucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75 configuous contiguous; (c) appearance variants of (a). Polymeptides (ABF68596-ABF68597) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polymeptides, polymucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polymeptide are useful in treating pancreatic cancer and stimulating an immune response. The polymucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour peparation of ribozyme molecules for inhibiting expression of the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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diagnosing, preventing and/or treating cancer, particularly pancreatic
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28-APR-2001; 2001US-0287112P.

16-MAY-2001; 2001US-0291631P.

21-JUL-2001; 2001US-0305484P.

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27-NOV-2001; 2001US-0313626P.
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The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (PI, human Nogo receptor (NGR) NTLRCT domain), or residues 27-309 of PI with 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive residues. The nucleic acid of the in yention has neuroprotective activity. The polynucleotide may have a use in gene therapy. The nucleic acid is useful for decreasing inhibition of axonal growth by a central nervous system (CNS) neuron. The NgR poptide or an agent inhibite the binding of Nogo to NgR or NgR poptide or an agent inhibite the binding of Nogo to NgR or NgR copendent signal transduction in the central nervous system injury, e.g. spinal cord injury. Expression of an NgR protein may be associated with trauma, stroke or a demyelinating disease, such as multiple sclerosis, monophasic demyelination, encephalomyelitis, woultifocal
                                                                                                                                                                                                                                                                                       Human, Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy, axonal growth; central nervous system; CNS; Nogo; spinal cord injury; cranial trauma; spinal trauma; spinal trauma; stroke; Krabbe's disease; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukcencephalopathy, panencephalitis, or Krabbe's disease. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system neuron, or in treating central nervous system disease, disorder or injury, e.g. spinal cord injury.
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                                                                                                                                                                                                                                                                                                                binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder.
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LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
                      Vitaliti A;
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Pred. No. 2.8e-293;
4; Mismatches 13;
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                                                                                                                                               protein; 1192
                                                                                                                                                                                                                                                                           Human NogoA protein SEQ ID NO:5.
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(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
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97.2%;
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Matches 1160; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleoitde is also useful for chromosome localization and for tissue expression studies. The present sequence represents the human MAGI protein
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                                                                                                                                                                                                   MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; stroke; cytostatic; cerebroprotective, neuroprotective.
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Pred. No. 5.1e-293;
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                                                  standard; protein; 1192
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N-PSDB; AAZ56886.
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Best Local Similarity
Matches 1159; Conserv
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        NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuropyrotective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy.
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                                                                                                                                                                                                                                                                                                                                         New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
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Pred. No. 5.1e-293;
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2000GB-00001550.
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N-PSDB; AAF90324.
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Matches 1159; Conserv
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24-JAN-2000;
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Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE by Dypetides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent interaction between these polypeptides, and determining if the test agent caute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas, carriers and in neoplastic (e.g. glioblastomas, carriers have many be carriable, keloid formation, fibrocystic conditions, tissue thypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may be useful in treating Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polynucleotide encoding the BACE polypeptide are useful in expensive to the modulation of a patient suffering from this capacitation of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polynucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy contining the internation of the modulation of degree represents the human Nogoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPPSTPAAPKRG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
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|SGGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP
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       system; axon regeneration; NogoA;
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Pred. No. 5.1e-293;
4; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                              Prinjha R,
                          disease; metastasis
                                                                                                                                                                                                                                                                                                        (GLAX ) GLAXO GROUP LTD.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                            18-JAN-2001; 2001GB-00001312.
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97.2%;
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    central
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Matches 1159; Conservative
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    tissue hypertrop
Nogo-associated
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nootropić; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; human; receptor.
      Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
                                                                                                                                                                            Beserman P,
                                                                                                                                                                            Cohen IR,
                                                                                                                                                                            Hauben E,
                                                                                                                     98MO-US014715.
98WO-US014715.
98US-00218277.
                                                                                                                                                            (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                             99US-00314161.
                                                                                                         2001US-00893348
                                                                                                                                                                           isenbach-Schwartz M,
balem G;
                                                                                                                                                                                                  2002-607255/65.
                                                                                                                                                                                                          N-PSDB; ABN86601
                                                                          US2002072493-A1
                                                                                                                      19-MAY-1998;
21-JUL-1998;
22-DEC-1998;
                                                            Homo sapiens
                                                                                                         28-JUN-2001;
                                                                                                                                             19-MAY-1999;
                                                                                         13-JUN-2002
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degeneration in the Promoting nerve regeneration and preventing neuronal degeneratior central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, analogs/peptides

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Mosonego

Page 53-56; 93pp; English.

The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central peripheral nervous system (NS). The method involves administering NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt crauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not autoimmune disease or neoplasm. The disease results in a degenerative continuance disease or neoplasm. The disease results in a degenerative continuance in the gray or white matter or both. The disease is disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disease, including but not limited the neuropathies associated with various diseases including but not limited the neuropathies associated with various diseases including but not limited the neuropathies associated with various diseases including but not limited the neuropathies associated with various diseases including but not limited the neuropathies associated with various diseases including but not limited the neuropathies associated with various diseases including but not limited the neuropathies associated with various diseases including but not limited the neuropathies associated with various diseases. pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangectasia, Friedreich's ataxia, amyloid polyneuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the human neurotransmitter receptor protein Nogo-A, an example of NS-specific to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute sensory neuropethy, chronic ataxic neuropethy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (19)A- and 19G gamma-

Sequence 1192 AA

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                      16;
Length 1192;
                       Indels
Score 5810; DB 5;
Pred. No. 5.1e-293;
4; Mismatches 14;
 98.1%;
97.2%;
                         Conservative
Query Match
Best Local Similarity
               Best Local Sim
Matches 1159;
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VPGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES 1079 1125 286 466 586 705 765 825 180 300 346 406 420 480 526 600 720 780 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALA-TQAEIBSIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLAMVPTYVGALFNGLT AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPAPPSTPAAPKRRG --VVXXXXXIMDLKEQPGNTISAGOEDFPSVLLETAASXPSLSP SSEKAKOSFNEKRVAVEAPMREEYADFKPFERVWEVKOSKEDSDMLAAGGKIESNLESKV DKKCPADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE PLIGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLXPAAQLCPSF EESEATPSPVL.PDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE SNDDLFISKEAQIRETETPSDSSPIEIIDEPPTLISSKTDSFSKLAREYTDLEVSHKSEI ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGH SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGOEDFPSVLLETAASLPSLSP SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV DKKCFADSLEOTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF EVVANMPEGLIPDLVQEACESELNEVIGIKIAYETKMDLVQTSEVMQESLYPAAQLCPSF EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE MAKVEQPVPDHSBLVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY SNDDLFISKEAQIRETETFSDSSPIELIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV VFGASLFLLLSLTVFSIVSVTAYIALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTKLVKEDEVV SSGA---096 241 361 587 1006 19 121 181 181 301 407 467 481 527 541 601 647 661 90/ 994 781 826 886 901 946 1020 61 227 287 347 421 g a g 셤 g 엄 셤 셤 g 8 8 g 셤 ò g ò g g ઠ 셤 ò 셤 8 à ò 셤 à à ò ò ò ઠે Š ઠે ઠે

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                                                                                               LSAASFKEHEYLGNLSTVLPTEGTLOENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM
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|SGGSVDETLFALPAASEPVIRSSAENMDLKEOPGNTISAGQEDFPSVLLETAASLPSLSP
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1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLT
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contactin-associated protein-1; Caspr; neuroprotective; gene t
CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.
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Best Local Similarity 97.2%;
Matches 1159; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a myelin-associated glycoprotein (MAG)

derivative comprising a mutation in or flanking MAG Ig-like domain 5

(Igd5), excluding the MAG derivative MAG (da-1)-Fc, where the mutation

reduces or eliminates the ability of the derivative to regulate neurite

outgrowth as compared to endogenous or soluble MAG without eliminating

to binding to neuronal surfaces. The inhibitors of MAG are useful for

promoting neural degeneration associated with injuries, disorders, or

treating neural degeneration associated with injuries, disorders, or

diseases. The disorder, disease, or condition is associated with

c apoptosis or results from a demyelinating disease and includes

amylotrophic lateral sclerosis, Alzheiner's disease, Parkinson's disease,

Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease,

kuru, multiple system atrophy, amylotrophic lateral sclerosis (Lou

Gehrig's disease), or progressive supranuclear palsy. The present

sequence represents the amino acid sequence of human NOGO-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New myelin-associated glycoprotein (MAG) derivative comprises a mutation in or flanking MAG Ig-like domain 5 (Igd5), excluding the MAG derivative MAG (d1-3)-Fc, useful promoting neural growth and regeneration.
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                                                                                                            human; myelin-associated glycoprotein; MAG; neural growth; neural regeneration; apoptosis; amylotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease; Huntington's disease; multiple sclerosis; Creutzfeldt-Jacob disease; kuru; multiple system atrophy; Lou Gehrig's disease; progressive supranuclear palsy.
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Pred. No. 5.1e-293;
4; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 9; 81pp; English.
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97.2%;
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(DOME/) DOMENICONI M.
(CAOZ/) CAO Z.
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N-PSDB; ADR13965.
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                                                                                                                                                                                                                                                                                    US2004121341-A1.
                                                                                                                                                                                                                                                 Homo sapiens
                                                                             Human NOGO-A
                                        23-SEP-2004
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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene crelative to expression of the gene relative to expression of the gene relative to expression of the gene relative to expression of the gene relative to expression of the gene relative to expression of the gene relative to expression of the gene relative to expression of the agent and identifying fat cell mumber or size in the subject comprises a mammal, preferably a human. The collypeptide to the agent, detecting binding of the agent to the polypeptide and an agent, exposing the polypeptide to a change in an activity of the polypeptide, treating a subject of a changes in an activity of the polypeptide, treating a cumber or size comprises an antibody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the comprise providing a useful for identifying compounds that influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents a human polypeptide used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
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                                                                                                      Human; fat cell number; fat cell size; obesity; diabetes; anorectic;
antidiabetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; SEQ ID NO 429; 275pp; English.
                                                                                                                                                                                                                                                                                               09-OCT-2002; 2002US-00267502
                                                                                                                                                                                                                                                                                                                                           09-OCT-2002; 2002US-00267502.
                                                                                                                                                                                                                                                                                                                                                                                   (LIFE-) LIFE SCI DEV CORP.
                                                              Human polypeptide #65
                    (first
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                                                                                                                                                                                                            US2004071700-A1
                                                                                                                                                                    Homo sapiens.
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1125 300 480 959 346 406 420 466 540 586 9 646 9 705 765 780 825 840 885 900 945 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM GSSFSVSPKAESAVIVANPREEIIVKNKDEEKLVSNNILHXQQELPTALTKLVKEDEVV GSSFSVSPKAESAVIVANPREELIVKNKDEEEKLVSNNILLHNQQELPTALTKLVKEDEVV EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE EAMSVSLKKVSGIKEBIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVY ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALA-960 TQAEIESIVKPKVLVKBAEKKUPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV -- VVXXXXXXIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSBLEYSEM SSEKAKDSFNEKRVAVEAPMREEYADPKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV DXXCFADSLEQTNHEXDSESSNDDTSFPSTPEGIXDRSGAYITCAPFNPAATESIATNIF PLIEDPTSENXTDEKKI EEKKAQI VTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSBVMQESLYPAAQLCPSF EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLOMEELSTAVY SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGH 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIXKGVIQAIQKSDEGHPFRAYLES EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLT 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLT TOABIBSIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178 SSGA----901 181 946 1066 287 421 481 541 587 841 1126 1140 227 347 407 527 601 647 661 904 721 99/ 781 826 886 181 241 301 467 RESULT 13 셤 윱 q a ď g 8 셤 8 ઠે ઠે ð ઠે 셤 δ 원 ò 요 ò 셤 ò g ò 원 g g 유 8 ઠે ò ò ò

ADK67502 ID ADK67502 standard, protein, 1192 XX

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                                                                                                                                                EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE
                                                                                                                                                                                                             EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE
                                                              EVVANMPEGLIPDLVQEACESELNEVIGIKIAYETKMDLVQTSEVMQESLYPAAQLCPSF
                                                                                 EVVANMPEGLIPDLVQEACESELNEVIGIKIAYETKMDLVQTSEVMQESLYPAAQLCPSF
                                                                                                                            EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE
                                                                                                                                                                                         EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE
                                                                                                                                                                                                                                                                                                                                       EYENKEKLSALPPEGGKPYLESFKLSLINTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY
 PLLEDPTSENXTDEKKI EEKKAQI VTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE
                                                                                                                                                                                                                                                                               MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI
                                                                                                                                                                                                                                                                                                                     EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVY
                                                                                                                                                                                                                                                                                                                                                                                                      ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rat; human; Nogo-A; truncated; affinity; membrane-bound
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                                                                                                                                                                                                                                                                                                                                                                                              polypeptide having BACE1 activity, useful in preparing a composition treating amyloidosis or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polypeptide having BACE1 activity. The protein is useful in preparing a composition for treating amyloidosis or Alzheimer's disease. This sequence corresponds to the RTM-4A protein.
                                                                                           therapy; BACE1 activity; RTN4; RTN3; amyloidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
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||||| SGGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP
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Pred. No. 3.5e-292;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 52; SEQ ID NO 7; 42pp; English.
                                                                                                                                                                                                                                                                   17-APR-2002; 2002US-0373284P.
                                                                                                                                                                                                                                      08-APR-2003; 2003WO-US008829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.8%;
Best Local Similarity 97.0%;
Matches 1157; Conservative
                                                                                                                                                                                                                                                                                                   (PHAA ) PHARMACIA & UPJOHN
                             (first entry)
                                                                                           neuroprotective; gene
Alzheimer's disease.
                                                           Human RTN-4A protein
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                                                                                                                   SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI
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                     EYENKEKL.SAL.PPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEBLSTAVY
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26-JAN-2001;
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                                                                                                                                                                                 The present invention relates to an isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein from the rat and from the human. The truncated polypeptide is useful for identifying a compound having detectable affinity to a Nogo-A protein. The present sequence is a Nogo-A polypeptide of the invention.
                                                                        New isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein, useful for identifying a compound having detectable affinity to a Nogo-A protein.
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|SGGSVDETLFALPAASEPVIRSSAENMELKEQPGNTISAGQEDFPSVLLETAASLPSLSP
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Pred. No. 2.6e-290;
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                                                                                                                                                Claim 1; Fig 6B; 80pp; English.
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Matches 1148; Conservative
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                                     WPI; 2004-376159/35
Fiedler
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for genetic The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or Human, vaccination, gene therapy, nutritional supplement; stem cell proliferation, haematopoiesis, nerve tissue regeneration, immune suppression, immune stimulation, anti-inflammatory, leukaemia. human polypeptides, useful in

ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGH ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALA-

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SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI

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tendon
physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                         Length 1246;
                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                         . Score 5526.5; DB 4;
; Pred. No. 2.8e-278;
13; Mismatches 39;
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Best Local Similarity
Matches 1123; Conserv
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286 120 180 226 346 406 466 586 646 705 765 825 101 161 221 281 341 401 461 521 526 581 641 701 761 821 9 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEDEDDLEELEVLERKPA SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAAPAAPPSTPAAPKRRG GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPEROPSWDPSPVSSTVPAP AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAAPAAPPSTPAAPKRRG SSGA-------VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV DKKCFADSLEQTWHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKWDLVQTSEVMQESLYPAAQLCPSF **EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE** EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY EYENKEKLSALPPEGGKPYLESFKLSLDNTXDTLLPDEVSTLSKKEKIPLQMEELSTAVY MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDBEEEEEEEEBBDEDBLEBLEVLERKPA LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF PLLEDPTSENXTDEKKI EEKKAQI VTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXOOELPTALTKLVKEDEVV MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI Gaps 33; Indels Conservative 342 Н 762 42 61 102 121 222 282 287 347 402 407 462 467 522 527 582 587 642 647 702 904 991 227 181

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time: 175.11

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VGALFNGLTLL-----ILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI

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1006

1001 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV

TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV

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988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1047
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Best Local Similarity 99.0
Matches 189; Conservative
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Sequence 9180, Ap
Sequence 6, Appli
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Sequence 8, Appli
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Sequence 8, Appli
Sequence 5000, Ap
Sequence 8859, Ap
Sequence 563, App
Sequence 45132, A
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4600, Ap
4601, Ap
32, Appl
1246, Ap
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Appli
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3, Appli
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1976.818 Million cell updates/sec
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5923
1 MEDLDQSPLVSSSDSPPRPQ......VKDAMAKIQAKIPGLKRKAE 1178
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-08-700-607-7
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US-09-513-9960-60
US-09-149-016-8859
US-09-270-767-45132
US-09-270-767-45132
US-09-709-607-3
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-08-714-741-32
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US-09-345-473E-40
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Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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276.5
267.5
                                                                                                                                                                                                                                              Minimum DB :
Maximum DB :
                                            OM protein
                                                                                                                                        Sequence:
                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
No.
                                                                   Run on:
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Sequence 6978, Ap Sequence 10933, A Sequence 13, Appl Sequence 5, Appl Sequence 5, Appl Sequence 8902, Ap Sequence 8903, Ap Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 5, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl S
                                                                                                                                                                                                                                                                                                                                   Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TILLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                    ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-055
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 199 amino acids
TYPE: amino acid
                                         MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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                    U.S.
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Gaps

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15.7%; Score 931; DB 2; Length 199; 99.0%; Pred. No. 1e-49; tive 0; Mismatches 2; Indels

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957 KVLEKEAEKKLPSDTEKEDRSPSA-------IFSADLGKTSVVDLLYWRDIK 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                676 EAPYISIACDL------IKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVED 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 PAPYID---DLSEEQRRAPQITTPVKITLTEIEPSVE-----TTTQEKTPEKQDICLK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 SSAESGD------SEIELVSEDPMAAEDALPSGYVSFGHVGGPPPSP 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 ASPSIQYSILREEREAELDSELIIESCDASSAS-----EESPKREQDSPPMKPSALD 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LPPDVSALGHTQAEIESIVKP 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         723 SSPDSEPVDLFS---DDS------IPDVPQKQ-----DETVMLVKESLTETSF 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        762 ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMBELS 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------EVKARSGPPTIPSPLDHEA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIOPKVEEKISFSD 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822 TAVYSNDDLFISKEAQIRETETFSDSSPIEIIDBFP----TLISSKTDSFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGPELPPGDGAL----EPETPMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   588 ESEATPSPVLPDI --VMEAPLNSA-----VPSAGASVIQPSSSPLE---ASSVNY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.3%; Score 787.5; DB 2; ilarity 31.9%; Pred. No. 4.5e-40; Conservative 91; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                922 DF-----SKNGSATSKVLL---
                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
TELECHONE: 415-855-0555
TELECHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 -KGLSYETAENPRPVGQLADRP-
                               1: Incyte Pharmac
3174 Porter Drive
                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 776 amino acids
TYPE: amino acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pha:
STREET: 3174 Porter D:
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: GenBank
CLONE: 307307
                                                                                                           u.s.
                                                                                                                            ZIP: 94304
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Best Local Simi
Matches 229;
                                                                                                           COUNTRY:
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Sequence 9124, Application US/09949016

Sequence 9124, Application US/09949016

Sequence 9124, Application US/09949016

Sequence 9124, Application US/09949016

Sequence 9124, Application US-0919916

SERNEAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
                                                                                                                                               1107
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                                                                                                           128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 AVLMWVFTYVGALFNGLTLILLALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
      9 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLIVPSIVSVTAYIALALLSVTISFRIYKGVI
                                                                    QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKF
                                                                                         69 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 KDKVVDLLYWRDIKKTGVVFGASLFILLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKF
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Pred. No. 1e-49;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08700607
Patent No. SBS8708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.7%;
99.0%;
                                                                                                                                                                                                                             1168 AKIPGLKRKAE 1178
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                                                                                                                                                                                                                                                                   AKIPGLKRKAE 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Human
US-09-949-016-9124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Fast:
SEQ ID NO 9124
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-700-607-5
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us-09-830-972-29.rai

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Sequence 9180, Application US/09949016
Factor No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE REPERENCE: CL001307
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 05/09/49,016
CURRENT PILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-37
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
                                         ----IFSADLGKTSVVDLLYWRDIK 1001
                                                                                                                         KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRA 1061
                                                                                                                                                                                                         YLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALF 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 996 YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDE 1055
                                                                                                                                                 497 AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGPELPPGDGAL----EPETPMLP 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   774 SALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIS 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GGPPPSPASPSI----IESCDASSAS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            834 KEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAG 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 EESPKRE----ODSPPMK-----PSALDA-----IREETGVRAEERAPSRRGLAEPG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SL---PCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGHTQAEI 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESIVKPKVLEKEAEKKLPSDTEKEDRSPSA-------IFSADLGKTSVVDLL 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 ETPMLP-----RKPEEDSSSNQSPAATKGPGPLGPGAPPPLLF---LNKQKAIDLL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                         NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
                                                                                                                                                                                                                                                                                                             11 KGSISEDELITA-----IKEAKGLSYETAENPRPVGQLADRPEVKARSGPPTIPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           715 - DHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMIBYENKEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           659 KEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQP--VP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%; Score 727.5; DB 4; Length 439; 36.8%; Pred. No. 9.7e-37; tive 68; Mismatches 138; Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9180
LENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 SFLDYPSTE------POPGPE----
                                         KVLEKEAEKKLPSDTEKEDRSPSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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US-09-949-016-9180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200;
                                                                                                                         1002
                                                                                                                                                                                                                                                                                            1122
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Best Local S:
Matches 200
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                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION.

JAPPLICANT: VENTER, J. Craig et al.

APPLICATT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 6998

TENNER. 176
                                                                                                 1062 YLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALF 1121
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                   1002 KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRA 106
                                         141 EELGTPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQMKAEAYKYIDIT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 -KGLSYETAENPRPVGQLADRP-----EVKARSGPPTIPSPLDHEA 403
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                                                                                                                                                                                                                                                                                                                            Sequence 6998, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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  920 SDDFSKNGSATSKVLLLPPDVSALGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPS 979
                                       -----RKPEEDSSSNQSPA 145
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                                                                                                    1085 VNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALPNGLTLLILALISLFSVPVIYERH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Gli, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: THO NOVEL HUMAN NSP-LIKE PROTEINS
                                                                                                                                                                                                                                                                                                                      1145 QAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
                                                                                                                                                                                                                                                                                                                                              323 QAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 356
                                    ----EPETPMLP-
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IRM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRANICH/COCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08700607
Patent No. 5858708
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Matches 129; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat.
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CORRESPONDENCE ADDRESS:
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                                                           GHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFT 1115
                                                                                                                                       1116 YVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKR 1175
803 EVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISS 862
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                                                                                  317 GHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLMHLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 705; DB 2;
Pred. No. 1.7e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 42.6
Matches 168; Conservative
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LENGTH: 356 amino acid
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CORRESPONDENCE ADDRESS:
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LIBRARY: General
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US-08-700-607-6
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US-08-700-607-6
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NAME/KEY: UNSURE
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                                                                                                                     US-09-513-999C-5000
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US-09-949-016-8859
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                                                                  1108 AVLAMVETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1167
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1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKF 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        988 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hilman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.3%; Score 671; DB 2; 66.3%; Pred. No. 1.4e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEMOVERSION 1.5
CURRENT APPLICATION DATA: US/08/700,607
APPLICATION WINBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0114 US
                                                                                                                                                                                                                                                      Sequence 8, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 Porter Drive CITY: Palo Alto COUNTY: CA COUNTY: U.S. ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IELEFAX: 415-855-0555
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 66.3%
Matches 124; Conservative
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                                                                                                                                                                    198 AKIPGAKRHAE 208
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IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 281046
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Sequence 8859, Application US/09949016

Patent No. 6812339

GENERAL INCORPARATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINHER: US/09/949,016

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,758

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                              Sequence 5000, Application US/09513999C

Sequence 5000, Application US/09513999C

Sequence 5000, Application US/09513999C

GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR PLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5000
LENGTH: 129
129 AVLAWILTYVGALFNGITILILMAVVSMFTLPVVYVKHQAQVDQYLGIVRTHINTVVAKIQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKXXIPLQMEELSTAVY 120
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Pred. No. 5.3e-32;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 106
OTHER INFORMATION: Xaa=Glu or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 107
CTHER INFORMATION: Xaa=Lys or Thr
US-09-513-999C-5000
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98.4%;
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                                                        1168 AKIPGLK 1174
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                                                                                                            189 AKIPGAR 195
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Best Local Similarity
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R APPLICATION NUMBER: 60/047,581
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,584
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,500
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,587
R APPLICATION NUMBER: 60/047,492
R APPLICATION NUMBER: 60/047,492
R APPLICATION NUMBER: 60/047,492
R FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                  R APPLICATION NUMBER: 60/047,598
R FILING DATE: 1997-05-23
A PPLICATION NUMBER: 60/047,613
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,582
R APPLICATION NUMBER: 60/047,582
R APPLICATION NUMBER: 60/047,582
R PILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/043,569
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,671
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,903
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PELICATION NUMBER: 60/043,674
LING DATE: 1997-04-11
PLICATION NUMBER: 60/043,669
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PLICATION NUMBER: 60/043,315
LING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICATION NUMBER: 60/056,886
ILING DATE: 1997-08-22
PPLICATION NUMBER: 60/056,877
ILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,878
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APPLICATION NUMBER: 60/056,662
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FILING DATE: 1997-08-22
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LING DATE: 1997-05-23
PPLICATION NUMBER: 60/047,632
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PPLICATION NUMBER: 60/047,601
LING DATE: 1997-05-23
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PLICATION NUMBER: 60/043,568
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PPLICATION NUMBER: 60/043,314
LING DATE: 1997-04-11
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LICATION NUMBER: 60/043,312
ING DATE: 1997-04-11
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LING DATE: 1997-04-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ING DATE: 1997-06-06
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EARLIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 FWMLMTYVGAVFNGITLLILAELLIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 182
                                                                                                                                                                                                                                                                                                                                                            3 SVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQA
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                           Length 192;
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                        Ouery Match 10.6%; Score 627.5; DB 4; Best Local Similarity 61.1%; Pred. No. 4.1e-31; Matches 116; Conservative 38; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8859
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/040,162
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,615
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,502
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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LING DATE: 1997-05-23
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APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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                                                                                       ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859
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US-09-149-476-563
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R PILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/057,761

R PILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/047,595

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599

R APPLICATION NUMBER: 60/047,588

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,588

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,585

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,585

R PILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/056,632
R FILING DATE: 1997-08-22
R PILING DATE: 1997-08-22
R PILING DATE: 1997-08-22
R PRILICATION NUMBER: 60/056,876
R PILING DATE: 1997-08-22
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R APPLICATION NUMBER: 60/047,593

R FILING DATE: 1997-05-23

R PELING DATE: 1997-05-23

R APPLICATION NUMBER: 60/043,518

R APPLICATION NUMBER: 60/043,578

R PILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,576

R APPLICATION NUMBER: 60/043,576

R APPLICATION NUMBER: 60/043,576
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,864
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,845
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,892
60/056,888
                                 APPLICATION NUMBER: 60/056,879
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,880
                                                                                      FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,894
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APPLICATION NUMBER: 60/056,911
                                                                                                                                                              FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,874
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/047,594
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,589
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,862
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/048,964

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1013 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE 1072
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REPERENCE: TO 8/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45132
LENGTH: 219
                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                               Length 168;
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8.8%; Score 522.5; DB 4;
Best Local Similarity 47.1%; Pred. No. 1.4e-24;
Matches 99; Conservative 47; Mismatches 61;
                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                            Query Match 9.1%; Score 541.5; DB 4 Best Local Similarity 60.5%; Pred. No. 6.5e-26; Matches 101; Conservative 34; Mismatches 31
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EARLIER APPLICATION NUMBER: 60/057,650
ERALIER FILING DATE: 1997-09-05
ERALIER PEDIJORION NUMBER: 60/055,884
ERALIER PEDLICATION NUMBER: 60/057,669
ERALIER FILING DATE: 1997-09-05
ERALIER FILING DATE: 1997-09-05
ERALIER PILING DATE: 1997-06-05
ERALIER APPLICATION NUMBER: 60/049,610
ERALIER FILING DATE: 1997-06-13
ERALIER FILING DATE: 1997-06-13
ERALIER FILING DATE: 1997-06-13
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US-09-949-016-7290
; Sequence 7290, Application US/09949016
; Patent No. 6912339
; GENERAL INFORMATION:
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Jennifer L.
TWO NOVEL HUMAN NSP-LIKE PROTEINS
    APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-I
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
                                                                                                                                                              COUNTR.

ZIP: 94304
COMPTER READABLE FORM:
MEDIUM TYPE: Diskette
"""TTER: IBM Compatible
""""TTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 47.7%
Matches 102, Conservative
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CITY: Palo Alto
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MOLECULE TYPE: pe
IMMEDIATE SOURCE:
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LIBRARY: THELL
TANK: 31870
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US-09-513-999C-6304
                                                                                                                                                  STATE: CA
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  APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307;
CURRENT FILING DATE: 2000-04-14

PRIOR PLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 7290

LENGTH: 588
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IGLFTIP1LYRQHQAQIDQYVGLVTNQLSHIKAKIRAKIPGTGALASAAAAVSGSKAKAE 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 164;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
8.7%; Score 514; DB 4; Length 588;
Best Local Similarity 28.2%; Pred. No. 1.9e-23;
Matches 169; Conservative 81; Mismatches 186; Indels 1
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US-09-949-016-7290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6304, Application US/09513999C
; Sequence 6304, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
    APPLICANT: Duclert, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
                                                              20;
          Score 513; DB 2; Length 241;
Pred. No. 6.1e-24;
                                                              55; Indels
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----KVPSKTPWNRQK 213
8.7%; Scor.
47.7%; Pred. No. b...
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Sequence 3, Application US/08700607; Patent No. 5858708; GENERAL INFORMATION: APPLICANT: Bandman, Olga APPLICANT: Au-Young, Janice APPLICANT: Goli, Surya K.

RESULT 14 US-08-700-607-3

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0; Gaps
                                                                                                             Query Match 5.9%; Score 347; DB 4; Length 68; Best Local Similarity 100.0%; Pred. No. 1.6e-14; Matches 68; Conservative 0; Mismatches 0; Indels
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6304
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6304
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Search completed: June 16, 2005, 12:33:39 Job time : 45.4839 secs

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OM protein - protein search, using sw model

June 16, 2005, 12:29:05 ; Search time 152.811 Seconds Run on:

(without alignments) 2960.058 Million cell updates/sec

US-09-830-972-29 Title: Perfect score:

5923 1 MEDLDQSPLVSSSDSPPRPQ......VKDAMAKIQAKIPGLKKKAE 1178 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1714042 seqs, 383979560 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

continued. Applications. Appli prodata/2/pubpaa/US10E_PUBCOMB.pep: prodata/2/pubpaa/US10 NEW PUB.pep: prodata/2/pubpaa/US11A_PUBCOMB.pep: prodata/2/pubpaa/US11A_PUBCOMB.pep: prodata/2/pubpaa/US11_NEW PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*/ ptodata/2/pubpa/US10C_PUBCOMB.pep: ptodata/2/pubpaa/US10D_PUBCOMB.pep: Published Applications AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 6, Appli	Sequence 6, Appli	Sequence 71, Appl	Sequence 2, Appli	Sequence 23, Appl	Sequence 429, App	Sequence 9, Appli	Sequence 9, Appli	Sequence 23, Appl	Sequence 7, Appli	Sequence 18, Appl
	ID	US-09-758-140-6	US-09-972-599A-6	US-10-060-036-71	US-09-789-386-2	US-09-893-348-23	US-10-267-502-429	US-10-327-213-9	US-10-466-258-9	US-10-810-653-23	US-10-408-967-7	US-09-893-348-18
	0B	6	σ	14	σ	0	15	16	16	16	15	σ
	Match Length DB	1192	1192	1192	1192	1192	1192	1192	1192	1192	1192	1163
*	Match	98.2	98.2	98.2	98.1	98.1	98.1	98.1	98.1	98.1	97.8	72.5
	Score	5815	5815	5815	5810	5810	5810	5810	5810	5810	5794	4296.5
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e 18, Appl e 10, Appl e 10, Appl e 431, App	6, Appli 24, Appl 72, Appl 8, Appli 24, Appli	Sequence 6, Appli Sequence 4, Appli equence 4, Appli Sequence 164, App equence 20, Appl	25, Appl 25, Appl 25, Appl 25, Appl 36, Appl 467, Appl 21, Appl	11 6 4 4 4 3 7 1 1 1 2 7 1 8 4 3 7 1 8 4 4 3 7 1 8 7 1 8 7 1 8 7 1 8 7 1 8 7 1 8 1 8
Sequence Sequence Sequence Sequence	Sequence o, Sequence 24 Sequence 24 Sequence 8 Sequence 8	Sequence 6, Sequence 4, Sequence 4, Sequence 16	Sequence 25, Sequence 25, Sequence 25, Sequence 25, Sequence 9, Sequence 21, Sequence 21,	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
US-10-810-653-18 US-10-633-423-10 US-10-427-741-10 US-10-257-502-431		D D	US-09-893-348-25-2 US-10-660-946-1 US-10-810-653-2 US-10-408-967-9 US-09-893-348-21 US-09-893-348-21	US-10-466-258-11 US-10-205-219-93 US-10-660-946-5 US-10-267-502-430 US-10-267-502-432 US-10-267-502-432 US-10-660-946-6 US-10-108-260A-2892 US-10-10-205-194-127 US-10-660-946-7
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ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Strittmatter, Stephen M.
APPLICANT: Strittmatter, Stephen M.
TITLE OF INVENTION: NO. US2002012965A10 Receptor-Mediated Blockade of Axonal Growth FILE REFERENCE: 4574-5073-US
CURRENT APPLICATION NUMBER: US/09/758,140
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/175,707
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR PILING DATE: 2000-05-29
PRIOR PELING DATE: 2000-05-29
PRIOR PILING DATE: 2000-09-29
US-09-758-140-6; Sequence 6, Application US/09758140; Patent No. US20020012965A1
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1192
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Gaps 16; 98.2%; Score 5815; DB 9; Length 1192; 97.2%; Pred. No. 3.4e-261; Indels Pred. No. 3.4e-261; 4; Mismatches 13; Best Local Similarity 97.2 Matches 1160; Conservative ઠે

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61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120

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us-09-830-972-29.rapb

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Sequence 6, Application US/09972599A

Patent No. US20020077295A1

GENERAL INFORMATION:
APPLICANT: STRITTMATER, STEPHEN M.
TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REPRESENCE: CO77 CIP US
CURRENT APPLICATION NUMBER: PCT/US01/01041

PRIOR APPLICATION NUMBER: PCT/US01/01041

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29

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Pred. No. 3.4e-261;
4; Mismatches 13;
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Best Local Similarity 97.2%;
Matches 1160; Conservative
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Length 1192;
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Best Local Similarity 97.2%; Pred. No. 5.9e-261;
Matches 1159; Conservative 4; Mismatches 14;
                                                                                                                                                                   APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANT: PRINHA, RABINDER KUMAR
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30165-C1
CURRENT APPLICATION NUMBER: US/09/789,386
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: U. K. 9916898.1
PRIOR APPLICATION NUMBER: U. K. 9816024.5
PRIOR FILING DATE: 1998-07-19
PRIOR APPLICATION NUMBER: US 09/359,208
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                   Sequence 2, Application US/09789386 Patent No. US20020010324A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2
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Pred. No. 5.9e-261;
4; Mismatches 14;
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APPLICANT: Kim, Jaeseob
TITLE OF INVENTION: Obesity Linked Genes
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 429
SEQ ID NO 429
                                                                                                                                                              Sequence 429, Application US/10267502
Publication No. US20040071700A1
GENERAL INFORMATION:
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97.2%;
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Matches 1159; C
                                                                                                                                      RESULT 6
US-10-267-502-429
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              16;
              Indels
           14;
Pred. No. 5.9e-261, 4; Mismatches 14,
97.28;
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Local Similarity
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61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPPSTPAAPKRG 180 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPPSTPAAPKRG 180 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPPSTPAAPKRG 180 181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASKPSLSP 226	GSSFSVERAESAVIVANPREEIIVKNKDEEKLUSNNILHKOOELPTALTKLVKEDEVV 3 GSSFSVERAESAVIVANPREEIIVKNKDEEKLUSNNILHKOOELPTALTKLVKEDEVV 3 GSSFSVERAKDSFNARAVAVAPAPAREETIVKNKDEEEKLUSNNILHNOOELPTALTKLVKEDEVV 3 SSEKAKDSFNAKRAVAVAPAPAREETADFKPFRVWEVKDSKEDSDMLAAGGKIESNLESKV 4 SSEKAKDSFNEKRVAVAPAPAREETADFKPFRVWEVKDSKEDSDMLAAGGKIESNLESKV 4 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 4		SPYLPDIVMEAPLNSAVESAGASVIQPSSSPLEASSVNYESIKHI SPYLDIVMEAPLNSAVESAGASVIQPSSSPLEASSVNYESIKHIKVSGIKEEIKEPENINAALQETEAPVISIACDLIKETKLSAEPP LKKVSGIKEEIKEPENINAALQETEAPVISIACDLIKETKLSAEPP VPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLI	766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825	946 TQABIESIVKPKVLEKEABEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005
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Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 646 Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 705 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKERIPLQMEELSTAVY 825 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840 Qy 826 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 865 Db 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900 QY 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNCSATSKVLLIPPDVSALGH 945 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALA- 959		TIKELKKEFLVUDDLVDSLKRAVLMWVFITVGALFNGLT II3: IDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178 IH	; PUBLICARION NO. USERVALIORIUM. ; GENERAL INFORMATION: ; APPLICANT: FILBIN, MARIE T. ; APPLICANT: DOMENICOMI, MARCO ; APPLICANT: CAO, ZIXUAN. ; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG) ; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION ; FILE REFERENCE: CUNY,003 ; CURRENT APPLICATION NUMBER: US/10/327,213 ; CURRENT FILING DATE: 2002-12-20 ; NUMBER OF SEQ ID NOS: 43 ; SOFTWARE: PATEILING VAT: 2.1	; SEQ ID NO 9 ; LENGTH: 1192 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-327-213-9 Query Match

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JAPPLICANT: EBSERMAN, Pietre

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JAPPLICANT: WOSONEGO, Alon

JAPPLICANT: WOSONEGO, ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USF

CURRENT APPLICANTION NUMBER: US/10/893,348

PRIOR FILING DATE: 1999-10-22

PRIOR PELING DATE: 1999-10-22

PRIOR PELING DATE: 1998-12-22

PRIOR PELING DATE: 1998-12-22

PRIOR PELING DATE: 1998-07-21

PRIOR PILING DATE: 1998-07-21

PRIOR PILING DATE: 1998-05-19

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 23

SEG ID NO 23
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Pred. No. 5.9e-261;
4; Mismatches 14; Indels 16;
                                                                   Sequence 9, Application US/10466258
Publication No. US20040132096A1
GENERAL INFORMATION:
TITLE OF INVENTION: ASSAY
FILE REFRENCE: P800966 GGW
CURRENT APPLICATION NUMBER: US/10/466,258
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 9
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97.2%;
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Best Local Similarity 97.2<sup>3</sup>
Matches 1159, Conservative
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CRGANISM: Homo sapiens
US-10-466-258-9
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US-10-466-258-9
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	121 SPLSAAAVSBSKLPEDDEPPARPPPPPASVSPQAEPVWTPPARAPPSTPAAPKRG 180 	181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226	227 LSAASFKEHBYLGNLSTVLPTEGTLQENVSEASKBVSEKAKTLLIDRDLTEFSELEYSEM 286 	287 GSSFSVSPKAESAVIVANPREBIIVKNKDEBEKLVSNNILHKQQELPTALTKLVKEDEVV 346 	347 SSEKAKDSFNEKRVAVEAPWREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406	407 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466	467 PLLEDPISENXTDEKKIEEKKAQIVTEKNISTKISNPFVAAQDSETDYVTTDNLIKVTE 526 	527 EVVANMPEGLIPDLVQEACESELNEVIGTKIAYETKMDLVQISEVMQESLYPAAQLCPSF 586	587 EESEATPSPVLPDIVMEAPLNSAVBSAGASVIQPSSSPLEASSVNYESIKHEPENPPYE 646 	647 EAMSUSL-KUSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 705 	706 MAKVEQPVPDHSELVEDSSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 765 	766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825 	826 SNDDLFISKEAQIRETETFSDSSFIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885 	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGH 94	TQABIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYMRDIKKTGV 100 	AYLES 106 AYLES 107	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKPAVLMWVFTYVGALFNGLT 112 	1126 LLILALISLESVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178

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1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFN 1107
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                                                                                                                                                                                       LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFN
                                                 VTEEVVANMPEGLIPDLVQEACESELNEVIGIKIAYEIKMDLVQISEVMQESLYPAAQLC
                                                                                                                                                                                                                                                                                                                                                       AVYSNDDLFISKEAQIRETETFSDSSPIELIDEFPTLISSKTDSFSKLAREYTDLEVSHK
                                                                                                                                                                                                                                                                                                                                                                                                                     SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAY
                                                                                                          PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENP
                                                                                                                                                                                                                                                                                           SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-10-633-423-10
i Sequence 10, Application US/10633423
i Sequence 10. Application US/10633423
i Publication No. US20040191240A1
i GENERAL INFORMATION:
A PAPLICANT: TOYPAUM, MASAYA
i APPLICANT: Yamashita, TOSHINide
i TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
FILE REFERENCE: 59150-8023 US00
CURRENT PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-03-29233
PRIOR FILING DATE: 2003-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 4289; DB 16;
Pred. No. 1.8e-190;
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73.9%;
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SOFTWARE: Patentin versic
SEQ ID NO 10
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Best Local Similarity
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TYPE: PRT
ORGANISM: Mus n
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                                                                                                                                       APPLICANT: BISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.
APPLICANT: BESERVAN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOALEM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKVDRKCLEDSLEGKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTK 523
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    RGSSG------AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.5%; Score 4296.5; DB 16; Length 1163; Best Local Similarity 74.0%; Pred. No. 7.9e-191; Matches 885; Conservative 104; Mismatches 156; Indels 51;
                                                                                                                                                                                                                               FILE REFERENCE: EIS-SCHWARTZ=2A
CURRENT APPLICATION NUMBER: US/10/810,653
CURRENT APPLICATION NUMBER: US/09/893,348
PRIOR APPLICATION NUMBER: US/09/893,348
PRIOR PILING DATE: 2001-06-28
PRIOR PLING DATE: 1999-05-19
PRIOR PLING DATE: 1999-05-19
PRIOR PLING DATE: 1999-12-2
PRIOR PLING DATE: 1998-12-2
PRIOR PLING DATE: 1998-12-2
PRIOR PLING DATE: 1998-12-2
PRIOR APPLICATION NUMBER: PCT/US98/14715
PRIOR APPLICATION NUMBER: PCT/US98/14715
PRIOR PLING DATE: 1998-07-21
PRIOR PLING DATE: 1998-07-21
PRIOR PLING DATE: 1998-05-19
                                                                                            Sequence 18, Application US/10810653
Publication No. US20040253218A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin version 3.1 SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Rattus norvegicus
                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-810-653-18
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MEDLDQSELVSSG-DSPP	09; Mismatches 153; Indels 50; Gaps 18; Qy 1064 ESEVAISEELVQKYSNSALGHVNCTIKELRELFUNDL RPOPAFKYQFVREPEDBEEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEB	VSSTVPA	PKRR 179 RE US	; Publication No. US20040191291A1 ; GENERAL INFORMATION: ; APPLICANT: Tohyama, Masaya ; APPLICANT: Yamashita, Toshihide	TITLE OF INVENTION: COMPOSITION AND METHOD FOR NE TITLE OF INVENTION: COMPOSITION AND METHOD FOR NE TILE REFERENCE: 59150-8023 TILE REFERENCE: 59150-8023 TILE REFERENCE: 59150-8023 TILE REFERENCE: 59150-8023 TILE OF INVERENCE INVENTE	VKNKDEEEKLUSNNILHKQQELPTALTKLVKEDEV 345	ADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES 404	US-10-427-741-10	Matches 883; Conservative 109; Mismatch Matches 883; Conservative 109; Mismatch Mi	Db	61	115	PYDLFSDDSIPDYPQKQDETVMLVKESLTETSFES 763	KLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA 823 	DD 284 SPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKS 883	DD DD DD DD DD DD DD D	SDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKT 1003 599	
	8 883; Conservative 109; Mi 1 MEDLDQSPLVSSS-DSPPRPQPAFK MEDLDQSLVSSSADSPPRPPPAFK MEDLDQSLVSSSADSPPRPPPFFFF	AAGLSAAPVPTAPAAGAPLMDFGND 	0 PSPLSAAAVSPSKLPEDDEPPARPP	GSSG GSGSVDETLFALPAASE	PLSAASFKEHEYLGNLSTVLPTEGT	MGSSFSVSPKAESAVIVANPREEII 	VSSEKAKOSFNEKRVAVEAPMRERY 	KVDKKCFADSLEQTNHEKDSESSND	IFPLEEDPTSENXTDEKKIEEKKAQ 	F TEEVVANMPEGLIPDLVQEACESEL			SEMAKVEQPVPDHSELVEDSSPDSE :	MIEYENKEKLSALPPEGGKPYLESF : ::: : VTQHKHKERLSASPQEVGKPYLESF	VYSNDDLFISKEAQIRETETFSDSS::	EIANAPDGAGSLPCTELPHDLSLKN	GHTQAEIESIVKPKVLEKEAEKKLP : : : : -ESQIEMGNIVKPKVLTKEAEEKLP	

16; Length 1162; 90; Indels 50; Gaps 18; AAPPVAPERQPSWDPSPVSSTVPA 119 EPVWTPPAPAPAPPSTPAAPKRR 179 FISAGGEDFPSVLLETAASXPSLS 225 /SEKAKTLLIDRDLTEFSELEYSE 285 SNPFFVAAQDSETDYVTTDNLTKV 524 ORSGAYITCAPENPAATESIATN 464 KMDLVQTSEVMQESLYPAAQLCP 584 EREREREDEDEDLEELEVLERKP 59 NERVE REGENERATION

457 524

584 576 643

928 1003

1047 1122

Search completed: June 16, 2005, 13:04:04 Job time : 158.811 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 16, 2005, 12:55:32; Search time 35.4224 Seconds (without alignments) 3199.767 Million cell updates/sec Run on:

US-09-830-972-29 5923 1 MEDLDQSPLVSSSDSPPRPQ......VKDAMAKIQAKIPGLKRKAE 1178. Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues Searched:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.		Query Match	Length	DB	ID	Description
	787.5	13.3	776	. 7	A46583	neuroendocrine-spe
7	688	11.6	208	7	I60904	neuroendocrine-spe
m	671	11.3	267	~	A60021	tropomyosin-relate
4	528	8.9	2484	7	T26216	hypothetical prote
S	519.5	8.8	2607	~	T26215	
9	340.5	5.7	222	~	T26213	hypothetical prote
7	331	5.6	7962	~	138346	-
60	325.5	5.5	5327	7	T13564	microtubule-associ
0	324.5	5.5	865	~	A47282	calcium-binding pr
10	320.5	5.4	873	~	A47283	calphotin - fruit
11	299.5	5.1	3488	~	T34418	g
12	299	5.0	3924	~	837431	ankyrin 2, neurona
13	290.5	4.9	1274	~	T16251	hypothetical prote
14	289	4.9	2364	~	A56577	microtubule-associ
15	289	4.9	2464	Н	QRMSP1	microtubule-associ
16	287.5	4.9	971	~	T19431	hypothetical prote
17	285.5	4.8	1621	~	A82255	
18	278	4.7	1948	~	S00485	O
19	274	4.6	3507	7	T34513	hypothetical prote
20	272.5	4.6	1829	7	T24583	
21	272.5	4.6	2361	~	T25752	_
22	271	4.6	2187	~	T30826	nascent polypeptic
23	270	4.6	1230	~	T22458	
24	267.5	4.5	1851	7	T19964	hypothetical prote
25	263.5	4.4	2409	ч	A60979	versican precursor
26	262.5	4.4	64	N	T29757	protein UNC-89 - C
27	261	4.4	55	7	B71603	RESA-H3 antigen PF
28	260.5	4.4	3381	7	T42389	versican precursor
29	259.5	4.4	1828	~	A40115	microtubule-associ

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cytadherence-acces	hypothetical prote	nucleolar phosphop	hypothetical prote	gravin - human	hypothetical prote	microtubule-associ	ankyrin 3, long sp	microtubule-associ	microtubule-associ	microtubule-associ	hypothetical prote	367K tegument prot	NF-180 - sea lampr	mucin-like protein	TCOF1 protein - mo
G64242	T15348	151618	T26517	JW0057	556852	T14007	A55575	ORHUMT	A37981	S13507	T04556	WZBEB6	151116	T30351	JC5630
~	N	N	~	7	~	~	0	٦	N	N	N	-	7	~	7
1616	5170	066	1634	1684	1189	1224	4377	1824	1830	1825	1890	3421	1110	1029	1320
4.4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1
258	257.5	256	256	255.5	253	252.5	252	250.5	250.5	248	248	248	246	244.5	243
30	31	32	33	34	32	36	37	38	38	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
, cz (neurosandocrine-specific protein, splice form A - human Nochtains neuroendocrine-specific protein, splice form B
	Cigrectes: noun sapiens (man) Date: 2-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004 Cigression: A46R83: 16A983
, K. T.	Throchock, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Var Bolde, H.J.; Van Bokhoven, A.J.; All J. J. J. J. J. J. J. J. J. J. J. J. J.
O 4 4	A)Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe A.Reference number: A46583; MUID:93293865; PMID:7685762
AA	A;Accession: A46583 A;Status: preliminary; translated from GB/EMBL/DDBJ
4.4	A:Molecule type: mRNA A:Residnes: 1-776 <rob1></rob1>
(4 6	A,Cross-references: UNIPROT:Q16799; GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307
* 4	A,Accession: 160903 A,Status: preliminary, translated from GB/EMBL/DDBJ
K 4	A;Molecule type: mRNA A.Residhes: 421-776 <rors< td=""></rors<>
. ∢	A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
U 4	C;Genetics: A:Gene: GDB:PTN1: NSP
. K K	A;Cross-references: GDB:203968; OMIM:600865 A;Map position: 14q21-14q22
•	Query Match 13.3%; Score 787.5; DB 2; Length 776;
	ative 9
O	Qy 588 ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNY 632
Δ	Db 141 BELGTPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQMKAEAYKYIDIT 200
a	Oy 633ESIKHEPENPPYEEAMSVSLKVSGIKEEIKEPENINAALOFT 675
Ω	DD 201 RPEEVKHQEQHHPELEDKOLDFKOKDTDISIKPEGVREPDK-PAPVEGKIIKDHLLEEST 259
ø	QY 676 EAPYISIACDLIKETKUSAEPAPDFSDYSEMAKVEQPVPDHSELVED 722
Q	DD 260 FAPYIDDLSEEGRRAPQITTPVKITLTEIEPSVETTTQEKTPEKQDICLK 309
ø	Qy 723 SSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSF 761
Ω	Db 310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEA 363
o	OY 762 ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELS 821
Ω	Db 364 -KGLSYETAENPRPVGQLADRPEVKARSGPPTIPSPLDHEA 403
a	QY 822 TAVYSNDDLFISKEAQIRETETFSDSSPIBIIDEFPTLISSKTDSFS 868

Db 404 SSAESGDSEIELVEDPMAAEDALPSGYVSFGHVGGPPPSP 4	444
869KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSD	92
445 ASPSIQYSILREEREAELDSELIIESCDASSASEESPKREQDSPPWKPSALD	496
AIRECTGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGPELPEPETPMLP AIRECTGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGPELPPGDGALEPETPMLP	958 551
957 KVLEKEAEKKLPSDTEKEDRSPSAFSADLGKTSVVDLLYWRDIK	1001 Cicomment: ints Heuronal-Specific mans was identified by hybridization to an Query Match 11.3%; Score 671; DB 2; Length 267;
552RKPREDSSSNQSPAATKGPGPLGPGAPPPLLFLNKQKALDLLYWRDIK	599 Best Local Similarity Matches 124; Conservat
OY TOOZ KIGVOFGASLFILDLSLIYESIVOSTAIIAMALDSVIISEKIIKGYIQALQKSDEGHFFRA 1 -	1001 Qy 988 KTSVVDLLYWRDIKKTGVVFGASLPLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1047
Qy 1062 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALF 1	1121 OY 1048 QAIQKSDEGHPRAYLESEVAISELVÖXXSNSALGHVNCTIKELRRLFLVDDLVDSLKF 719
1122 NGLTLLILALISLESVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 117	78 Db 69
Db 720 NGLTLILMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 776	DD 129 AVLAMLLTYVGALFNGTTLLLAAVVSMFTLPVVVVKHQAQVDQYLGLVRTHINTVVAKIQ
RESULT 2	Cy 1168 AKIPGLK 1174
louzona neuroendocrine-specific protein C - human C:Species: Homo sapiens (man)	Db 189 AKIPGAR 195
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004 C;Accession: 160904	
R; Roebrock, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaeke J. Biol, Chem. 268, 13439-13447, 1993	rs, F.C.; v
a novel	neuroendocrine-spe C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
A;Accession: I60904 A;Status: preliminary; translated from GB/EMBL/DDBJ	C;Accession: T26216 R;Aniscough, R. R;Aniscough, R. R;Aniscough, R. R;Aniscough, R.
וות כשמפאגאייות	. ונגרטנה. מדם
1.100000000000000000000000000000000000	7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
A;Crose-references: GDB:201968; OMIM:600865 A;Map position: 14q21-14q22	A;Residues: 1-2484 <wil> A;Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:WC</wil>
Query Match 11.6%; Score 688; DB 2; Length 208; Best Local Similarity 67.5%; Pred. No. 1.48-21;	Ajenetics: Cloue wosh, C.Genetics: CESP:W06A7.3c
Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps	0;
QY 988 KISVVDLLYWRDIKKIGVVEGASLELLESITVESIVSYTAIAALLESVIISFRIIKKIT DE 15	104/ Query Match 8.9%; Score 528; DB 2; Length 2484; 77 Best Local Similarity 20.9%; Pred. No. 1.3e-13;
	1107 Matches 2
Db 78 QAVQKTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKF 1	137 Db 1397 LEXXEVOL-DLGOXPHYIIDLHF-NIPOHEDYGNDYVPEGTESSERSOKADGNOE
Qy 1108 AVLAWWFTYVGALPNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKAVKDAMAKIQ 1	1167 Oy 39 EEBEEDEDEDLEELEVLERKPAAGLSAAP197
1168 AKIPGLKRKAE 1178	Db 1454 NQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVGCITDVDASDVNEQDEESTLKIL
Db 198 AKIPGAKRHAE 208	OY 68VPAPPAGAPLANDFGNDFVPPAPROPLAAPPVAPEKQEW
RESULT 3	Cy 109DESPVSSTVPAPSPLSAAAVSPSKIP-EDDEPPARPPPPPASVSPQAEPVW 159
A60021 tropomyosin-related protein, neuronal - rat C. Sparies, Dathus normanians (Norman rat)	DD 1570 TESEISEMAPQVSESTCPIPEPLADLKLPVEDDEKTPEPEPVVPGQVQERIIPIE 1624
C;Species: wartus norvegicus (norway rat) C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999	9 Qy 160 TPPAPA-PAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLE 216

Db 2467 KLPPIR 2472	RESULT 5 T26215 hypothetical protein W06A7.3a - Caenorhal	C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 1: C;Accession: T26215 R;Ainscough, R.	submitted to the EMBL Data Library, Augus A;Reference number: 220173 A;Accession: T26215 A;Sratus: preliminary: translated from G	A;Molecule type: DNA' A;Residues: 1-2607 <will a:creas-references:="" co3187:="" emri.<="" interot:="" th=""><th>A)Experimental source: clone W06A7 C;Genetics:</th><th>A;Gene: CESP:W06A7.3a A;Map position: 5 A;Introns: 1827/1; 1866/3; 1963/3; 1990/</th><th>Query Match 8.8%; Score Best Local Similarity 20.4%; Pred. 1</th><th>Matches 292</th><th>DD 1397 LEKVEVQPDLSQNSPAPHKIIDLHI</th><th>Qy 39 BERREDBDEDLEBI</th><th>DD 1454 NQEBEDVVABELNFHPIRQWRDEDVISI</th><th>Qy 68VPTAPAAGAPLMDFGNDFVPPAPR(</th><th>Db 1514 KVVPSEPSLLELDFTNDPKVIHY</th><th>Qy 109DPSPVSSTVPAPSPLSAA</th><th>Db 1570 TESEISEMAPQVSESTCPIPEPL</th><th>160</th><th>Db 1625 VEQÀPTIPQRPPRAPKSELPKVĀKPLI</th><th>209DPPSVLLETAASXP</th><th>. 255</th><th> </th><th>CY 313NKDEBEKLVSNNILHXQOE</th><th>Db 1788 IMGPGKSLNEDNDDDDGSECLDSIG</th><th></th><th>Db 1830 PSIRRDSFSSISSFGDRQKFRTAIENI</th><th>Qy 421 EKDSESSNDDTSFPSTPEGI</th><th>Db 1887 SMDSPSDLSPNAPPVGFENTAQFI</th><th>Qy 467 PLEDPTSENXTDEKK</th><th>512</th><th>1</th></will>	A)Experimental source: clone W06A7 C;Genetics:	A;Gene: CESP:W06A7.3a A;Map position: 5 A;Introns: 1827/1; 1866/3; 1963/3; 1990/	Query Match 8.8%; Score Best Local Similarity 20.4%; Pred. 1	Matches 292	DD 1397 LEKVEVQPDLSQNSPAPHKIIDLHI	Qy 39 BERREDBDEDLEBI	DD 1454 NQEBEDVVABELNFHPIRQWRDEDVISI	Qy 68VPTAPAAGAPLMDFGNDFVPPAPR(Db 1514 KVVPSEPSLLELDFTNDPKVIHY	Qy 109DPSPVSSTVPAPSPLSAA	Db 1570 TESEISEMAPQVSESTCPIPEPL	160	Db 1625 VEQÀPTIPQRPPRAPKSELPKVĀKPLI	209DPPSVLLETAASXP	. 255		CY 313NKDEBEKLVSNNILHXQOE	Db 1788 IMGPGKSLNEDNDDDDGSECLDSIG		Db 1830 PSIRRDSFSSISSFGDRQKFRTAIENI	Qy 421 EKDSESSNDDTSFPSTPEGI	Db 1887 SMDSPSDLSPNAPPVGFENTAQFI	Qy 467 PLEDPTSENXTDEKK	512	1
	217 TAASXPSLSPLSAASPKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLL 270 :	271 IDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIVKAKDEEEKLVSNNILHKQQ 330 1709 SPNTLAEYEEVPMMDMQSVPHSPQEKQEEIEALSEII 1745	331 ELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKE 387 			443 RSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEBKKAQIVTEKNTSTKTSN 502 	PFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETK	- LOFNAFFVGFENTAGF LEKLIQUE - DRFSAEGSI DSSGFEKVDHE YEDAAOI (POGGEFEKVDHE	THE STATE OF THE S	623 SPLEASSVNYESIKHEPENPPPYERAMSVSLKVSGIKBEIKEPENINAAL 672	1968 QDDGFVPIERNEANEATLKKNQKMSSHHNDVIEKNYFNDNAPTAAL 2013	673 QETEAPYISIACDLIKETKLSABPAPDFSDYSEMAKVEQPVPDHSEL 719	2014LESPIABERARKLVQDAVESASEYKKQAVDSGDEIGRELLDNVEQKIEQVKEP 2065	720 VEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLITETSFESMIEYENKEKLSALPPE 779	2066 IVDSLHKAYDGVGDFVHETVPNAVDDFVREAEKQLPESPVPEKIETPE 2113	GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEXIPLQMEELSTAVYSNDDLFISKEAQ	2114PLVDIHÖTVDKVHÖEVDNFLRREPTP-PFETDDVAPLSDDKPQFGNQTP 2161	838 IRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPC 897	×	2216VESLTERERM	958 VLEKEAEKKLPSDTEKEDRSPSAIFSADLG	2238 TPPKDISDEDVKPSTVNLGPSHHHSHPSSPHHSILKHHGDAWIDFKTVP 2286	990 -SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 1048	2287 PCVLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAAGFRVFKKVEA 2346	1049 AIQKSDEGHPFRAYLESEVALSEELVQXYSNSALGHVNCTIKELRRLFLVDDLVDSLKFA 1108	2347 QİKKTDSEHPFSELLAQDLTLPQEKVHAQADVFVEHATCIANKLKKLVFVESPLESIKFG 2406	1109 VLMMVPTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA 1168 2407 INT MET MYLAGBEGERT ALL TITLAGREGORENTANDEN ANT GGULF SANONITHE 2469		
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L:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:WC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDDSKS-----RVRFAPLNIKLGRTYSEEQQKEL 1678
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NIRQDLLPPQSSVSQYLRSSPNP---SQQLLVTNL 1886
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| HF-NIPKDHEDYGNDYVPFGTESSEESQKADGNQE 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: |: | SLQSLYBEVGCITDVDASDVNEQDEESTLKIL 1513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAVSPSKLP-EDDEPPARPPPPPASVSPQAEPVW 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRRGSSGAVVXXXXIMDLKEQPGNTISAGQE--- 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SLSPLSAASFKEHEY--LGNLSTVLPTEGTLOEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QELPTALTKLVKEDBVVSSEKAKDSFNEKRVAVEA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D--SDMLAAGGKIESNLESKVDKKCPADSLEQTNH 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IEEKKAQIVTEKNTSTKTSNPFFVAAQDS 511
                                                                                                                                                                                                                                                                                                                                                                                                                        QFVREPEDEEE----EE 38
                                  15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEVLERKPA----AGLSAAP-----
                                                                                                                                                                                                                                                                                                                                          519.5; DB 2; Length 2607;
No. 3e-13;
smatches 474; Indels 491; Gaps
abditis elegans
                                                                                                                                                    св/емвг/ррвл
                                                                                          ust 1996
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Db 2004 FNDNAPTAALLESPIAEEARKLVQDAVESASEYKKQAVDSGDEIGRELLDNVEQKIE 2060	Matches 66; Conservative 52; Mismatches 83; Indels 3; Gaps 2;
QY 567 QTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVWEAPLNSAVPSAGASVIQPSSSPLE 626	Ä.
Db 2061 QVKEPIVDSLHKAYDGVGDFVH-ETVPNAV-DDFVREAE2097	
Qy 627 ASSUNYESIKHEPENPPYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIACDL 686 Db 2098KQLPESPVPEKIETPEPLVDIHDTV 2122	QY 1031 LALLSVTISFRIYKGVIQAIQKSDEGHPRAYLESEVAISEELVQKYSNSALGHVNCTIK 1090
CY 687 IKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDV 741 Db 2123 DKVHDEVDNPLRREPTPPFETDDVAPLSDDKPQFGNQT 2160	OY 1091 BLRRLPLVDDLVDSLKPAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDH 1150
Qy 742 PQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLP 801	Oy 1151 YLGLANKNVKDAMAKIQAKIPGLK 1174
DEVSTLSKKEKIPLQMEBLSTAVYSNDDLFISKEAQIRETETFSDSSPIBIIDBFPTLIS 861	RESULT 7 138346
AREYTDLEVSHKSEIANAPD 890	elastic titin - human (fragment) C;Species: Homo sapiens (man) C;Date: 29-May.1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004 C;Accession: I38346
Qy 891 GAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS 924	R.Labeit, S.; Kolmerer, B. Science 270, 293-296, 1995 A.Title: Titins: giant proteins in charge of muscle ultrastrúcture and elasticity. A;Reference number: A57430; MUID:96026330; PMID:7569978
944	A.Accession: 138346 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA
2317 KSLPLLDNLLSLVVYLSISLIIHVKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNI 2376	A, Residues: 1-7962 <res> A; Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101</res>
Qy 945HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK 1002 Db 2377 VLRVGLNVALVVGVAVSAHEAYKLTKSSGVLRKKEVLDVIYWRDAKK 2423	C;Genetics: A;Gene: GDB:TTN A;Cross-refarences: GDB:127867; OMIM:188840
Qy 1003 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAY 1062 :: : :	Query Match 5.6%; Score 331; DB 2; Length 7962; Best Local Similarity 20.0%; Pred. No. 6.3e-05;
Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFN 1122	SEDSDEDLEELEVLERKPAAGLSAAPVPTAPA 7
2464 IMQUELIFÇERVIRAÇANVEVERHILLANKANALAYEVESFEESIKEGIYINSHILIKOFFS 23	SEPEEYV
GETLAILGELGEVEN VERNORATION COMMUNICATION CO	QY 74 AGAPLMDFGNDFVPPAPRGPLPAAP-PVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSK 132
RESULT 6 126213	
hypothetical protectn W06A7.3D - Caenorhabditis elegans C;Species: Caenorhabditis elegans C:Date: 15.Ort-1909 Hermians revision 15.Ort-1909 #text channe 09.Till-2004	DD 62/3 VPEEPKNEVPEKNINFEKVINGEEPLEARVIENHOUIIQEENVLANDAFFEANKVEEL 6352 Ov 176 PKRRGSSGAVVXXXXKIMDLKEOPGNIISAGOEDFPSVLLETAASXPS-LSPL 227
	6333 PKRAVPEEKVLKTKPREEPPAKVTEFRKRVVKEEKVSIEAPKREPQPIKEV
submitted to the EMBL Data Library, August 1996 A,Reference number: Z20173	Qy 228 SAASFKEHEYLGNLSTVLPTEGTLQEN-VSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
A/Accession: 120213 A/Actures preliminary; translated from GB/EMBL/DDBJ A.Molevile type: DNA	
A.Residues: 1-222 <wil> A.Residues: 1-222 <wil> A.Crose-references: UNIPROT: Q23188; EMBL: Z78066; PIDN: CAB01523.1; GSPDB: GN00023; CESP: WCASE FEREINE STREET SOURCE: clone W06A7</wil></wil>	Qy 287 GSSFS
C;Genetics: A;Gene: CESP:W06A7.3b A;Map position: 5 A:Trons: 27/1: 77/2: 201/2	Qy 310 IVKNKDEBEKLVSNNILHKQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAP 365
ch 1 Similarity	Qy 366 MREEYADFKPFRVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE 425 : : :: :

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요	6548 VPVPRKEVAPPVRVPEVPKELEPEEVAPEEEVVTHVE-EYLVEEEERYIHEEE-E 6600	Ouerv	Match
ò		Best Match	Best Local Similarity Matches 275; Conservat
qq	6601 FITEBEVVPVIPVKVPEVPRKPVPEEKKPVPVPKKKEAPPAKVPEVPKKPEE 6652	ò	28 VREPEDERER
ò	486 KKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNL 521	q	1277 MEQVKDKEEHEC
q	6653 KVPVLIPKKEKPPPAKVPEVPKKPVPEEKVPVPVPKKVEAPPAKVPEVPKKPVPEKKVPV 6712	è	76 APLMDFGNDFVI
ò	522TKVTBEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEV 571	셤	1337 KDREDTGSIESI
ପୁ	6713 PAPKKVEAPPAKVPEVPKKLIPEEKKPTPVPKKVEAPPPKVPKKREPVPVPVALPQEEEV 6772	È	127 AVSPSKLPEDDE
ò	572 M-QESLYPAAQLCPSFEESBATP593	qq	1396GSVKEDTE
q	6773 LFEEBIVPEREVLPEBEEVLPERERVLPERERVLPERERIPPERERVPPEREVLPERE 6830	ò	178 RRGSSGAVVXXX
ò	594SPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESI- 635	q	1452 RRESIAKTHKDE
eg G	6831 BFVPEEEVLPEVKPKVPVPAPVPEIKKKVTEKKVVIPKKEBAPPAKVPEVPKKVEEKRII 6890	È	230 ASFKEHEYLGNI
ò	636 KHEKEPENIN 669	qq	1511KEPSRRESI
qq	6891 LPKEEEVLPVEVTEEPEEPISEEIPEEPPSIEEVEEVAPPRVPEVIK 6939	ò	290 FSVSPKAESAVI
È	670 AALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEP 729	qq	1568 ESAKPPIEFRE
q	6940 KAVPEAPTPVPKKVEAPPAKVSKKIPEEKVPVPVQKKEAPP 6980	ò	347 SSEKAK
ò	730 VDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFK 789	ପ୍ଧ	1626 STEKSRRESVAE
QΩ	6981 AKVPEVPKKVPEKKVLV	ò	399 ESNLESKVDKKC
È	790 LSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDSSP 849	q 0	1685 KDESMSK
QO	7010TVLEEKVSVAFRQEVVVKERLELEVVEAEVEE-IPEEEEFHEVEEYFEEGE 7059	È	456 AATESI
ò	850 IEIIDEPPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLK 907	qq	: 1733 ESTTQSKEAGS
q	7060 FHEVEEFIKLEQHRVEEEHRVEKVHRVIEVFEAEEVEFKAPPKAPPKGPEISEK 7113	ò	SOO TSNPFFVAAQDS
ò	908 NIQPK	qq	1793 ASRPASVAES
qq	7114 IIPPKKPPTKVVPRKEPPAKVPEVPKKIVVEEKVRVPEEPRVPP 7157	۵	556 KIAYETKMDLVÇ
ò	944 GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSP 978	qq	1846 KSKEESRRESVA
qq	7158TKVPEVLPPKEVVPEKKVPVPPAKKPEAP 7186	ò	613 AGASVIQPSSSF
DECITA	α	qq	1906 RPASVAESIKDE
T13564	nile-seenciated nrotein homolog . fruit fly (Drosowkila melanosaster)	ò	670 AALQETEAPYIS
N, Alter	N.Alternate names: hypothetical protein EG:49E4.1	qq	1966 SVAEKSPLP
C; Date:	C:Date: 13-Aug-1999 #Bequence_revision 13-Aug-1999 #text_change 09-Jul-2004 C:Accession: M13564	à	730 VDLFSDDSIPDV
R; Spanor	C. Arccessium: 12304 anhmitted to the EMRI Date Library annil 1909	qq	2010I
A; Descr.	A; Description: Sequencing the distal X chromosome of Drosophila melanogaster. A;Reference number: 217689	λ.	785 LESFKLSLDNTK
A; Acces	A.Accession: T13564 A.Atatus: preliminary: translated from GR/RMRI./DDR.1	qu	2059 AESIKDEAEKSK
A; Moleci	A; Molecule type: DNA A: Pacidine : 1.5127 / CDA	δ	841 TETFSDSSPIEI
A; Cross-re	A;Restudes: 1-321/ CSFA; Arcetauces: UNIPROT:076891; EMBL:AL031128; PIDN:CAA20006.1 A:Genetics:	qq	2113 -ESMAESGKAQS
	.cross-references: FlyBase:FBgn0025392 Introns: 24/2: 52/3: 104/3: 179/1: 232/1: 1669/3: 2566/1: 4798/3: 5272/1	ò	899 ELPHDLSLKNIC
A; Note: C:Super	G:49E4.1 mily: Drosophila 576K microtubule-associated protein homolo	qq	2168SARDDC
 		ò	950 IESIVKPKVLEK

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SPPTIEEAIEVEVQAKQEAQKPVPAPEEAIKTEKSPLASK-ETSRPESAT 1395
                                                                                                                                                                                                                                                                                                                                                                          | : | | : | : | 132
SIKDEKSPLASEBASRPASVAESVKDEAEKSKEESRRESVAEKSPLPSKE 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                        --SARDDÓSPLESKGASRPESVVDSVKDEAEKQES------RRESK 2205
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                                                                                                                                                                         /PPA-----PRGPLPAAPPV-APERQPSWDPSPVSSTVPAPSPLSAA 126
                                                                                                                                                                                                                                                                                                                                             CXXKIMDLKEQPGNTISAGQE-----DPPSVLLETAASXP-SLSPLSA 229
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                                                                                                                                                                                                                                                           )EPPARPPPPPASVSPQAEPVWTPPAPAPPSTPA-----APK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSFNEKRVAVE-APMREEYADFKPFERVWEVKDS--KEDSDMLAAGGKI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CFADSLEQTNHE--KDSESSNDDTSFP-STPEGIKDRSGAYITCAPFNP 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIATNIFPLLEDPTS-----ENXTD--EKKIEEKKAQIVTEKN--TSTK 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SETDYVITDNLTKVTEEVVANMP----EGLTPDLVQEACESELNEVTGT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLEASSVNYESIKHEPENPPYEEAMSVSLKVSGIKEEI---KEPENIN 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEP 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPQKQDETVMLVKESLTETSPESMIE--YENKEKLSALP-PEGGKP--Y 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDTLLPDEVSTLSKKEKIPLQMEE----LSTAVYSNDDLFISKBAQIRE 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  III--DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCT 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPKVEEK-----ISFSDDFSKNGSATSKVLLLPPDVSALGHTQAE 949
                                                                                      BEEEE---DEDEDLEELEVLERKPAAGLS-----AAPVPTAPAAG
                                                Gaps
                                            Indels 219;
5.5%; Score 325.5; DB 2; Length 5327; 23.6%; Pred. No. 6.1e-05; attive 151; Mismatches 520; Indels 219;
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Db 321 TPAPEPETIAPPVVAETPEVASVAVA-ETTPPVV-PPVAAESI-PAPVVATTPV 371 Qy 580 -AQLCPSFEESEATPSPVLPDIVMEAPLASASVIOPSSSPLEASSVNYESIKHE 638 :	Qy 861 SSKTDSFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP	RESULT 10 A47281 calphotin - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Accession: A47283 K;Ballinger, D.G.; Xue, N.; Harshman, K.D. Froc. Matl. Acad. Sci. U.S.A. 90, 1356-1540, 1993 A;Title: A Drosophila photoreceptor cell-specific protein, calphotin, binds calcium and A;Recence number: A47283 MUD:93165730; PMID:8434015 A;Contents: photoreceptor cells A;Contents: photo
Db 2206 TESVIPPKAKDDKSPKEVLQPVSMTETIREDADQPMKPSQAESRRESIAESIKASSPRDE 2265 Qy 1001 KKTGVVFGASLFLLSLTVPSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFR 1060 Db 2266 KSPLASKEASRPGSVAESIKYDLDKPQIIKDDKSTE-HSRR 2305 Qy 1061 AYLESEVAI-SEELVQKYSNSALGH 1084 Db 2306 ESLEDKSAVTSEKSVSRLGH 1084 Db 2306 ESLEDKSAVTSEKSVSRLGH 2330 RESULT 9 A47282 C;Species: Drosophila melanogaster C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A. Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993 A;Title: Calphotin: a Drosophila photoreceptor cell calcium-binding protein. A;Fitle: Calphotin: a Drosophila photoreceptor cell calcium-binding protein.	A Accession: A47282 A Status: preliminary A Molecule type: nucleic acid A; Molecule type: nucleic acid A; Molecule type: nucleic acid A; Residues: 1-865 cMAR> A; Cross-references: UNIPROT:002910; GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157032 A; Experimental source: photoreceptor cells A; Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBIP:124956) C; Genetics: A; Gene: FlyBase: Cpn A; Cross-references: FlyBase: FBgn0010218 C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Superfamily: collagen alpha 1(2) chain; fibrillar collagen carboxyl-terminal homology; C; Superfamily: collagen alpha 1(2) chain; fibrillar collagen carboxyl-terminal homology; C; Superfamily: 20:13%; Pred. No. 5.6e-06; Best Local Similarity 22:3%; Pred. No. 5.6e-06; Matches 229; Conservative 128; Mismatches 375; Indels 297; Gaps 49;	S PAAGLSAAPVPTAPAAGAPLADFGNDFVPRARPGAPENAPENGPENDPSWDSSTVP 118 118 118 118 118 119 118 119 1

us-09-830-972-29.rpr

-AASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLT 276	EFSELEYSEMGSSFSVSPKAESAVIVANPREBIIVKNKDEBEKLVSNNILHKQQE 331 	LPTALTKLVKEDEVVSSEKAKOSFNEKRVAVEAPNREEYADFKPFERVWEVKOSKEDSDM 391 -	LAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCA 451 :	PFNPAATESIATNIFPLLEDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDS 511 	ETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEV 571	MQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVFSAGASVIQPSS 622 :	SPLEASSUNYESIKHEPENPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYIS 681 :	IACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPV 730 	DLFSDDSIPDVPQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESF 788	KLSLDNTKDTLLPDBVSTLSKKEKIPLQMEBLSTAVYSNDDLFISKEAQIRETETF 844 :: :	SDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP 901	HDLSLKNIQPKVEEKISFSDDFSKWGSATSKVLLLPPDVS 941 :-		KYAEPVISEAPAAEVPITAGDNPDNTSVGISEVV-PTIAEKPVEEVPTSEIPEQSSSPSD 811	IFSADLGKTSVVDLLYWRDIKKTGV 1005 :	
218 -AA 155 PAA	277 EFS 200 P	332 LPT : 227 IPE	392 LAA :: 273 VSV	452 PFN 304 PET	512 ETD 321	572 MQE 365 AAE	623 SPL : 424 PPV	682 IAC 484 TPP	731 DLF 543 DLI	789 KLS :: 596 AVA	845 SDS 645S	902 694 AVE	942 ALG	753 KYA	981 IFS 	
දු පු	S G	è a	& g	& · 원	o S	è q	& a	a S	8 S	& 8	& 43	රු සි	ò	gp Gp	රු අ	

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RESULT 11
T34418
T34418
Cybetical protein F12F3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34418
B;Fulton, B, Wohldmann, P.
Submitted to the EMBL Data Library, July 1998
A;Reference number: 221521
A;Reference number: 221521
```

ATD---SEKVSKOKEODEPTKPAVSETOMVTEADKSKKOKETDEKLKLDAE1AAKTKOEA 1029 1084 AKKAABV--BAAKKOKEKDEQLKLDTEAASKKAAABKLELEKQAQIKKA---AGADAVKK 1138 :| | | | :: | | | | : : | | | : : | | | : : : | | : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | 294 343 814 EANIKKTAEVEAAKKQKEKDEQLKLETEVVSKKSAAEKLELEKQAQIKKAAEAD---AVK 870 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Crose-references: 1-3488 - FUL>
A;Crose-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3
A;Experimental source: strain Bristol N2; clone F12F3
A;Genetics: CESP:F12F3.3
A;Map position: 5
A;Map position: 5
A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1 ETEVGAKKKPDAEKPIDLSKAKKDSKSKKSDEPBASTEEKSTTEKPINDKTSKKSAEKKT 459 VPPAPR---GPLPAAPPVAPERQPSWDPSPVSSTVPA------PSPLSAAAV 128 164 697 698 VIDKSKKTIEDQTKVATDSKLEKAADTTKQIETETVVDDKSKKKVLKKKTEKSDSF-ISQ 756 GKIESNLESKVD--KKCFAD--SLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCA 451 511 EIDYVITDNLIKVIEEVVANMPEGLIPDLVQEACESELNEVIGIK-----IAYEIKMDL 565 |:|: :| | : :| | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | | : : | : : | | : : | : : | | : : | : : | | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : : | : : | : : : | : : | : : : | : : : : | : : : | : : : | : : : | : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : 460 VKPXKEVTGKPLEAKKPVEDKKDASQPSSSKESSPPTDGKKKKQIPKALFIPDEISSRFG SPSKL------PEDDEPPARPP--PPPPASVS------PQAEPVWTPPAP AP----AAPPSTPAAPK----RRGSSGAVVXXXXXIMD----LKEQPGN-----TPDDKSRKKEGLPPAKKSEKKDEVTAEKOSTEALIESKKKEVDESKISEQQPSDKNKSEV ----TISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVL---PTEGTLQEN 640 VGVPEKAAGPETKKDV--SEIEEVPKKKTIKKKTEKSDSSISQKSNVLKPADDDKSKSDD VSEASKEVSEKAKTLLID-----RDLTEFSELE------YSEMGSSFSVSP KAESAVIV--ANPRE----BIIVKNKDEEEKLVSNNILHXQQELPTALTKLVKED---------EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAG 928 BSEPTSKKTIDTKDVGATE-PADB--TPKKKIIKKK----TEKSDSS-----ISQKS 520 DPSTWHSETNITTIRGREGSADAKTPLVEPLSASVSMKVFTLVESAKEKABPSPKRRSE 1 MEDLDQSPLV--SSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEEEEEEEEEF ----LERKPAA----GLSAAPVPT-----APAAGA------PLMD-----FGNDF PFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDS 683 ACDLIKETKLSAEPAPDFS----DYSEMAKVEOPVPDHSEL------VE 566 VQTSEV-MQESLYPAAQLCPSFEESEATPSPVLPD-IVMEAPLNSAVPSAGASVIQPSSS 624 PLEASSVNYESIKHEPENPPPYE-EAMSVSLKVSGIKEEIKEPENINAALQETEAPYISI Gaps Indels 387; Length 3488; 5.1%; Score 299.5; DB 2; ilarity 20.6%; Pred. No. 0.00039; Conservative 187; Mismatches 475; Query Match Best Local Similarity Best Local Simi Matches 272; 452 512 973 400 86 129 165 580 55 202 255 757 295 396 344 d ò 유 g ઠે g ठे 셤 ò g ઠે 셤 셤 셤 g g g g q ઠે Š ઠે ç ે ò 8 ò ઠ ò

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A;Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and B: A;Reference number: A49462; MUID:94075409; PMID:8253844
A;Accession: A49462
A;Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1884 SPSGRTEKHPPVSPGRTEKRLPVSPSGRTD-----KHÓPVSTAGKTEKHLPVSPSG 1934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VSSTVPAPSPL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LLIDRDLTEFSELEYSEMGSSFSVSPKAES--AVIVANPREEIIVKNKDE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 DSPP-----RPQPAFKYQFVREPEDEEEEEEEEEDEDLE-----ELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1648 DIPPDETOSTOKOHKPSLGIKKPVRRKLKEKOKOKEEGLOASAEKAELKKGSSEESLGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 TPPAPAPAAPPSTPAAPKRR---GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---FGNDFVPPAPRG----
                                                                                                  A;MoJecule type: mRNA
A;Residues: 1-3924 <RES>
A;Cross.references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                     A;Map position: 4q25-4q27
C;Superfamily: ankyrin; ankyrin repeat homology
K;Kywords: alternative splicing
F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>
F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MAZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 5.0%; Score 299; DB 2; Length 3924; Best Local Similarity 21.5%; Pred. No. 0.00048; Matches 258; Conservative 167; Mismatches 417; Indels 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 PAAGLSAAPVPTAPAAGAPLMD------
                                                                                                                                                                                                                                                                                                                                                                                                                                  F;129-161/Domain: ankyrin repeat homology <AN03>
F;162-190/Domain: ankyrin repeat homology <AN04>
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                                                                                                                                                                                                                                                                                                                                                                            :63-95/Domain: ankyrin repeat homology <AN01>
                                                                                                                                                                                                       A,Gene: GDB:ANK2
A,Cross-references: GDB:127607; OMIM:106410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 -----PLPAA-PPVAPERQPSWDPSP-
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ankyrin repeat h
ankyrin repeat h
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A; Residues: 1-1443,3585-3924 <OTT>
A; Residues: 1-1443,3585-3924 <OTT>
A; Crose-references: EMBLX56558
B; Tree, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward, Genomics 10, 858-866, 1991
A; Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A; Reference number: A40334; MUID:92009921; PMID:1833308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
!Wolecule type: mRNA
!Statiues: 1-3924 «CHA»
!Cross-references: UNIPROT:Q01484; EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid N;Contains: ankyrin 2, short form
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A;Title: Isolation and characterization of CDNAs encoding human brain ankyrins reveal A;Reference number: A39643; MUID:91302466; PMID:1830053
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Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
                                                                                                                                         EGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK-------EKIPLQME
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                                                                                                            -VMLVKESLTETSFESMIEYENKEKLSA
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            DSSPDSEPVDLF------SDDSI--
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A;Cross-references: GB:M37123; NID:g176
R;Chan, W; Kordeli, R
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Date: 06-Jan-1995 #sequence
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A;Accession: B39643
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Molecule type: mRNA
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atch 4.9%; Score 290.5; DB 2; Length 1274;	Maccnes ZZI; Conservative LZ6; Mismatcnes 417; indels 313; Gaps	13 SDSPPRPQPAKKYQFVREPEDBEBEBEBEBEBEBDBEBLEELBVLERKRAAGLSAAPVPT	2 SRAPPTPIKNPAKKWKPPWESVDEEEBMEVDEETPAPSKLEKKPSLKRKDAPTKP 56	71 APAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSP	57 VPSPGAPSPVPIKNPVKKWKAPWEDDEPMEEAPAAPVP	131 SKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPPSTPAAPKRRGSSGAVVX	95 AKKVRDPSPKKVPAKPRDASPKKIMAAKKEPETLPAVPP-TPVKNPVKKFKAPWED	188 XXXXIMDLKEQPGNTISAGQBDFPSVLLETAASXP-SLSPLSAASFKEHEYLGNLSTVLP : :	150 DEVDVEDVKDAPTVPAKKTPVLKKKEPAAAKPRDPSPKKAAPSKEHDPIVPP	247 TEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELBYSEMGSSFSVSPKA ::	203 TPIKNPAKKWKPPWEDDEVPTEEIKEPEPATRKVPALKKKEPSTSVKPVS	297 ESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTKL 339	253 DPSPTKKVPVKKEPEVPPTFIKNPTKKWKPPWEDETPVEEVKEPPVPEKKAPV 305			390 DMLAAGG	362EVKKPSAPEKKTPVLKRKEPEPSSTTPSSDPSPKKAAPAVKPRDSSPKK 410	450 CAPFNPATESIATNIFPLEEDPISENXTDEKKIEE-KKAQIVTEKNTSTKTS 501	411 ATPLQADPKÄQEVPPTPVKNPVKKYKPPWEVDDEDPVEEVKQPEAPAKKTPVLKRK 466	SO2 NPFFVAAQDSETDYVTTDNLTKVIEEVVANMPEGLTPDLVQ 542	467 EPAAKDTAKPATSKTPETPEKKDPVKPRDSSPKKVAAKPDSAQAPAT 513	543BACESELNEVTGTKIAVETKMDLVQTSEVMQESLYPAAQLCPSFEES 589	: : : :	590 EATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAM 649	574 DPSPKKVAPTAPEKKTPVLAKKEPAGPADSKTKEPEKSKPRDPSPKKAP 623	650 SVSLKVSGIKEBIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSD 702
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hypothetical protein F35A5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16251
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redic		Indels	AGAPL	 !AGVTE	TPEDD	SDE	MDIKE	: : : : : : : : : : : : : : : : : : :		ASTIS	AKTILITORITERS	SPIEK	XIC	SOSVT	EKRVA	I:A	KCFAD.		LEDPT.	KEDFG	TKTSN	DKSAT	KIAYE	EVDDS.	VLPDI	MSIEF	PENPP	PTEEP	IACDL	LASEK	VEQPVPDHSELVEDS-	ATAEP	-SPDSEPVDLFSD-	EDYDY	
acus I	Length		EDEBEBEBEBEBEDEDL-EELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAP	1009 EAEQSEEEGEEEDKAEDAREEGYEPDKTEAEDYVWAVADKAAEAGYTEEQYGY	RGPLPAAPPV-APERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPA	LGTSAKOPGIOSPSREPA SIHDETLPGGSESBATASDERNREDOPREFTA	SVSPOAEPVWTPPAAPAPPSTPAAPKRGSSGAVXXXXXKTWDIKEOPGNTISAGOED	: RDV		1157 VNITKXESSLYSOBYŠKPAVAŠENGLSEGSKTDATDGKYJNASAŠTISPESSMERF		SALRDAYCSBEKELKASAELDIKDVSDERLSPAKSPSLSPSPPSPIEKTPLGERSV-NFS	ELEYSEMGSSFSVSPKAESAVIVANPREEIIVKNK	LTPNEIKVSAEGEARSVSPGVTQAVVEEHCASPEEKTLEVVSPSGSVTGSAGHTPYYQSP	- DEBEKLUSINI LHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADF	EFSEAKDE-NERASLSPMDEPVPDS	VKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE : ;		SSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXT	GKNGKQGFPDRESPVSDLTSTGLYQDKQEBKSTGFIPIKEDFGPEKKTSDVETMS	EEKKAQIVTEKNTSTKTSNPFFVAAQDSETD	SQSALALDERKT.GGDVSPTQIDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGVAEDT	YVITDNLIKVTEBVVANMPEGLIPDLVQEACESELNEVIGIKIAYETKMDLVQTSEVM	YSHMEGVASVSTASVATSSFPEPTTDD-VSPSLHAEVGSPHSTEVDDSLSVSVVQTPTTF	SPEESEATPSPVLPDIVMEAPLNSAV	QETEMSPSKEECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSFAMD	PSSSPLEASSVNYESIKHEPENPPPY	rsrospohptlgasvihitengptevdyspcdiodsslshkippteepsytodnolskli	APYISIACDLIKETKLSAE	SVSQVEASPSTSSAHTPSQIASPLQEDTLSDVVPPREMSLYASLASEKVQSLEGEKLSPR		SDISPLTPRESSPLYSPGFSDSTSAAKETAAAHQASSSPFIDAATAEPYGFRSSMLFDTM	SPDS	1838 QHHLALNRDLTTSSVEKDSGGKTPGDFNYAYQKPENAAGSPDEEDYDYESQEKTIRTHDV	
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protein search, using sw model OM protein June 16, 2005, 12:33:51; Search time 159.813 Seconds Run on:

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US-09-830-972-29 5923 1 MEDLDQSPLVSSSDSPPRPQ......VKDAMAKIQAKIPGLKRKAE 1178 Perfect score: Sequence:

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seq length: 0 seq length: 200000000 Minimum DB Maximum DB 0 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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% Query Match	98.2	81.9	72.5	72.4	72.2	61.8	43.6	42.7	37.7	29.3	25.9	S	25.6		25.5	25.5	25.2	22.5	20.3	19.6	19.5	16.7	15.7	15.7	15.6	15.5	15.4	15.0	14.6	13.6	13.4
Score	5815	4851	4296.5	4289	4277.5	3658.5	2580.5	2527	2233	1735	1534.5	1531	1518.5	1517.5	1510	1508.5	1492	1331.5	1201.5	1163	1152.5	992	931	927	922	919	915	887	867	804.5	792
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06jrv4 xenopus lae 064548 rattus norv 06iffy xenopus tro 090638 gallus gall 016799 homo sapien 06fry1 xenopus lae 06jrw1 xenopus lae 06jrw2 xenopus lae 08fv484 mus musculu 06jrw2 xenopus lae 08k700 mus musculu 06jrw2 xenopus lae 08frv2 xenopus lae 08frv2 xenopus lae	
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ALIGNMENTS

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SEQUENCE FROM N.A. (ISOFORM 4).
Jin W.-L., Ju G.;
"Developmentally-regulated alternative splicing in a novel Nogo-A.";
Exhmitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             [1]—
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
PRINJHA R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G., Michalovich D., Simmons D.L., Walsh F.S.;
"Inhibitor of neurite outgrowth in humans.";
Nature 403:383-384(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;
Tagami S., Equchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
"A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplaemic reticulum and reduces their anti-apoptotic activity.";
Oncogene 19:5736-5746(2000).
                                                                         28-FEB-2003 (Rel. 41, Created)
25-OCT-2004 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nego protein) (Foocen) (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific protein) (NSP) (Neuroendocrine specific protein) (NSP) (My043 protein).
Name-RTN4; Synonyms-ASY, KIAA0886, NOGO; HOMO sapiens (Human).
                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
RTN4_HUMAN
ID *RTN4_HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQG3; Q94962; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;
AC Q9Y506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

MEDLINE=20237542; PubMed=10773680;

Yang J., Yu L., Bi A.D., Zhao S.-Y.;

"Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14-->2p13 by radiation hybrid mapping ";

Cytogenet. Cell Genet. 88:101-102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
TISSUB=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in human.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).
TISSUB-Fibroblast;
YUESUGO M.;
"Isolation of a cell death-inducing gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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TISSUE=Brain, Ovary, Pancreas, AMU 3).

TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;

RE TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;

RE Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIAUSNER R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buscrow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapletcon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.M., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Rilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,

A Raha S.G., Grimwood J., Schmutz J., Myers R.M.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Hutterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

B Hutterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

R Hannes ChNA sermences "... Analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 3).
TISSUBE-Unball:acal cord blood;
MEDLINE=20499367; PubMed=1042152; DOI=10.1101/gr.140200;
Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
To J., Huang Q.-H., Zhou J., Hu G.X., Gu J., Chen S.-J.,
"Cloning and functional analysis of cDNAs with open reading frames for
                                                                                                                                                                                                                                                                                                         Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 5:355-364(1998).
                                                            Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 3).
Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                                                                                                                                                                     Yu J., Han L.H.; "Novel human cDNA clones with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 previously undefined genes expressed in CD34+ hematopoletic stem/progenitor cells."; Genome Res. 10:1546-1560(2000).
                                                              Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., X
Luo B., Hu R., Chen J.;
"Human neurcendocrine-specific protein C (NSP) homolog gene.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sha J.H., Zhou Z.M., Li J.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
                                                                                                                                                                                                                                                                                               MEDLINE=99156230; PubMed=10048485;
                             SEQUENCE FROM N.A. (ISOFORM 3).
TISSUE=Pituitary;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold=Q9NQC3-4; Sequence=VSP_005654; TiSSUB SPECIFICITY: Isoform 1 Is specifically expressed in brain and testis and wealty in heart and skeletal muscle. Isoform 2 is widely expressed excepted for the liver. Isoform 3 is expressed in brain, skeletal muscle and adipocytes. Isoform 4 is testis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          block the regeneration of the nervous central system in adults. Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2. This is likely consecutive to their change in subcellular location, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.

SUBDAT: Binds to RTM4R. Interacts with Bcl-xl and Bcl-xl SUBCELJULAR LOCATION: Integral membrane protein. Endoplasmic reticulum and control to the membrane of the endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regeneration.";
J. Neurosci. Res. 67:559-565(2002).
-!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
                                                                                                                                                                                                                                                                                       Fournier A.E., Grandpre T., Strittmatter S.M.; "Identification of a receptor mediating Nogo-66 inhibition of axonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134; Ng C.E.L., Tang B.L.; "Nogos and the Nogo-66 receptor: factors inhibiting CNS' neuron
                                                              aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINCLARITY: Contains 1 reticulon domain. CAUTION: Ref.11 sequence differs from that shown due to frameshifts in positions 1149 and 1156.
                    GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M., "Identification of the Nogo inhibitor of axon regeneration
                                                                                                                                                                                                                           TISSUE=Brain;
MEDLINE=21069055; PibMed=11201742; DOI=10.1038/35053072;
MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms=4;
Name=1; Synonyms=RTN 4A, Nog0-A, RTN-XL;
Name=2; Synonyms=RTN 4B, Nog0-B, RTN-XS;
Name=2; Synonyms=RTN 4B, Nog0-B, RTN-XS, Foocen-M;
IsoId=Q9NQC3-2; Sequence=VSP 005655;
Name=3; Synonyms=RTN 4C, Nog0-C, Foocen-S;
IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through 2 putative transmembrane domains. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG17976.1; -.
BAA74909.2; ALT_INIT.
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                                                                                              Reticulon protein.";
Nature 403:439-444(2000)
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AB020693;

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313 NKDEEEKLVSNNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD 372
  TQAELESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV
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Catarrhini; Hominidae; Homo
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05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
RNT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform F) (RTN4 isoform Aa).
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98.9%; Pred. No. 7.3e-169;
ive 1; Mismatches 8;
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                                                                                                                                                                          PRELIMINARY;
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Submitted (MAY-2002)
                                                                                                                                                                                                                                              Name=RTN4;
Homo sapiens (Human)
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                                                                                       MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDLEELEVLERKPA
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                              Score 5815; DB 1;
Pred. No. 7.3e-204;
4; Mismatches 13;
                              Query Match

Best Local Similarity 97.2%;
Matches 1160; Conservative
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AAH07109.1;
BC001035;
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MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
OCTID T., Huber C., van der Putten H., Schwab M.E.;
Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4.";
Mol. Biol. 325:299-323(2003).
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VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES
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LFSDDS1PDVPQKQDETVMLVKESLTETSFESMLEYENKEXLSALPPEGGKRYLESFKLS
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                                         FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTS
                                                                                FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLGDPTSENKTDEKKIEEKKAQIVT
                                                                                                           EKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEV
                                                                                                                       EKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEV
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                                                                                                                                                            AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSL-KVSGIKEEIKEPENINAA
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                                                                    FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVT
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                              FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCPADSLEQTNHEKDSESSNDDTS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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QJAKI1; QJAKIO; QJROD9; QJWUE9; QJWUF0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
(Glut4 vesicle 20 kba protein).
Name=Rtn4; Synonyms=Nogo;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           help (By
                                                             MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6; MOFFIS N.J., ROSS S.A., New U.M., Lane W.S., Lienhard G.E.; "Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name-4; Synonyme=Fooden-M2; Incompage 1 and Part 1 and 2 are present in optic TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are present in dorsal root ganglion, sciatic nerve and PC12 cells after longer exposure. Isoforms 2 and 3 are detected in kidney, cartilage, skin, lung and spleen. Isoform 3 is expressed at high leyel in skeletal muscle. In adult animals isoform 1 is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;
GrandPre T., Li S., Strittmatter S.M.;
"Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
Nature 417:547-551(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the
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block the regeneration of the nervous central system in adults
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EMBL; AJ242963; CAB71029.1; -.
EMBL; AF132045; AAD31019.1; -.
EMBL; AF132046; AAD31020.1; -.
EMBL; AF132046; C.:integral to endoplasmic reticulum membrane; IDA.
GO; GO:0030176; C.:integral to endoplasmic reticulum membrane; IDA.
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
Spillmann A.A., Christ F., Schwab M.E.,
"Nogo-A is a myelin-associated neurite outgrowth inhibitor and antigen for monoclonal antibody IN-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
STRANFWISHEAR KYOLO; TISSUE=Vascular smooth muscle;
ILO T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in rat: one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein. Anchored arough 2 putative
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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    (ISOFORM 3), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLUIAR LOCATION: Integral membrane proteinembrane of the endoplasmic reticulum through atransmembrane domains (By similarity).
ALTERNATIVE PRODUCTS:
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Name=1; Synonyms=Nogo-A, NI-220-250;
IsoId=Q9JK11-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mainly in the nervous system.
SIMILARITY: Contains 1 reticulon domain.
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Isold=Q9VRI.-2; Sequence=VSP_0056SB;
Name=3; Synonyms=Nogo-C, VP20;
Isold=Q9JKI1-3; Sequence=VSP_005656,
SEQUENCE FROM N.A. (ISOFORM 3), AND PART'
STRAIN=Sprague-Dawley, TISSUE=Adipocyte,
                                                                                                                                                                                                                                         iochim. Biophys. Acta 1450:68-76(1999)
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                                                                                                                                  L-EPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK
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                                                                                                                    YSEMAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFE
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        PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENP
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SETAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129SvcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102284; AAM73506.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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Submitted (MAY-2002)
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SEQUENCE FROM N.A
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05-JUL-2004 (
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
72.5%; Score 4296.5; DB 1; Length 1163;
Best Local Similarity 74.0%; Pred. No. 1.4e-148;
Matches 885; Conservative 104; Mismatches 156; Indels 51;
                                                                                                                                                                                                                                                                                                 /Frid=vSP 005657.
Missing (in isoform 2).
/Frid=vSP 005658.
Missing (in isoform 4).
/Frid=vSP 005659.
Missing (in Ref. 3).
Missing (in Ref. 3).
Missing (in Ref. 3).
                   anti-apoptosis;
axon extension;
                                                                                                                                                                          Cytoplasmic (Potential)
Reticulon.
                                                                                                               Cytoplasmic (Potential)
                                                                                                                                                                                                                                             Missing (in isoform 3) /FIId=VSP_005656.
GO; GO:0005515; F:protein binding; ISS.
GO:0019987; P:negative regulation of anti-ap
GO; GO:0030517; P:negative regulation of axon ex
InterPro; IPR003388; Reticulon.
PROSITE; PS50845; RETICULON; 1.
PROSITE; PS50845; RETICULON; 1.
Alternative splicing; Direct protein sequencing;
Endoplasmic reticulum; Transmembrane.
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Potential.
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  815 IYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDDS----PKEYTDLEVSNKS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jin W., Long M., Li R., Ju G.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
EMBL, AX114152, AAM77068.1; --
MGD; MGI:1915835; Rtn4.
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01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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                                                                                                                                                                       Gaps
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                                                                                                                   855697FBEE11781F CRC64;
                                                                                                                                          72.4%; Score 4289; DB 2;
.larity 73.9%; Pred. No. 2.6e-148;
Conservative 109; Mismatches 153;
         MGD; MGI:1915835; Rtn4.
GO; GO:00055783; C:endoplasmic reticulum; ID;
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
InterPro; IPR003388; Reticulon;
Pfam, PF02453; Reticulon; I.
PROSITE; PS50845; RETICULON; I.
SEQUENCE 1162 AA; 126612 MW; 855697FBEE:
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Best Local Simi
Matches 883;
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STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8
NCBI_TaxID=10090;
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MGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXOOELPTALTKLVKEDEV
         VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES
                                      KVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN
                                                                  IPPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKV
                                                                                                TEEVVANMPEGLIPDLVQEACESELNEVIGIKIAYETKMDLVQTSEVMQESLYPAAQLCP
                                                                                                                            SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENPP
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                   promoters
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Oertle T., Huber C., van der Putten H., Schwab M.E.; "Genomic structure and functional characterisation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                           61.8%; Score 3658.5; DB 2; 69.5%; Pred. No. 2.1e-125; ive 108; Mismatches 148;
                                                                                                                                    EMBL/GenBank/DDBJ
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=1295vcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDE EMBL, AY102280; AAM73502.1;
EMBL, AY102286; AAM73507.1;
MGD; MGI:1915835; Rtn4.
GO; GO:00055783; C:endoplaemic reticulum; IDP GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0001525; P:neurogenesis; IMP.
                                   nan and mouse nogo/rtn4.";
Mol. Biol. 325:299-323(2003)
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Pfam; PF02453; Reticulon; 1.
PROSITE; PSS0845; RETICULON; 1.
                                                                                                                                    to the
                                                                                               STRAIN=129/SvcJ7;
Van der Putten H.;
Submitted (MAY-2002)
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                                                                                  SEQUENCE FROM
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Last sequence update) Last annotation update)

Created) PRT;

23, 23, 27,

01-MAR-2003 01-MAR-2003 05-JUL-2004 RTN4.

COSCEPTION

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399 KVDKKCFEDSLEQKGHGKDSESRNENASFPRTPELVKDGSRAYITCDSFS-SATESTAAN 457
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                                                                                                                                                                                                                              DB 2; Length 720;
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                                                                                                                       Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056373; AAH56373.1; -.
Hypothetical protein: Protein: Protein: SEQUENCE 720 AA; 77435 MW; 80AB78728F16EAB2 CRC64;
                       Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                         107;
                                                                                                                                                                                                                          43.6%; Score 2580.5; DB: 70.8%; Pred. No. 2.4e-86; iive 69; Mismatches 107
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                                         [2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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ies 527; Conservative
                       Natl. Acad.
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Submitted (AU
      mouse
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Matches 527
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MEDINE-2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2518825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2518 R.J. Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

MEDINE R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

MEDINE R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

MEDINE R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

MEDINE R.F., Jordan H., Moore T., Mark J., Rubin G.M., Milahy S.J.,

MEDINE S.S., Morden P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MEDINE S.M., Mordan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MILATON D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

MILING M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

MILING M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Makealey R.W., Tuckhman J.W., Green B.D., Dickson M.C.,

Makealey R.W., Marka M.J.,

Makealey R.W., Malaka U., Smailus D.E., Schnerch A., Schein J.E.,

M. Generation and initial analysis of more than 15,000 full-length human
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SVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAAQE
                                                               EPPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVE
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutenesia; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12.7, Medner T., Schaefer C.F., Bhat N.K.,

MEDLINE=22388257; PubMed=T., Medner T., Medner T., Schaefer C.F., Bhat N.K.,

MEDLINE=22388257; PubMed=T., Medner T., Medner T., Schaefer T.E.,

MEDLINE=22388257; PubMed=T., Medner M., Medner M., Medner M., Medner M., Medner M., Medner M., Medner M., Medner M., Gay L.J., Hulyk S.W.,

Miting M., Medner M., Sodergren E.J., Lu X., Gibbs R.A.,

Miting M., Medner M., Schaefer E.D., Dickson M.C.,

Medriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Medriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Medner M., Medner M., Smailus D.E., Schnerch A., Schein J.E.,

Medner M., Medner M., Medner M., Medner C., Schnerch M., Schein J.E.,

Medner M., Medner M., Smailus D.E., Schnerch A., Schein J.E.,

Medner M., Medner M., Medner M., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., Medner C., M
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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Last sequence update,
Last annotation update)
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PROSITE; PS50845; RETICULON; 1.
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EMBL; BC032192; AAH32192.1; -.
MGD; MGI:1915835; Rtn4.
01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
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355 GANSLPCSELPCDLSFKNTYPKDEAHV--SDEFSKSRSSVSKVPLLLPNVSAL-ESQIEM
                                                                                            1011 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAIS
                                                                                                                                                                                            EELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILA
                                                                   ESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         832 ISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                 LISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 578;
                                                                                                                                                                                                                                                                                                                                                                                             65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Tozaki H., Hirata T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB073672; BAC75974.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR00388; Reticulon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578 AA; 63696 MW; 832670C171E4AC61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.7%; Score 2233; DB 2; 78.4%; Pred. No. 8.3e-74; iive 52; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
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649

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95 PAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQ 154
470 SVVDLLYWRDIKKIGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                             1050 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                  530 IQKSDEGHPFRAYLESDVAVSEELIQKYSSVVLGHINGTVKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                          1110 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK
                                                                                                                                                                                                                                                            590 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLVNKNVKDAMAKIQAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AEPVWTPPAAPAAPPSTPAAPKRRGSSGAVVXXXXXIMDLKEQPGNTISAGQEDFPSVL
                                                ---VLLIPPDVSALGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKT
                                                                                                               SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EOSPDISSSHSGDERREPAQPGERKFWDDLDDVLDLTGGAGQFSQPFSGSHPARDIEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 EEEEEEEEDEDEDLEELEVLERKPAAGLSAAPV-PTAPAAGAPLMDFGNDFVPPAPRGPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Wholemount embryos;

X PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;

A Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanweh Petrausch B., Oertle T., Schwab M.E., Stuermer C.A.;

T dentification of two NGGO/RTN4 genes and analysis of Nogo-A expression in Kenopus laevis.";

Mol. Cell. Neurosci. 25:205-216(2004).

R EMBL, AY116196; AAQ12645.1; --.

R GO; GO:0005783; C:endoplasmic reticulum; IEA.

R InterPro; IPR001388; Reticulon.

R Pfam; PF02453; Reticulon.

R PROSITE; PS50845; RETICULON; 1.

R PROSITE; PS50845; RETICULON; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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25.9%; Score 1534.5; DB 2;
Best Local Similarity 36.9%; Pred. No. 4.7e-48;
Matches 463; Conservative 157; Mismatches 353;
                                                                                                                                                                                                                                                                                                                                                                                                                      1055 AA
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                                                                              FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISE 1071
                                                                                                                                           ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILAL 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PEGLIPDLVQEAYESEMHDBAACTKLAYETKIDLVQTSESVQETLKPVTQLCPSFEDSEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSL-KVSGIKEEI----KEPENINAALQETEAPYISIACDLIKETKLSAEPA-PDFSDYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTK-DTLLPDE--VSTLSKKEKIPLQMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 SHKSE---IAN-APDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSK---
                SIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASL
                                  Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                   ELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Caltharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX494005; AAS1847.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF09453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                            1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.3%; Score 1735; DB 2; Length 658; 58.0%; Pred. No. 1.3e-55;
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29.3%; Score 1735; DB 2; Deliyel v
Best Local Similarity 58.0%; Pred. No. 1.3e-55;
Matches 388; Conservative 83; Mismatches 164; Indels
                                                                                                                                                                                                                           72075 MW; 14B7A000C5E8CDA5 CRC64;
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Last annotation update)
NOGO-A (Fragment).
                                                                                                                                                                                                                                                                                                                          658 AA
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                                                                                                                                                                                                                                                                                                                                                                                                   Neurite outgrowth inhibitor
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                                                                                                                                                320 VGYEVSDVAEKFQVDV--GRL--NLESAVKHE-----EKSSEEMEIDSISDDIS-PLIP 368
                                                                                                                                                                                                                                                                                                                                                                                                      680 FDQKSEESSPSKSYLDSFQPEICVSKATSDLFAKGLTTLLQEK--PLQMEELDEGL-SLE 736
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                                                                                                                                                                                                                      S-----TKTSNPFF-VAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESEL 549
                                                                                                                                                                                                                                                                           STGIPKQKYESNIDLVQTAANSVQEKVSPTAQAPARLEETDSVSSPVLPDIVMEAPLAS 527
                                                                                                                                                                                                                                                                                                                                                  668 INAAL------QETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQP--VPDH 716
                                                                                                                                                                                                                                                                                                                                                               SELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLT----ETSFESMIEYENKEK 772
                                                                                                                                                                                                                                                                                                                                                                                                                                    LSALPPEG--GKPYLESFKLSLDNTKDT--LLPDEVSTLSKKEKIPLQMEELSTAVYSND 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSK---LAREYTDLEVSHKSEI 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                737 KIPCTKYSPVSE----SPEPRPSPVPEDLSSKLGDIQKEVLIAKOPEDKVOKNRSNL 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGH 945
                                                                       -----YVVDHPT 260
                                                                                                               SQQETISEHAKLYSQSAKEMFSGMLQSV-APPHEEFTDIKEVYDPYVDFKPFMSSKSGD 319
                                                                                                                                                                                                                                          SVGFGLKVATVNPFYNESAQESE--YVTTHVATHVSTK-----PEGPTPDIVQEAYESEA 467
                                                                                                                                                                                                                                                               550 NEVTGTKIAYETKMDLVQT-SEVMQESLYPAAQLCPSFEESBATPSPVLPDIVMEAPLNS 608
                                                                                                                                                                                                                                                                                                         AVPSAGASVIQPSSSPLEAS-SVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPEN 667
         LETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRD 274
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ALETV---ALKPDISPVGIKPPARVEKTKAEPEKPPSYEEAVT------EVLQNQD
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                                                                                                                                  RVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTP
                                                                                                                                                                            EGIKDRSGAYITCAPFNPAATESIATNI-FPLLEDPTSENXTDEKKIEEKKAQIVTEKNT
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                           176 LOSTASLSSLPSLSTDSSKEHAETVAFPTGLAATEALOEPTD
                                                                     ----NMYSVSRITSHLPLSDNLESKAL-DQVKEEVIFSEKG-
                                                                                           ALTKLVKEDEV-VSSEKAKDSFNEKRVAVEAPMREE-
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392 AA.

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RESULT 12 Q96B16 ID Q96B16

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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altaoner R.D., Colline F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Butchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Caraninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rotiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
and mouse Chan and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAAPPSTPAAPKRRG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEEEEEEEDEDEDLEELEVLERKPA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
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                               Last sequence update)
Last annotation update)
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7; Mismatches 3;
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EMBL; AX102278; AAM64247.1; -.
EMBL; AX102278; AAM64247.1; -.
EQO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
01-DEC-2001 (TrEMBLrel. 19, Created)
1-DEC-2001 (TrEMBLrel. 19, Last sequenc
25-0CT-2004 (TrEMBLrel. 28, Last annotat
Reticulon 4, isoform D (RTN4 isoform B2)
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Mol. Biol. 325:299-323(2003)
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TISSUES-Whole-mount embryos;

TISSUES-Whole-mount embryos;

TISSUES-Whole-mount embryos;

X PubMed=1501938; DOI=10.1016/j.mcn.2003.09.021;

Klinger M., Diekman H., Heinz D., Hirsch C., Hannbeck von Hanwehr S., Petrausch B., Oerle T., Schwab M.E., Stuermer C.A.;

I "Identification of two NOGO/RTM4 genes and analysis of Nogo-A expression in Xenopus lacvis.";

I Mol. Cell. Neurosci. 25:205-216(2004).

IR EMBL; AY316197; AAQ82646.1; -.

R GO; GO:0005783; C:endoplasmic reticulum; IEA.

InterPro; IPR003388; Reticulon.

R Pf048; SS50845; ExEICULON; 1.

R PROSITE: PS50845; EXEICULON; 1.
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                                         PPARDEKTKABPEKPPSYEEAVTEVLODGGPAAAADLGDSKQ-GAVVKEAEAAPISPYIS
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
NCBI_TaxID=8355,
                              -SVNYESIKHEPENPPPYEEAMSVSLKVSG--IKEEIKEPENINAALQETEA-
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KIPCTKYSPVSE-----SPEPRPSPVPEDLSSKLGDIQKEVLIAKQPEDKVQKNRSNL
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                                                344 T-----DYDMFAT--VEQNIPFSFGGGHVAGNKTDEKKIEDIEAQ-----KTSVGFGL
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TQAEIESIVKPKVLEKEAE-KKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTG
                                                         VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLE
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                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Wholemount embryos;

X PubWed=15019938; DOI=10.1016/j.mcn.2003.09.021;

A Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehn Petrausch B., Oertle T., Schwab M.E., Stuermer C.A.;

I "Identification of two NOGO/RTN4 genes and analysis of Nogo-A expression in Kenopus laevis.";

Mol. Cell. Neurosci. 25:205-216(2004).

R EMBL, AY316195; AAQ8264.1; -.

R GO; GO:0005783; C:endoplasmic reticulum; IEA.

R InterPro; IPRO03188; Reticulon.

R Pfam; PF02453; Reticulon.

R PROSITE; PS50845; RETICULON; 1.

S PROSITE; PS50845; RETICULON; 1.
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Mao, Y.M., Xie, Y. and Zheng, Z.H.
Direct Submission
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Coganism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="011a12"
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-MODEL=frame+_pl. model -DEV=xlp
-MODEL=frame+_pl. model -DEV=xlp
-G=/CGM2_1/USPTO_spool_p/US09830972/runat_16062005_153944_19011/app_query.fasta_1.654_
-G=/CGM2_1/USPTO_spool_p/US09830972/runat_16062005_153944_19011/app_query.fasta_1.654_
-DEVALIDED-1 -QFWT=fastap -SUFFTX=rge -MINNATCH=0.1 -LOOPCH=0 -LOOPEXT=0
-UNITS=bits -START=1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OOTFWT=ptc -NORM=ext -HEAFSIZE=500 -MINNEN0 -MAXIEN=2000000000
-USER=US09830972 @CGN 1 1 5783 @runat_16062005_153944_19011 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NGG_SCORES=0 -MINTALD=0 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AF320999 Homo sapi
AF333336 Homo sapi
AX766050 Sequence
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                    nucleic search, using frame_plus_p2n model
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AF320999.1 GI:11878277
 /protein id="AAG43160.1"
| Ma_xref="101:1202034"
| /translation="WDEG1rpUQBACESELNEVTGTKIAYETKMDLVQTSEVMQBS
| LYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYE
                                                          SIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENIMOLFKKQKLLIYLLHYDLIKET
KLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDET
VMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVST
                                                                                                       LSKKEKI PLQMEELSTAVYSNDDLFISKEAQIRETETFSDSSPIBIIDEFPTLISSKT
DSFSKLARBYTDLEVSHKSBIANAPDGAGSLPCTELPHOLISKINIOPKYBEKISSBDD
PSKNGSSATSKVLLLPPDVSALATQABIESIVKPKVIVKEAKKLPSDTKKEDRSPSAI
FSKAELSKTSVVDLLYMRDIKKTGVVFGASLFILLISLIVPSIVSVTAXIALALLSVTIS
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Conservative:
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ACCESSION VERSION

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WEVKOSKEDSDMLAAGGKIESNLESKVOKKCPADSIEQTNHEKOSESSNDDTSFPST
BEGIKORGGATITCAPPNAPATESI TAYNI PPILLEDPYSBMYNDEKIEREKAQUTTEK
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INAALQETERPY IS TACDLI KETKLSAEPAPDFSDYSEMAKVEQPVPDHSBLVEBSEV
DSEPVDLFSDDSIPDVKQDETVMLVKESLTETSFESMIEYTENKEKLSALPPEGGKP
YLTSFKLSLDMYKDTLLPBSFTLSSKTASTATENESVESMAKVEQPVPDHSBLVEDSSP
ETESPSSSPIE II DEBYSTLSKKEN PLOLGMEESSTAVSSNDDLETSFESLETSKE
LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDDVSALATQAEIESIVKPKV
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VSNNIILHNQQELPTALTKLVKEDEVVSSEKAKDSFNEKRAVAVEAPMREEYADFKPFER
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LTVESIVSYTAIALALLSVTISFRIYKGVIQJADGKSDEGHPFRAXLESEVAISEELV
GYSNSALGHYNCTIKELRELPLVDDLVDSIKEAVLMWYFTYVGALFNGITLILALI
SLFSVPVIYEHQQQIDHYLGLANKNYKDAMAKIQAKIPGKRKAE"
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                                                                        Jin, Waster and Ju.G.

Developmentally-regulated alternative splicing in a novel Nogo-A Developmentally-regulated alternative splicing in a novel Nogo-A Unpublished

Upublished

Jin, W.-L. and Ju.G.

Direct Submission
Submitted (12-NOV-2000) Institute of Neurosciences, No. 17 Chang West Road, Xian, Shanxxi 710032, China
Location/Qualifiers
      Euteleostomi;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2883)

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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="alternatively spliced"
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/mol_type="mRNA"
/db_xref="taxon:9606"
1. .2883
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VVDLLYWRDIKKTGYVFGASLFLLLSLTVFSIVSYTAYIALALLSYTISFRIYKGVIQ
AIQKSDEGHPRAYLESEVAISEELVQKYSNSALGHYNCTIKELRRLFLYDDLVDSLK
FAVLWWYFTYYGALFRGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNYKDAMA
KIQARIFGLKKKAE"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 03002602-A 5 09-JAN-2003;
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Homo sapiens
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LOCUS
DEFINITION
ACCESSION
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CETWORDS
SOUNCE
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AUTHORS
TITLE
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Homo sapiens testis specific reticulon 5 protein mRNA, complete
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1 (Dases I to 3431)
2hou, Z.M., Sha, J.H., Li,J.M., Lin,M., Zhu,H., Zhou,Y.D., Wang,L.R., Zhu,H., Wang,Y.Q. and Zhou,K.Y.
Expression of a novel reticulon-like gene in human testis
1857060
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ABASLBQTNHEKDSESSNDDTSFPFERDKIKORSAGATITAFPERPRAAFESIATNIFPL
IGDPFTSENKTDEKKLEEKKAQIVTEKNTSTRTSNPFLVAAQDSETDYYTTDNLTKVTFPL
EVVANMPEGLTPDLVQEACESELSEVTGTKIAYETKNDLVQTSEVWQESLYPBAQLCP
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PSDYSEMASVSIKKVSGIKEETKEPRINAALOSTBAPPYISIACDLIKETKLSABPAPD
PSDYSEMAVULVKSSIKELVEDSISPVDLFSDDSIPDVPQKQDETVMLVKESLI
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YTDLEVSHKSBIANAPDGAGSLPCTELPHDLSLKNIQPKVEBKISFSDDFSKNGSATS
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YLGNLSTVLPTEGTLQENVSEASKEVSEKAKTILIJDRDLTEFSELEYSEMGSSFSVSP
KAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVVSSEKAK
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Sha,J.H., Zhou,Z.M. and Li,J.M.
Direct Submission
Submitted (04-JAM-2001) Key Lab of Reproductive Medicine, Nanjing
Medical University, Han Zhong Road 140, Nanjing, Jiangsu 210029,
                  LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu1leLeu
                                                                                                                           2674 TrGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACTACTGATTTTG
                                                                                                                                                               AlaLeuIleSerLeuPheSerValProValIleAyrGluArgHisGlnAlaGlnIleAsp
                                                                                                                                                                                                   'product="testis specific reticulon 5 protein"
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1. .3491
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PC C12P21/08,C12N15/00,C12N5/00
CC Protein similar to neuroendrocrine-specific protein, and Cencoding cDNA
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Protein similar to neuroendrocrine-specific protein, and Patent: JP 2002522016-A 1 23-JUL-2002; SMITHKLINE BEECHAM PLC
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/organism='Homo sapiens (human)'.
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.
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Michalovich,D. and Prinjha,R.K.
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                   Location/Qualifiers
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/mol_type="unassigned DNA"
db_xref="taxon:9606"
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JP 2002522016-A/1.
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

HSA251383 LOCUS

RESULT 6

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3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          3010 TCAGTTGTTGACCTCCTGTACTGAGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC
                                                                                                                                                                       21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                            IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                    1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                                                                                                                         41 AlaLeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitaliti, A. and Zurini, M. Nogo a binding molecules and pharmaceutical use thereof Patent: WO 2004052932-A 4 24-JUN-2004; Novartis AG (CH)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
1. 3579
/note="unnamed protein product; Human NogoA"
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                                          US-09-830-972-29_COPY_990_1178 (1-189) x HSA251383 (1-3579)
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SGQDPPSVLULBTAAABLPSISPIGAABSKEHSTIGMISTVIPTEGTLGBNVSBRASKEV
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VENNIILHNQQELPTALIKLVKEDEVVSSEKAKDSFNEKTWARDAPRRETSADFKPFRR
VENKTOKSEDSDMLAARIESINDESSNDTSEPSTPRESSENDTSFSPST
PEGTIKONPGAYITGAPGASTESILESKTVOKKCHSANDSLEQTWINDEKKIEERKAQIJVTER
NTSTKTSNPFLVAAQDSETDYVTTONLTKVTEEVVANMPEGLTPDLVQEACESELNEV
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INAALQETERAPYISIACDLIKETKLSARPAPPSDFSDYSEMAVSGIKKVEGPVPDHSELVEDSSP
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TLESFKLSLAVYKNTLLPBEVSTLSKKEKIPLQMELGTYVSNNDDLFFSKEAQIRET
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LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALATQAEIESIVKPKV
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LTVFSIVSVTAYIALALLEVTISKTYTSKGVIQAJOKSDEGHPPRAYLESEVAISBELV
GYSSNSALGHYNCTIKELRELFLODDLVDSIKFAVLMWYFTVYGALFRGITLLILALI
SLFSVPVIYERHQADIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
                                                                                                                               PRI 22-JUL-2000
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Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
                                                                                                                                                                                                                                                                               Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                              Prinjha,R., Moore,S.E., Vinson,M., Blake,S., Morrow,R., Christie,G., Michalovich,D., Simmons,D.L. and Walsh,F.S. Inhibitor of neurite outgrowth in humans Nature 403 (6768), 383-384 (2000)
                                                                                                                 HSAZ51383 3579 bp mRNA linear
Homo sapiens mRNA for Nogo-A protein (Nogo gene).
AJ251383
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Conservative:
Mismatches:
Indels:
Location/Qualifiers
1. 3579
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1. 3579
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evidence=experimental
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Homo sapiens (human)
Homo sapiens
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/gene="Nogo"
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Michalovich, D.
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FEATURES

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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL MEDLINE PUBMED

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DSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMIEVEKKLSALPPEGGKY
YLESFKLSLDMYKDTLLPDEVSTLSKKEKIPLQMEBLSTAVSNDDLFTSKERALPPEGGKY
TLESFBSDS PIEIIDEFPTLISSFENDFSKRARETYDLEVSHKSEIANAPDGAGSLPCTE
LPHDLSLKNIQPRVEREKISFSDDFSKRGSATSKYLLLPPDVSALATQAEIESIVKTRV
LVKEAEKKLFSDTEKEDRSPSAIFSKYLLLYSVVDLLYWRDIKKTGVVFGASLFLLLS
LTVFSIVSVYTAYIALLSVTISFRIYTKGVIQAIQKSDEGHPFRAYLESEVAISEELV
SKYSNSALGHYNYCTIKELRELFLYDDLVDSLKRAYLWWYFTYVGALGELTLILLALI
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SEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKL
                                                                                  VSNNI LHNQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFER
WWEVKOKSENSEDSMLAAGGKIESNLESKVOKKCFASLEQUPHEKODESSNDTOFSPST
PEGI KORSGAY I TCAPENPAATES I ATNI FPLLGDPYSENKTDEKKI BEKKAGI VTEK
NTSTKTSNPFLVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELMEV
TGTKTA PATKMOLVQYSENWOESLY PRAAQLCBSEBESBATPSPVLLDV VMGAPLANSAV
PSAGASVI QPSSSPPLASASVAYES I KHEPENPP PYERAMSVSI KYCSGI KEETKEPEN
I NAALQETEAPY I SI ACDLI KETKLSAEPAPPSDYSSHAKVEQPVPDHSELVEDSSP
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/db_xref="G1:15385810"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="unnamed protein product; Human mRNA for Nogo
protein (KIAA0886, GenBank Accession No. AB020693)"
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/mol_type="unassigned RNA"
/db_rref="taxon:9606"
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Patent: WO 0151520-A 5 19-JUL-2001;
YALE UNIVERSITY (US)
4053 bp
Sequence 5 from Patent W00151520.
AX195249
AX195249.1 GI:15385809
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XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 5 (6), 355-364 (1998)
10048485
                          3384 TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATA 3443
                                                                                                                                                        /product="KIAA0886 protein"
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/bc.xref="C1:4078974"
/translation="YPRLSRPSPGOSSPTPTTARGSETRPRRRRQULQHHLHPPAMED
LDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDDEBLEELEVLERKPAA
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Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.
Ohara,O., Submission.
Direct Submission.
Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
                                                                   120
                                                                                                                                  LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140
                                                                                                                                                                                                                                                                       HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys1leGlnAlaLys 180
                                                                                                                                                                                                       AlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                        LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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4053 bp mRNA linear
Homo sapiens mRNA for KIAA0886 protein, partial cde.
AB020693.1 GI:4240260
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/clone_lib="pBluescriptII SK plus"
/dev_stage="adult"
1. .4053
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="hk07722"
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ELEYSEMGSSFSVSPKAESAVIVANPREEIIIVKNVDEEEKLVSNNILHNQGELPTALT
KLVKEDEVVSSEKKDSFRKKUSTVARAPMEREIIOTAKNOSKEDSDMLAAG
GKIESNILESKUDKKCFADSLEGTHHEKNOSESNDDTSFPSTVPEGIKDRSAGYITAPF
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ETDYVTTONLTKVTEBVVANMPEGLIPDLVQBACGSELNBTVTGTKIAYETNDLUGTS
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SSWYYESIKHEPRNPPPTSENSCHYPDLSELNBSSPDSEPVDLFSDSSPLEA QKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLL PDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDSSPIEIIDEPPT LISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEK RSPSAIFSAELSKTSVVOLLYWRDIKKTGVVFGASLFLLLSLTUFSIVSVTAYIALAL LRYTISRYTYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKE LRELFLYDDLVDSLKFRYLWWPTYTYGALFNGLTLLIIALISLFSVPVIYERHQAQID HYLGLANKNVKDAMAKIQAKIPGLKRKAE" ISPSDDFSKNGSATSKVLLLPPDVSALATQAEIESIVKPKVLVKEAEKKLPSDTEKED

Length:

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ercent Similarity	Simil.	arity:	100.00%	Conservative:	. 0	
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3-09-830-972	0-972.	-29_COPY_9	_990_1178 (1-189)	x AB020693 (1-4	(1-4053)	
_	1	Servalval	AspleuLeuTyrTrp	ArgAspileLysLys1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
0	3144		GACCTCCTGTACTGG	AGAGACATTAAGAAGA	TCAGTTGTTGATCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC	3203
_	21	SerLeuPhe	LeuLeuLeuSerLeu	ThrValPheSerIle	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
0	3204		CTGCTGCTTTCATTG	ACAGTATTCAGCATTC	AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATT	3263
_	41	AlaLeuAla	LeuLeuSerValThr	IleSerPheArgIleT	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	09
0	3264		CTGCTCTCTGTGACC	ATCAGCTTTAGGATAI	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT	3323
	61	IleGlnLys	SerAspGluGlyHis	ProPheArgAlaTyrI	lleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
•	3324	ATCCAGAAA	TCAGATGAAGGCCAC	CCATTCAGGGCATATC	ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA	3383
_	81	SerGluGlu	LeuValGlnLysTyr	SerAsnSerAlaLeuC	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
0	3384		TTGGTTCAGAAGTAC	AGTAATTCTGCTCTTG	TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATA	3443
_	101	LysGluLeu	ArgArgLeuPheLeu	ValAspAspLeuValA	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
0	3444	AAGGAACTC	AGGCCCTCTTCTTA	GTTGATGATTTAGTTC	AAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGTAAGTTTGCAGTG	3503
_	121	LeuMetTrp	ValPheThrTyrVal	GlyAlaLeuPheAsnG	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
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	161	HisTyrLeu	GlyteuAlaAsntys	ABNValLyBABDAlaM	HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
•	3624	CATTATCTA	GGACTTGCAAATAAG	AATGTTAAAGATGCTA	CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA	3683
_	181	1leProGly	IleProGlyLeuLysArgLysAlaGlu	Glu 189		
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A070 bp mRNA linear PRI 23-SEP-2003 Homo sapiens RTN4 isoform F (RTN4) mRNA, complete cds; alternatively spliced.
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Gentle,T., Huber,C., van der Putten,H. and Schwab,M.E.
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                              2705 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2765 TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2885 TIGATGIGGGIATTIACCIATGITGGIGCCTIGITIAAIGGICTGACACTACTGATTITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                                                                                                                                                                                                                 2645 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                         61 11eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                           41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
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4060 bp mRNA linear PRI 23-SEP-2003
Homeo sapiens RTN4 isoform G (RTN4) mRNA, complete cds;
alternatively spliced.
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LGDPFSEKWTOBKKIEKKAQIVTERWYTSTKTSWPFLVAAGDSETDYTTDMLTKYTE
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SFESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENP
PSPERMWSVEVLPVLFULWEETKEPENTNAALQETEAPYISTACDLIKTSTKLSREPENP
PSPYERMAKVEQPPHSELVLEDSSPDSSPVLLFAPYISTODLIKTSTKLSREPAPD
FSDYSEMAKVEQPPHSELVLEDSSPDSSPDSEPVDLFSDDSIPDVPQKQDSTVWLVKESLIT
ETSFESMIEYENKEKLSALPPEGGKPYLBSFKLSLDNTKOTLLPDEVSTLSKKEKIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="RIN4"

Cocte="RTN4-G; alternatively spliced"

Coctes start=1

/product="RIN4 isoform G"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QMEELSTAVYSNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLARE
YTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS
KVLLLPPDVSALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTS
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AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLK
FAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA
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KAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQOELPTALTKLVKEDEVVSSEKAK
DSFNEKRVAVEAPMREEYADPKPFERVWEVKOSKEDSDMLAAGGKIESNLESKVDKKC
                                                                                                                                                                                                                                            Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.
Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 4060)
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Van der Putten, H.
Direct Submission
Submitted (17-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
3 (bases 1 to 4060)
Oertle, T and Schwab, M.E.
Direct Submission
Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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                                            2775 TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATA 2834
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                                                                                                                                                                                                                                                                                                                                                                                                     141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Valenzuela,D., Yuan,O., Hoffman,H., Hall,J. and Rapiejko,P. Secreted proteins and polynucleotides encoding them
Patent: UP 2002537757-A 32 12-NOV-2002;
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                                                                                                                                                                                                                                                                   LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu
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Secreted proteins and polynucleotides encoding them.
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SPEESRATESPVLPDIVWBAPLNSAVPSAGASVIQPSSSPLAASSVNTESIKHEPENP
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VVDLLYRRRDIKKTGVVFGASLPCTELPHDLSLKVNIQPKVEEKISFSDDFSKVTS
KVLLLPPDVSALATQAREISENINGSVLVKRARKTST INDRVINGS V
NVDLLYRRDIKKTGVVFGASLPLLLLSLLVKRS IVSUTNAT IALALLEYTTSFRIYT VKGVIQ
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Oertle, T. and Schwab, M.E.
Direct Submission
Submitted (17-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
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Matches:
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Indels:
Gaps:
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gene="RTN4"
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IGDPTSENKTDEKKIEEKKAQI VTEKNTSTKTSNPFLVAAQDSETDYYTTDNLTKVTE
EVVAAMPEGITPDLVQEACESELNEVTGTKIAXETKNDLVQTSEWOGSLYPAAQLCP
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YTDLEVSHKSEALAQAEIESTVKPKTUVKEAREKLPSPTEKENBRSPAFFSAELSKTS
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KAESAVIVANPREEIIVKNKDBEEKLVSNNILHNQQELPTALTKLVKEDEVVSSEKAK
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FADSLEQTWHEKDSESSNDDTSFPSTPEGI KORSGAY I TCAPFNPAATES I ATN I FPL
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Matches:
                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                       /tissue_type="testis"
|. .4102
location/Qualifiers
                                                                                                                                                                                                note="synonym:
.175
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3137. .4102
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'gene="RTN4"
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/gene="RTN4"
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4102 bp mRNA linear PRI 23-SEP-2003 themo sapiens RTN4 isoform Aa (RTN4) mRNA, complete cds; alternatively spliced.
AY123245
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Van der Putten, H.
Van der Putten, H.
Direct Submission
3 (bases 1 to 4102)
3 (bases 1 to 4102)
Direct Submission
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Submitted (17-MAY-2002) Brain Research Institute, University of Submitted (17-MAY-2002) Brain Research Institute, University of Submitted (17-MAY-2002) Brain Research Institute, University of Switzerland
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                                                                                                                                         SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                   US-09-830-972-29_COPY_990_1178 (1-189) x BD270070 (1-4093)
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J. Mol. Biol. 325 (2), 299-323 (2003)
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/product="RTN4 isoform E"
/protein id="AAM64252.1"
/db_xref="G1:26800584"
/translation="MOLKEQPGNTISAGQEDPPSVLLETAASLPSLSPLSAASFKEHE
XLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSP
KAESANIVANPREEIIVKNKDEEEKLVSNNILHNQOELPTALTKLVKEDEVVSSEKAK
DSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKC
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(Dases 1 to 4109)

Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.
Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4

J. Mol. Biol. 325 (2), 299-323 (2003)
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/gene="RTN4"
/note="RTN4-E; alternatively
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="2"
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1.4109
/gene="RTW4"
1.016="synonym: NOGO"
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LGDPTSENKTDEKKIEEKKAOIVTEKNYSTKTSNPPIJVAAQDSETDYVTTDNILTKVTE
EVVANMPEGLIPDIVORAGGSELNEYTGYKIAVETKAPTRONILOGTSENOGSELYPAAGLCP
SFEBSEATPSPYLDIVORAGGSELNEYTGYKIAVETKAPADLCP
SFEBSEATPSPYLEVEDSINTSAVPSAGASVIQPSSSPLEASSWYESIKHEPENP
PPYERAMSWSCHKKLSALPPEGKEYLESPYDLFSDDSIPDVPQKQDETVMLYKESLT
ETSPESMIEYENKEKLSALPPEGGKEYLESFKJSDDYTKDTLLDPBVSTLSKKRIPL
QMEELSTAVYSNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLARE
YTDLEVSHKSEIAMAPGAGSLPCTELPHDLSLKWIQPKWEEKISFSDDFSKNGSATS
KVLLLPPDVSALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTS
VVDLLYWRDIKKTGYVFGASLPLLLSLTVGFSIVSTALALLSLTYETTINTKULY
ALOKSDEGHPFRAYLESENAISEELVQKSNSALGHVNCTIKELREFLEYDDLVDSLK
FAVLMWVFTYVGALFNGLTLLILALSLTYSTSVPDYTERHQAQIDHYLGLANKNVKDAMA
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Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 4160)
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1 (Dases 1 to 4160)
Oertle,T. and Schwab, M.E.
Direct Submission
Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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Van der Putten, H.
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FAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA
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                                                                                                                                                                                               Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Genomic structure and functional characterisation of the promoters
                                                                                                                            Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 4123)
Van der Putten, H.
Van der Submission
Submitted (O'T-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
3 (bases 1 to 4123)
Oertle, T. and Schwab, M.E.
Direct Submission
Submitted (17-MAY-2002) Brain Research Institute, University of
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| Gene="RTN4"
| 197. .3157
| Gene="RTN4"
| note="RTN4"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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Eukaryota, Metazoa, Chordata,
Ammalia, Eutheria, Primates,
(bases 1 to 4123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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AY123247
AY123247.1 GI:26800580
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                                                                           Homo sapiens (human)
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                                                                                                                                 2985 TTGATGTGGGTATTTACCTATGTTGGTGCCCTTGTTTAATGGTCTGACACTAGTTTTG 3044
                                                                                                                                                                                                                                     3105 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 3164
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                                                2925 AAGGAACTCAGGCGCCTCTTCTTAGTTGATTTAGTTGATTCTCTGAAGTTTGCAGTG 2984
                                                                                                                                                                                                        141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
                                                                                                                                                                                                                                                                                                               HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tagami, S., Eguchi, Y., Kinoshita, M., Takeda, M. and Tsujimoto, Y. A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity Oncogene 19 (50), 5736-5746 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (122-MAR-2000) Yutaka Eguchi, Osaka University Graduate School of Medicine, Blomedical Research Center, Department of Medical Genetics; Yamadasoka 2-2, Suita, Osaka 567-0871, Japan (B-mail:eguchi@Gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363, Fax:+81-6-6879-3369,
                                                                                                    LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu
LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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Eguchi,Y., Tagami,S. and Tsujimoto,Y.
Direct Submission
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             INAALQETEAPYISIACDIIKETKISAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSP
DSEPVOLFSDISIPOVPOKODETWALVKESLTETSFESMI EYRIKKEKISALPPEGGKP
YLESFKLSLDNTKOTTLIPDEVSTLSKKEKI PLÇMEELSTAAVYSNDOLFI SKRAQIRET
ETFSDSSPIEIIDFSPTLISSKTOSFSKLARRYTDLEVSHKSBIAMAPDGAGSLPCTB
LPHDLSLKNI QPKVEEKI SFSDDFSKNGSATSKVLLLPPDVSALATQAEIESI VKPKV
LVKBAKKLASTPEKEDRSPSAL FSAELSKTSVVDLLYWRDIXKTGVVFGASLFLLLS
LIVESI VSVLAY I ALALLSVTI SFRI YKGVI QAI QKSDEGHPPRAYLESEVAI SEELV
QKYSNSALGHVMCTI YEBLRELEVDDLVDSLKRAVLMWYFTYVGALESEVAI SEELV
SLFSVPVI YERHQAQI DHYLGLANKVVDAMAKI QAKI PGLKRKAE"
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PSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPEN
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens reticulon 4a mRNA, complete cds.
AF148537.1 GI:10039550
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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ERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPWT
PPAPAPAAPPSTPAAPKRGSSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTIS
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                                                                                                           2 (bases 1 to 4632)
Zhou,Y., Vu,L. and Zhao,S.Y.
Direct Submission
Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3151 TCAGTTGTTGACCTCCTGTACTGAGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC
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                              сргомовоме
                              (RTN4) to
      Yang,J., Yu,L., Bi,A.D. and Zhao,S.Y.
Assignment of the human reticulon 4 gene (RTN4)
2D14-->2D13 by radiation hybrid mapping
Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
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Matches:
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/note="RTN4a"
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4789 bp mRNA linear PRI 23-SEP-2003
Homo sapiens RTN4 isoform A (RTN4) mRNA, complete cds;
alternatively spliced.
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Genomic structure and functional characterisation of the promoters
of human and mouse nogo/xtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4789)
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
141 AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp
                                                                                                                                                                                                                                                                                                                                     HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
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                                                    SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
                                                                                                                      LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Homo sapiens"
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1. 4789
/gene="RTN4"
/note="synonym: N
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Oertle, T. and Schwab, M.E.
Direct Submission
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/gene="RTN4"
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Homo sapiens
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Van der Putten, H.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Regulation of mammalian cells
Patent: WO 2004076622-A 436 10-SEP-2004;
National Institute of Advanced Industrial Science and Tec hnology (JP)
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                                                                                                                                                                                               SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
                                                                                                     LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                       LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu1leLeu
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                                                                   3391 rcraagaagrragaagracagraarrcracrcrragraargraacracara
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Matches:
Conservative:
Mismatches:
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    /db_xref="taxon:9606"

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3734 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAA 3793
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Mismatches:
Indels:
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Jones, K.A., Volkmuth, W. and Walker, M.G.
Bone remodeling genes
Patent: US 6426186-A 106 30-JUL-2002;
Location/Qualifiers
                                                                                    DNA
                                                                                   AR220865
Sequence 106 from patent US 6426186.
AR220865
AR220865.1 GI:23327742
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QKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALI
SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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Matches:
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

LOCUS

BC016165

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EDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP
ERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWT
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LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGAL
FNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEE
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1 (bases 1 to 1784)

2 Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

3 Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Altschul, S.F., Zeeberg, B., Buetow, K.H.; Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Morce, T., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Wuzny, D.M., Sodersen, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchaz, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,

Generation and initial analysis of more than 15,000 full-length
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This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                   1784 bp mRNA linear PRI 29-JUN-2004 Howo sapiens reticulon 4, transcript variant 4, mRNA (cDNA clone IMAGE:3505850), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andy Chan, Steve S. Chand, Milliam Chow, Alison Cloutier, Ruth Reatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Parka Olson, Diana Palmquist, Anca Petrescu, Anna Litsa Prahbu, Parvaneh Saeedi, Mr Sancos, Angelique Schnerch, Ursula Skalska, Buane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-0CT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) MA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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trausberg, R.
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PUBMED REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

JOURNAL

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1337 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 1396

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Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
HERZEGOVINA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysLysThrGlyValValPheGlyAla
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                                                                                                                                                                                                                         41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLygGlyValIleGlnAla
                                                                                                                                                                                                                                                  974 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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                                                                                                                                                                                                                                                                                                  61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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Christie,G., Michalovich,D., Simmons,D.L. and Walsh,F.S.
Inhibitor of neurite outgrowth in humans
Nature 403 (6768), 383-384 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 bp mRNA linear
Homo sapiens mRNA for Nogo-C protein (Nogo gene).
AJ251385
                                    US-09-830-972-29_COPY_990_1178 (1-189) x AY102278 (1-2389)
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Nogo gene; Nogo-C protein.
Homo sapiens (human)
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Michalovich, D.
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/product="RTN4 isoform B2"
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                                                                                                          2389 bp mRNA linear PRI 23-SEP-2003 Almo sapiens RTN4 isoform B2 (RTN4) mRNA, complete cds; alternatively spliced.
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ERQPSWIDSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWT
PPAPRAAPREPETPAAPKRGSSGSVDETLFALFALBASEPVIRSSAVVDLLYWRDIKKTG
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LESEVAISEELVQXYSOSALGHYNCTIKELRELVDDIVDSIKFAVLMWVFTYVGAI
FNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKWVDMAKIQAKIPGEKKAE
                                                                                                                                                                                                                                                                           Eukaryogia, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(base 1 to 2389)

Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E. Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4

J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland
Location/Qualifiers
1. 02389
/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="tamena"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Oertle, T. and Schwab, M.E.
Direct Submission
Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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/gene="RTN4"
/note="RTN4-B2; alternatively spliced"
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                     IleProGlyLeuLysArgLysAlaGlu 189
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/note="synonym: NOGO"
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/gene="RTN4"
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3 (bases 1 to 2389)
Van der Putten,H.
Direct Submission
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1. .2389
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/gene="RTN4"
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Homo sapiens
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DB:
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AUTHORS
TITLE
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VERSION
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                                          /evidence=sperimental
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Conservative:
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Sequence 2 from patent US 5858708.
AR028522 AR028522.1 GI:5940495
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927.00
100.00%
100.00%
99.57%
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Best Local Similarity:
Query Match:
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Homo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone IMAGE:4291127), complete cds.
BC007109
BC007109.1 GI:13937989
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                                         and Hillman, J.L. human neuroendocrine-specific
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Matches:
Conservative:
Mismatches:
                                                                                                  Patent: US 5858708-A 2 12-JAN-1999;
Location/Qualifiers
1. 799
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Unclassified.
1 (Dases 1 to 799)
Bandman, O., Au-Young, J., Goli, S.K.
Polynucleotides encoding two novel
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IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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JP 2002522016-A/3.
Homo sapiens (human)
Homo sapiens sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moorer, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Moreran, K.D., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
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/db_xref="MIM:604475"
112. 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov beries: TRAL Plate: 21 Row. h Column: 12

This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein

This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: (Dickson, Mark) mcd@pax11.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (30-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLOWIECH
CDNA Library Preparation: CLOWIECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Homo sapiens
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  SOURCE
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PRI 22-JUL-2000

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         1036 TATCTAGGACTTGCAAATAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1095
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LGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
HERZEGOVINA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Prinjha,R., Moore,S.E., Vinson,M., Blake,S., Morrow,R.,
Christele,G., Michalovich,D., Simmons,D.L. and Walsh,F.S.
Inhibitor of neurite outgrowth in humans
Nature 403 (6768), 383-384 (2000)
                                                                                                                                                                               1122 bp mRNA linear
Homo sapiens mRNA for Nogo-B protein (Nogo gene).
AJ251384
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                  1119
                                                       ProGlyLeuLysArgLysAlaGlu 189
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Nogo gene; Nogo-B protein.
Homo sapiens (human)
Homo sapiens
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/gene="Nogo"
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927.00
100.00%
100.00%
99.57%
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Michalovich, D.
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DB:
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ACCESSION
VERSION
KEYWORDS
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MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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HSA251384
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E 1 (bases 1 to 1122)

Michalovich, D. and Prinjha, R.K.

Protein similar to neuroendrocrine-specific protein, and encoding protein similar to neuroendrocrine-specific protein, and encoding Patent: JP 202522016-A 3 23-JUL-2002;

SMITHKLINE BEECHAM PLC
OS Homo sapiens (human)
PN JP 2002522016-A/3
PN JP 2002522016-A/3
PP 21-JUL-1999 JP 2000561310
PR 21-JUL-1999 GB 9916898.1 PI
DAVID MICHALOVICH, RABINDER KUMAR PRINJHA
PC
C12N15/09,CO7K14/47,CO7K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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PC C12P21/08,C12N15/00,C12N5/00
CC Protein similar to neuroendrocrine-specific protein, encoding cDNA encoding cDNA
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Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1. .1122
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9
                        AUTHORS
TITLE
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       REFERENCE
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Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Blakesley,R.W., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
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McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
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LGHVNCTIKELRELFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.B. Consortium/Link at: http://image.llnl.gov
Series: IRAL Plate: 4 Row: c Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 5902015
This clone has the following problem: The cds is short compared to
the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOGO, ASY, NI220/250, NSP, RTN-X"
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                                                                                                                      cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:12654418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         choriocarcinoma"
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Mismatches:
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/mol type="mRNA"
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/db_xref="MIM:604475"
186_ 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector: pOTB7"
                        On Aug 19, 2003 this sequence
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/gene="RTN4"
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Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Hale, S., Garzia, A.B., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Mulahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, B., Ketteman, M., Youchman, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samilus, D.E.,
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Generation and initial analysis of more than 15,000 full-length
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Homo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone IMAGES:3139770), complete cds.
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                                                                                                         101
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                                                                                                                                                                                                                                                                                        102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 735
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1151)
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Submitted (17-MOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                               796 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
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                                                                           62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
  Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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COOTHAL/02, COOTH21/04, C12NS/104, C12NS/10 PC
COTHAL/02, C12NS/06, C12NS/06, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16, C12NS/16
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M GREENE,
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(Chases I to 1213)

Moore, P.A., Shi, Y., Rosen, C.A., Ruben, S.M., Lafleur, D.W., Olsen, H.S., Bner, R., Brewer, L.A., Young, P., Greene, J.M., Petrie, A.M., Yu, G.L., Ni, J. and Peng, P., Greene, J.M., Petrie, A.M., Yu, G.L., Ni, J. and Peng, P., Greene, J.M., Petrie, A.M., Yu, G.L., Ni, J. and Peng, P., Greene, J.M., B6 human secreted proteins

L Patent: JP 2002514090-A 78 14-MAY-2002;
HUMAN GENOME SCIENCES INC

OS Unidentified

PN JP 2002514090-A/78

PD 14-MAY-2002

PP 11-JUN-1999 US 60/049549,113-JUN-1997 US 60/049560 PR 13-JUN-1997 US 60/049660 PR 13-JUN-1997 US 60/049660 PR 13-JUN-1997 US 60/049600 PR 13-JUN-1997 US 60/049600 PR 13-JUN-1997 US 60/049601 PR 13-JUN-1997 US 60/049601,113-JUN-1997 US 60/049601 PR 13-JUN-1997 US 60/049601,113-JUN-1997 US 60/05999 US 60/05999 PR 12-SEP-1997 US 60/058971 PR 12-SEP-1997 US 60/058971 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/058972 PR 12-SEP-1997 US 60/05897
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BD194907
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CEYWORDS
SOURCE
ORGANISM
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427

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487

81

121

607

141

667

161

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(EB (bases 1 to 1466)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F., Diatchenko, L., Maruslina, K., Earmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Mazny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalkak, U., Schmutz, J., Myers, R.M., Butterfield, S., Krzywinski, M.I., Skalkak, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse conna sequences
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAL Plate: 58 Row: d Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24431932 This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers
                                       BC071848 1466 bp mRNA linear PRI 30-JUN-2004 Homo sapiens reticulon 4, mRNA (cDNA clone IMAGE:4635625), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Straubberg, R.
Direct Submission
Direct Submission
Submitted (01-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Conteact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Emsil: ggapbs-r@mail.nih.gov
                                                                                                                                        GI:47939581
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Homo sapiens
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BC071848.1
              BC071848
LOCUS
DEFINITION
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SOURCE
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AUTHORS
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                                                                Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 LeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValileGlnAlaile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 GAACTCAGGCGCCTCTTCTTAGTTGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValValAspLeuLeuTyrTrpArgAspIleLysLysTyrGlyValValPheGlyAlaSer
                                                                                                                                Ruben, S.M., Ni, J., Rosen, C.A., Ebner, R., Young, P., Moore, P.A., Feng, P., LaFleur, D.W., Olsen, H.S., Yanggu, S., Brewer, L.A., Greene, J.M., Ferrie, A.M. and Yu, G.L.
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Matches:
Conservative:
Mismatches:
Indels:
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1210
/note="n equals a,t,g, or c"
                                                                                                                                                                                                                                 Patent: EP 1439189-A 79 21-JUL-2004;
Human Genome Sciences, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/db_xref="taxon:9606"
1172
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100.00%
100.00%
99.57%
                   sapiens (human)
                 Homo sapiens
Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(E. (bases 1 to 1485)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschult, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, F.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Voung, A.C., Shevchenko, Y.,
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Chuman, and mourse and marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 14 Row: n Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
            PRI 29-JUN-2004
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1485 bp mRNA linear PRI 29-JUN-21 Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone IMAGE:3901353), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysis
This clone has the following problem: The cds is short compared the longest cds in the locus.

Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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/tissue_type="Pancreas, epithelioid carcinoma"
/clone_lib="NIH_MGC_70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteat: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/mol type="mRNA"
/db xref="taxon:9606"
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                                                                                                         BC010737.1 GI:14789600
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/gene="RTN4"
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                                                                                                      VERSION
KEYWORDS
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                                   DEFINITION
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COMMENT
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                                                                                                                                                                                                                                                                                                                             GAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSK
LPEDDEPPARPPPPASVSPQAEPVWTPPAPAPPSTPAAPKRGSSGSVVVDLL
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IPGLKRKAE"
                                                                                                                                                                                                                                                                                                         translation="MEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAA
                                   NOGO, ASY, NI220/250, NSP, RTN-X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 GTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 601
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                              /product="RTN4 protein"
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Query Match:
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, Diversity of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:fl.cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
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                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                            Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T., Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R., Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H., Onogawa,S., Kaerlyama,S., Satoh,N., Matsunaw,H., Takahashi,E. Kataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takahashi,E. Terashima,Y., Watanabe,M., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.
                                                                                                                                          Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Homo sapiens cDNA FLJ27302 fis, clone TMS04776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="thymus"
/clone Tib="TMS"
/note="cloning vector: pME18SFL3"
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Mismatches:
Indels:
                                                          oligo capping; fis (full insert sequence)
Homo sapiens (human)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1525)
Sugano, S. and Suzuki, Y.
                                         GI:34527696
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                                                                                                      Homo sapiens
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TITLE
JOURNAL
    DEFINITION
                    ACCESSION
VERSION
                                                          KEYWORDS
                                                                                                                                                               REFERENCE
                                                                                                                                                                                    AUTHORS
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LGHVNCTIKELRRLFLVDDLVDSLKFAVLAMVPTYVGALFNGLTLLILALISLFSVPV
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    NOGO, ASY, NI220/250, NSP, RTN-X"
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/db_xref="GI:14789601"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
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/note="synonyms: NSP-CL,
/db_xref="LocusID:57142"
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6. .1127
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                                                                                 gene="RTN4"
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                                                                                      141
                                                                                                                                      142 LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                       121
                                                                                                                                                                                                                                                                                                                                           DE231889.1 GI:33041659
JP 2002511231-A/3.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1610)
Lin,H. and Cao,L.
Lin,H. and cao,L.
Patent: JP 2002511231-A 3 16-APR-2002;
CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OS HOMO sapiens (human)
PN JP 2002511331-A/3
PN 16-2002511331-A/3
PD 16-34P-2002
PP 18-DEC-1998 JP 2000526635
PR 30-DEC-1997 US 60/10540
PI HAISHAN LIN LI CAO
PC C12N15/09,A61K38/00,A61P43/00,C07K14/47,C07K16/18,C12N5/10,
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 911 GAGGAGTTGGAAGTACAGTAATTCTGCTCTTGGTCATGTAAATGTGAAGAAAAGAAAAAG
                                      GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                    122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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/organism='Homo sapiens (human)'
Location/Qualifiers
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Location/Qualifiers
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C12N15/00,A61K37/02,C12N5/00
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeulysPheAlaValLeu
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Patent: WO 2003058021-A 303 17-JUL-2003;
Xantos Biomedicine AG (DE)
Location/Qualifiers
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|mol_type="unassigned DNA"
|db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T.,
Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1617)
Yang, J., Yu, L., Bi, A.D. and Zhao, S.Y.
Assignment of the human reticulon 4 gene (RTM4) to chromosome 2p14-->2p13 by radiation hybrid mapping
Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
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Yang,J., Yu,L., Dai,F.Y., Cui,W.C., Zheng,L.H. and Zhao,S.Y.
Direct Submission
Submitted (27-AUG-1998) Lab of Human Gene Research, Institute of Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433, P.R.China
                              GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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/db_xref="GI:10039643"
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Homo sapiens reticulon 4c mRNA,
AF087901.1 GI:10039642
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 1654)

2 Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Hordon, M., Malek, J.A., Gunarane, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A., Fahey, J., Hellen, B., Garcia, A.M., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schmerch, A., Scheili, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.R. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 19 Row: d Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24431932 This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                                                                                     Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone MACE:4082756), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuraċ
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteat: MGC halp desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
                                                                       1253 CCTGGATTGAAGCGCAAAGCTGAA 1276
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/clone="IMAGE:4082756"
                                   182 ProGlyLeuLysArgLysAlaGlu 189
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                                                                                                                                                                                                                                                                                                                      BC012619.1 GI:15214977
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1654)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1013 GAACTCAGGCGCTCTTCTTAGTTGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 1072
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                                            Chaese 1 to 1619)
Sugano, S. and Suzuki, Y.
Birect Submission
Direct Submission
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:flcdna@ins.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                    Pax:81.3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of Beconomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    893 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 713 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="DMC07157"
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Mismatches:
Indels:
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Matches:
  VEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.E., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, W.M. B., Bonaldó, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Gudin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Wullahy, S.J., Bosak, S.A., McEwan, P.J.,
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Sanchez, A., Whiting, M., Madan, A., Youchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M.,
Butterfield, Y.S., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M.,
Generation and mouse comha sequences
Droce, Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurament: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgabcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                             1668 bp mRNA linear PRI 29-JUN-2004
Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone
IMAGE:3862911), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone distribution: MGC clone distribution information can be fou through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 21 Row: h Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein
This clone has the following problem: The cds is short compared the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (04-APR-2002) National Institutes of Health, Mammalian
Submitted (04-APR-2002), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1668
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1251 CCTGGATTGAAGCGCAAAGCTGAA 1274
                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
1 (bases 1 to 1668)
                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                    DEFINITION
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                    RESULT 40
BC026788
                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMARK
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOGO, ASY, NI220/250, NSP, RTN-X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1011 GAACTCAGGCGCCTCTTCTTAGTTGATTTTAGTTGATTCTCTGAAGTTTGCAGTGTG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          891 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-972-29_COPY_990_1178 (1-189) x BC012619 (1-1654)
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Matches:
Conservative:
Mismatches:
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/db xref="LocusID:57142"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProGlyLeuLysArgLysAlaGlu 189
                                                                                                                                                                                                                                                                                                             /gene="RTN4"
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927.00
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1691)
1 Lo,T. and Schwartz,S.M.
Cloning of a member of the reticulon gene family in human: skeletal unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | codon start=1
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| LGHVKTIKELRRLELYDDLVDSIKFAVLMWYFTYVGALFNGLTLLILALISLFSVPV
| IYERHQAQIDHYLGLANKVVDAMAKIQAKIPGLKRAE"
                                                                                              PRI 18-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 213
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                                                                                             AF132048 1691 bp mRNA
AF00 sapiens foocen-s mRNA, complete cds.
AF132048 GI:4838518
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 1691
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121. 720
                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1691)
Ito, T. and Schwartz, S.M.
Direct Submission
Submitted (27-FEB-1999) Pathology,
Pacific NE, Seattle, WA 98195, USA
Location/Qualifiers
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 CCTGGATTGAAGCGCAAAGCTGAA 1305
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927.00
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                                                                                                                                                                                      Homo sapiens
Homo sapiens
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Best Local Similarity:
                      1282
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DB:
                                                                                                          DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                             AUTHORS
TITLE
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AUTHORS
TITLE
JOURNAL
                                                        RESULT 41
AF132048
LOCUS
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IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
                                                                                                              RTN-X"
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        MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
        141

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                                                                                                            NOGO, ASY, NI220/250, NSP,
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Matches:
Conservative:
Mismatches:
Indels:
                                                                      1. .1668
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//note="synonyms: NSP-CL, N
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                                                                                                                                                               187. .1308
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: al Row: g Column: 2 This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="WDGQKKNWKDKVVDLLYWRDIKKTGVVFCASLFLLLSLTVFSIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 cagaaarcagargaaggccaccarrcaggcararcrggaarcrgaagrrgcrararcr 384
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                         1. .1698
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Rlausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausher, R.D., Collins, F.S., Wagner, L., Schemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wans, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skaiska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone IMAGE:3933041), complete cds.
                                                                                                                 514 AIGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
                                                                                                                                                                                                                                                                                                                GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
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contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anura
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Contact: MGC help desk
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TIGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 332
                                                                               333 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 392
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eguchi,Y., Tagami,S. and Tsujimoto,Y.

Direct Submission

Submitted (12-MAR-2000) Yutaka Eguchi, Osaka University Graduate
School of Medicine, Biomedical Research Center, Department of
Medical Genetics; Yamadaoka 2-2, Suita, Osaka 567-0871, Japan
(E-mail:eguchi@gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363,
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                                                                                                                                                                                                                     453 GAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                                                                            GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="brain"
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/product="RTN-x8"
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/gene="RTN-x"
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Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
Yu,J. and Han,L.H.
Direct Submission

Losting (06-Aug-1999) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai Location/Qualifiers

Location/Qualifiers

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/organism="Homo gapiens"
/db xref="maxNA"
/db xref="maxNA"
/db xref="maxNA"
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IGHVNCTIKELRRLETYDDLVDSLKPAVLMWYFTYVGALFNGITLLILALISLFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGIKKRAE"
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Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.
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Matches:
Conservative:
Mismatches:
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Homo sapiens clone SP1507 unknown mRNA.
AF177332
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                                                                                                                                                                                                                   Submitted (27-201-2003) Brain Research Institute and Department Submitted (27-201-2003) Brain Research Institute and Department Biology, University of Zurich and ETH Zurich, Winterthurerstr.190, Surich 8057, Switzerland Sequence update by submitter On Oct 27, 2003 this sequence version replaced gi:32331288.
                                                                  Octle, T. and Schwab, M.E.
Direct Submission
Submitted (LeCT-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
Zurich 8057, Switzerland
3 (bases I to 1721)
Octle, T. and Schwab, M.E.
Direct Submission
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Bos taurus RTN4-C (RTN4) mRNA, complete cds.
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LGHVNCTIKELRRLFLVDDLVDSLKFAVLMWYFTYVGALFNGLTLLILALISLFSVPV
IYERNQAQIDHYLGLANKOVKDAMAXIQAKIPGLKRRKAE"
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                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 54 Row: c Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28557782
This clone has the following problem: The cds is short compared to the longest cds in the locus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      804 GITGITGACCICCIGIACIGGAGAGACATTAAGAAGACIGGAGIGGIGTITGGIGCCAGC 863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ValValAspLeuLeuTyrTrpArgAspIlelysLysThrGlyValValPheGlyAlaSer
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  Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="Eye, retinoblastoma"
/clone_lib="NIH MGC_16"
/lab_host="DH10B-R"
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Conservative:
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/product="reticulon 4, iso
/protein id="AAH68991.1"
/db_xref="GI:46362519"
/db_xref="LocusID:57142"
/db_xref="MIM:604475"
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'db_xref="LocusID:57142"

'db_xref="MIM:604475"
                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4634289"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer (C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Rah, S.S., Loquellano, N.A., Peters, G.J.,
Mockernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchen, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Brown and mouse cDNA sequences
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                                                                                                                  161
                                                       578
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 1728)
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Submitted (05-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                519 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTATTTTGGCT
                                                                                                               142 LeuileSerLeuPheSerValProValileTyrGluArgHisGlnAlaGlnIleAspHis
MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 2052)

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Submitted (17-JUN-1998) Masuo Yutsudo, Osaka University, Dept. of
                                                                                                                                                                                                                                                                                   268 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGAGTGGTTTGGTGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCAGATAAAG
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Matches:
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Homo sapiens ASY mRNA, complete
AB015639
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/gene="RTN4"
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                                                              Alignment Scores:
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                                                                                                              191
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Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1800)
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Oertle, T. and Schwab, M.E.
Direct Submission
Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Switzerland
3 (bases 1 to 1800)
2 van der Putten, H.
Direct Submission
Submitted (07-MXY-2002) Nervous System Research, Novartis
Inc., Basel, Switzerland
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I (bases 1 to 2335)
Yang, J., Yu, L., Bi, A.D. and Zhao, S.Y.
Assignment of the human reticulon 4 gene (RTN4) to chromosome Cytogenet. 2p13 by radiation hybrid mapping
Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
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Mismatches:
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AF148538
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                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 2235)
Zhou,Y., Yu,L. and Zhao,S.Y.
Direct Submission
                                                                                                                AF148538.1 GI:10039552
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                                                                              DEFINITION
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   Osaka
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   Yamadaoka, Suita,
Tumor Virol., Res. Inst. Microb. Dis.; 3-1 Yamadaoka
565-0871, Japan (B-mail:)Yutsudo@biken.osaka-u.ac.jp,
Tel:81-6-879-8313, Fax:81.6-879-8315)
Location/Qualifiers
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Mismatches:
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67. .1188
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AY102277 23-SEP-2003 Homo sapiens RTM4 isoform B1 (RTM4) mRNA, complete cds; alternatively spliced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          82 GluGlubeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.
Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                                                                                                                                                                                                                                                              915 CAGAAATCAGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 974
                                                                                                                                                                                                  Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2332)
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Van der Putten, H.
Direct Submission
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
                                                                              855 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
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                                         US-09-830-972-29_COPY_990_1178 (1-189) x AF132047 (1-2276)
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Oertle, T. and Schwab, M.E.
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2276)
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                       GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                937 GAGGAGITGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                            GlubeuargargLeuPheLeuValaspaspLeuValaspSerLeuLysPheAlaValLeu
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Cloning of a member of the reticulon gene family in human:
ubiquitous type
Unpublished
Loyases 1 to 2276)
S Ito, T. and Schwartz, S.M.
Direct Submission
Loyases 1 to 2769
S Ito, T. and Schwartz, S.M.
Direct Submission
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Conservative:
Mismatches:
Indels:
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Homo sapiens foocen-m mRNA, complete cds.
AF132047
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/product="foocen-m"
/protein_id="AAD31021.1"
/db_xref="GI:4838517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 ProGlyLeuLysArgLysAlaGlu 189
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Conservative:
Mismatches:
Indels:
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                                                                                                                                             DNA
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
479. .1354
                                                                                                                                      Sequence 3170 from Patent EP1396543. CQ783030.1 GI:45502969
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                                                                 ProGlyLeuLysArgLysAlaGlu 189
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/codon_start=1
/product="RTN4 isoform B1"
/protein_id="AAM64246.1"
/db_xref="G1:Se800562"
/translation="MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDBEEEEEEEED
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RRQFSWDFSPSVSSTVPARPSBCAAAVSOSSKLEPBOBPPARGPPPPPAGVSOGAEPVWT
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             Location/Qualifiers
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                             1280 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAAGAATC 1339
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Princes for synthesizing full length cDNA clones and their use
Patent: EP 1396543-A 3170 10-MAR-2004;
Research Association for Biotechnology (JP)
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Submitted (12-MAR-2002) Takao Isogai, Helix Research Institute, Genomice Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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Sugiyama, T., Suzuki, Y., Sato, H., Nagai, K., Sugano, S., Ishii, S.,
Swai-Ho, Y., Salto, K., Yamamotco, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
Ninomiya, K.
Unpublished
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                     LeuAlaLeuLeuSerValThrIleSerPheArg1leTyrLysGlyValIleGlnAlaIle
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AK075039
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Homo sapiens (human)
Homo sapiens
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Isogai, T. and Otsuki, T.
Direct Submission
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REFERENCE
AUTHORS
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                                                                                                                                                           1148 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 1207
.028 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGGTAAAG 1087
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JP 2002017375-A/2868
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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her for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD127437.1 GI:21222382

DP 2002017375-A/2868.

JP 2002017375-A/2868.

Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1694)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Makamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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                                                                                                                     MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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PN JP 2002017375-A/2868
PD 22-JAN-2002
PP 7-JAN-2002
PP 07-JUL-2000 JP 200253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHI PI ISHII, YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI TETSUJI OTSUKI, HISASHI KOGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2868 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AUTHORS
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                                                                                                                         /note="compared to AF148538, AF132047 and AC016171.4"
/replace=""
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                                                                               /tissue type="ovary, tumor tissue"
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Matches:
Conservative:
Mismatches:
Indels:
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                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OVARC1001030"
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                                             Euteleostomi;
                                                                                                                                          comparion between human neuroblastoma with good prognosis, in comparion between human neuroblastoma with good prognosis and leuroblastoma with bad prognosis patent: JP 2001321175-A 22 20-NOV-2001; CHIBA PREF,HISANITSU PHARMACEUTICAL CO INC
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1. .1980
/organism='Homo Bapiens (human)'
Location/Qualifiers
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Catarrhini; Hominidae;
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                                        Eukaryota; Metazoa; Chordata; Craniata; Vert.
Mammalia; Eutheria; Primates; Catarrhini; Hoi
1 (bases 1 to 1980)
Nakagawara, Nakagawara, Nuclaic acid sequence characterized in that potentiated in human neuroblastoma with good
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                           Homo sapiens (human)
JP 2001321175-A/22
20-NOV-2001
12-MAY-2000 JP 2000140387
AKIRA NAKAGAWARA
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Homo sapiens (human)
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1 (bases 1 to 994)

Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.

Extended cDNA of secretory protein
Patent: JP 2002508182-A 45 19-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                               SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
                                   41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                          61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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3 peptide 35. .160
JyA_signal 901. .906
JyA_site 979. .994.
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JP 2002508182-A/45.
Homo sapiens (human)
Homo sapiens
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BD139293
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Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma and poor prognostic human neuroblastoma and poor prognostic human neuroblastoma and poor prognostic human perent: WO 0166733-A 22 13-SEP-2001;

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                                                                         1485
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                                       AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp 160
                                                                                                            HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1980)
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     1366 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG
                                                             C12N15/12,C12Q1/68
Nucleic acid sequences characterized by their enhanced
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD097380
BD097380
NO 0166733-A/22.
Homo sapiens (human)
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99.47%
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PC C12N15/12,C1
CC Nucleic acic
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submitted (11-OCT-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashianih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tell:81-3555-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY
RGYOQAIQSASDEGHPPRAYLESSEVALSEELVQKYSNSALGHVNCTIKELRRLFLVDDL
VDSIRFAVLAWVFTYVGALFRGLTLLILALISLFSVFVIYERHQAQIDHYLGLANKNV
KDAMAKIQAKIPGLKRKAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  776 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCGATATCT 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="brain parietal lobe"
/clone_lib="macaque brain cDNA library QnpA"
/dev_stage="adult"
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                             /organism="Macaca fascicularis"
|mol_type="mkm4"
|db xref="taxon:9541"
|clone="QnpA-18952"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="hypothetical protein"
protein_id="BAB16739.1"
db_xref="G1:10801644"
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98.40%
98.60%
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Best Local Similarity:
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Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
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Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
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clone:QnpA-18952.
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is (full insert sequence).
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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                                                                                  4.39e-86
918.00
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                                                                    Alignment Scores:
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                                                                                                                                           Query Match
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AB049853
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stepeton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1649 CATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAA 1708
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Mus musculus
Musrayota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2958)
                                                                                                                                                                                                                                                                          1409 TCAGAGGAATIGGTICAGAAATATAGTAATICTGCTCTTGGTCATGTGAACAGCACAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1469 AAAGAATTGAGGCGTCTCTTTAGTTGATGATTAGTTGATTCCCTGAAGTTTGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp
                                                                                                              1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                           1289 GCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1349 AICCAGAAAICAGAIGAAGGCCACCCAITCAGGGCAIATIIGGAAICIGAAGIIGCCAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 HisTyrLeuGlyLeuAlaAsnLysAspAlLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                       1169 rcagricricaccrccrgracrggagagacarraagaagacrggagrggrgrgcc
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                                                                                                                                                                                                                                          21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                            41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC032192 2958 bp mRNA linear R
Mus musculus reticulon 4, mRNA (CDNA clone MGC:38204
IMAGE:5323152), complete cds.
                                                         US-09-830-972-29_COPY_990_1178 (1-189) x AB073672 (1-1738)
0
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KLEPENPPPYEEAMSVALKTSDAKEEIKEPESFNAAAQEAEAPYISIACDLIKETKLS
                                                                                                                     1015
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The partial sequence of mouse nogo-A cDNA clone#4109
Unpublished
2 (Bases 1 to 1738)

Tozaki, H. and Hirata, T.

Tozaki, H. and Hirata, T.

Submission
Submitted (29-00T-2001) Hirokazu Tozaki, Division of Brain
Function, National Institute of Genetics; Yata 1111, Mishima,
Basizuoka 411-8540, Japan (E-mail:htozaki@lab.nig.ac.jp,
URL:http://www.nig.ac.jp/home-j.html, Tel:81-55-981-6721(ex.6721),
Fax:81-55-981-6722
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
896 GAACTCAGGCGCCTCTTCTTAGTTGATGTTAGTTGATTCTCTGAGGTTTGCAGTGTTG
                                                         MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                           956 ATGIGGGTATTTACCTATGITGGTGCCTTGTTTAATGGTCTGAGCTTTTGGCT
                                                                                                                                                                                                                                                                                             TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProGlyLeuLysArgLysAlaGlu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/gene="Nogo-A"
<1. _1738
/gene="Nogo-A"
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AB073672
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REFERENCE

REMARK COMMENT

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/note="Reticulon; Region: Reticulon. Reticulon, also know as neuroendocrine-specific protein (NSP), is a protein of unknown function which associates with the endoplasmic reticulum. This family represents the C-terminal domain of the three reticulon isoforms and their homologues" /db_xref="CDD:pfam02453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1943 CATTATCTAGGACTTGCAAACAAGAGGGTTAAGGATGCCATGGCCAAAATCCAAGGAAAA 2002
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Mus musculus reticulon 4, mRNA (CDNA clone IMAGE:5366860), partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/gene="Rtn4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgrl.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Peargon,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 56 Rows k Column: 2.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="LocusID:68585"
/db_xref="MGI:1915835"
/translation="MPEGLTPDLVQEACESELNEATGKIAYETKVDLVQTSEAIQES
/translation="MPEGLTPDLVQEACESELNEATGKIAYETKVDLVQTSEAIQES
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DGIKLEPENPPPYEEAMSVALKTSDAKKEIKSPRSFNNAAQERKEAPYISIACDLIKET
KLSTEPSPEFSNYSEIAKFEKSVPDHCELVDDSSPESEPVDLFSDDSIPEVPQTQEEA
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KKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDDS
PKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVSDEFSKSRSSV
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SVODLLYWRITKKTGVVFGASLFLLSLTVFSTI VSVTALALLSVT ESFRI YKKVI
QALOKSDEGHPFRAVLESEVAL I SELLOKYSNSALGHVNST I KELRRLFLVDDLVDSL
KFAVLMWV FTY VGALFNGLTLLILAL SELFSI PVI YERHQAQI DHYTLGIANKS VKDAM
                                                                                                                                                                                                                          Direct Submission
Submitted (06-UN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                  Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailu's, D.E.,
                                                                                                                                                                                                                                                                                                                                                                        Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="synonyms: ASY, NOGO, NSP-CL, C130026I10Rik"
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/clone="MGC:38204 IMAGE:5323152"
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'db_xref="G1:21618981"
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/organism="Mus musculus"
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product="Rtn4 protein"
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/strain="FVB/N"
                                                                                            Proc. Natl. Acad. Sci.
22388257
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FEATURES

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2 (bases 1 to 4063)
Oertle, T. and Schwab, M.E.
Direct Submission
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Van der Putten, H.
Direct Submission
98.41%
98.28%
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              I. (Dasges I. Co. 2012)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKernan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wuzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerd, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Hellen, R. (B.S.) (26), 16899-16903 (2002)
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcampai.nih.gov/
Contact: nisc_mgcampai.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Gunn,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskeli,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Peargeon,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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Submitted (06-UN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk in the many state of the many state of the many state of the many state of the many state of the many state of the many state of the many state of the many state of the many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many state of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many states of many state
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/db_xref="taxon:1090"

/clone="thAGE:5366860"

/tissue_type="Eye, retina, mouse strain C57Bl\6"

/clone_lbb=nUHQC_94"

/lab host="DH108"

/note="Vector: pCMV-SPORT6"
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/organism="Mus musculus"
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99.47%
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TITLE
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PUBMED
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Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.
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                                                                                                                                                                                                2317 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla11e
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                                                                                                                                                                                                                                                                                 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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                                                                                                         US-09-830-972-29_COPY_990_1178 (1-189) x BC032272 (1-3815)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(B I (bases 1 to 4518)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschult, S.F., Zeeberg, B., Buetow, K.H., Schefer (C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Mulak, J.A., Gungaratne, P.H., Richards, S., Sanchez, A., Whiting, M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helten, E., Ketteman, A., Young, A.C., Shevchenko, Y., Shevchenko, Y., Butterfield, Y.S., Karzywinski, M.I., Skalska, U., Sanilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J. A., Schein, J. Schein, J. Schot, L. A., Schein, J. Schein, J. Schot, L. A., Schein, J. S., Grouse, S.J. and Marra, M.A., Schein, J. Schein, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Schot, J. Sc
                                                                                                                                                                                                                                         2964 TIGATGIGGGTATTTACTIACGTIGGTGCCTTGTTCAATGGTTTGACACTACTGATTTA 3023
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Mus musculus cDNA clone MGC:73436 IMAGE:6847916, complete cds.
BC056373
2844 TCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATA 2903
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                                                                  LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
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Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
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Submitted (11-A02-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                        2904 AAAGAATTGAGGCGTCTCTTCTTAGTTGATTAATTTAGTTGATTCCCTGAAGTTTGCAGTG
                                                                                                                                                                                               121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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Web site: http://genome.uiowa.edu
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC056373.1 GI:33604147
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DEFINITION
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
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codon_start=1
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Indels:
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Matches:
                                                                                             1. 4063
/organism="Mus musculus"
/mol type="maxna"
/strain="129/SvcJ7"
/db_rref="taxon:10090"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="AAM73502.1"
db_xref="GI:23379809"
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                                                                                                                                                                                                                                                                                                    . .4063
'gene="Rtn4"
'note="synonym: nogo"
                           Inc., Basel, Switzerland
Location/Qualifiers
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3174. .4063
/gene="Rtn4"
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Best Local Similarity:
Query Match:
DB:
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/db_xref="G1:23379817"

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LPSLSPLSTVSFKEHGYLGNLSAVASTEGTI EETLMEASRELPERATNPFVNRESAEF
SVLEYEGGGSSFNGSFNGESAML VENTKEEVI VRSKDKEDLVCSAALHNPQESPATLT
KVVKEDGVNS PEKTWIN I FNEMKANSVVAPVREEYADFKEPRQAMEVKOTYEGSRDVLAA
RANMESKVDKKCFEDSLEQKGHGKDSESRNENASFPRIPELVKDGSRAYITCDSFSSA
                                                                                                                                                                                                                                                                                                                                        3519 CATTATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAGCAAA 3578
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Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E. Genomic Structure and Functional Characterisation of the Promoters of Human and Mouse nogo/rtn4

J. Mol. Blol. 325 (2), 299-323 (2003)
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Inc., Basel, Switzerland
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Oertle, T. and Schwab, M.B.
Direct Submission
Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
                                                                           3399 TIGATGIGGGTATTTACTTACGTIGGTGCCTTGTTCAATGGTTTGACACTACTTTA
                                                                                                                                                                                                      3459 GCTCTGATCTCACTCTTCAGTATTCCTGTTATATGAACGGCATCAGGCGCAGAAGAT
                                                                                                                                                                                                                                                                                                      161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                       141 AlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
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/gene="Rtn4"
/note="NOGO-A; RTN4-A; alternatively spliced"
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/mol_type="mRNA"
/strain="129/SvcJ7"
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/chromosome="11"
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/note="synonym: nogo"
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Mus musculus (house mouse)
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LPSLSPLSTVSFKEHGYLGNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEF
SVLEYSEMGSSFNGSPKGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLT
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RANMESKVDKKCFEDSLEQKGHGKDSESRNENASFPRTPELVKDGSRAYITCDSFSSA
TESTAANI FPVLEDHTSENKTDEKKI EERKAQI ITTEKTSPKTSNPFLVAIHDSEADYV
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SYPTPAQLCEBFEBRARTPSPVLLPVI VMEAPLINSLLBSTGASVAQPSASPLEVPSPVS
YDGIKLEPENPPPYEBAMSVALKTSDSKEBIKEPESFRAAAQEAEAPYISIACDLIKE
TKLGTEPSPPERSVEIAKFEKSVPDHCELVDDSSPESI
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Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu.I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Ishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.
Scheetz,T., Smith,C., Snir,B., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ServalvalaspLeuLeuTyrTrpArgAspIleLysLysThrGlyvalvalPheGlyAla
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                                                                                                                                                                                                                                                                                                                                                                /.organism="Mus musculus"
/mol_type="mRNA"
/strain="c57BL/6"
/db xref="taxon:10090"
/clone="MGC:73436 IMAGE:6847916"
/tissue type="Brain, mouse, 13.5,14.5,16.5,17.5 dpc"
/clone_Tib="NIH BMAP_FY0"
/lab host="DH10B"
/note="Vector: pYX-ASC"
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Matches:
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Best Local Similarity:
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8 셤 ò 셤 8 8 8 셤 à 요 ò

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Mus musculus (house mouse)
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Best Local Similarity:
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DB:
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ACCESSION
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KEYWORDS
SOURCE
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ORGANISM
                                                                                                                                                                                             source
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                                                                       REFERENCE
AUTHORS
TITLE
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LOCUS
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KEYWORDS
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             TIDNISKVTEAVVATMPEGLIPDLVQEACESĒLMEATGTKIAVETKVDLVQTSEAIQE
SIYPTAQLCBEFERARATPSPVLPDIVMEAPLNSLLESTGAGVAQPSASPLEVPSPVS
YDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESPNAAQBARAAVISIACOLIKE
TKLSTBEPEBENPPSTBIAKFEKSVPHCELVDDSSPESEPVDLFSDSIPEVQTGEE
AVMLMKESLITEVSETVŢĢKKHKERLSASPQEVCKPYLESFQPNLHITKOAASNBIPTI
TKKETISLQMEBENTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDD
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Mismatches:
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Sequence 382 from patent US 6607879.
AR379837
AR379837.1 GI:40087471
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Matches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1671 GAIGIGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGC 1730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIl
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                                                                   and immunological
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188
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Unthiorismitied.

1 (bases 1 to 2610)

Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.

Compositions for the detection of blood cell
response gene expression
Patent: US 6607879-A 382 19-AUG-2003;

Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                           1. .2610
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Mus musculus RTN4 (Rtn4) mRNA,
AY102282
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99.47%
99.47%
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140

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IYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRRAE"
                                                                                                                                                                                                                                1167 freargreserartractracerresecrretrearestricacactactacrearitra 1226
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Mouse vp20/RIN4C cDNA
C. Craggs; P.D. and Morris, N.J.
Mouse vp20/RIN4C cDNA
C. (bases 1 to 734)
Morris, N.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (05-DEC-2000) School of Biochemistry and Genetics, The
Medical School, Newcastle University, Newcastle upon Tyne, Tyne a
               81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlle
                                                                                                                                                      161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                     IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                      141 AlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
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Mus musculus vp20/RTN4C protein mRNA, complete cds.
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Matches:
Conservative:
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Indels:
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67. 666
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AF326337
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RRGSGSVDETLPALPAASAPVIPSKLPEDDEEPARPPAPAGASPLABPAAPFETPAAF
IVSVTAYIALLSVTISFRIYKGVIQAIOKSDEGHPFRAVLESEVAISEELVOKYSN
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1377. .2266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Gemomic Structure and Functional Characterisation of the Promoters
of Human and Wuse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2266)
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
Inc., basel, Switzerland
Location/Qualifiers
1. .2266
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Certle, T. and Schwab, M.E.
Direct Submission
Submitted (07-MAX-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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Matches:
Conservative:
Mismatches:
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Van der Putten, H.
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IYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGKRAE"
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/gene="Rtn4"
/note="NOGO-C; RNT4-C; alternatively spliced"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/db_xref="GI:23379815"
                                 organism="Mus musculus"
                                                                               db_xref="taxon:10090"
                                                                                                                                            note="synonym: nogo"
Location/Qualifiers
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                                                                                              chromosome="11"
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AY102283.1 GI:23379814
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
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                               US-09-830-972-29_COPY_990_1178 (1-189) x AF326337 (1-734)
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J. Mol. Biol. 325 (2), 299-323 (2003)
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Oertle, T. and Schwab, M.E.
Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer:
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Sequence I from Patent WO03002602.
AX766046 GI:32260128
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Rattus norvegicus
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                                                                                                                                      AY102281 2209 bp mRNA linear ROD 29-JAN-2003 Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.
                                                                                                                                                                                                                                                                                                                                                                   Oertle, T., Huber, C., van der Putten, H. and Schwab, M.B.
Genomic Structure and Functional Characterisation of the Promoters
of Human and Mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 2209)
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3 (Dasea 1 to 2209)
Van der Putten, H.
Direct Submission
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [ (bases 1 to 2209)
Oertle,T. and Schwab,M.E.
Direct Submission
Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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Location/Qualifiers
i. 1209
/ Organism="Mus musculus"
/ mol type="mRNA"
/ strain="129/SvcJ7"
/ db xref="taxon:10090"
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1320. .2209
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/gene="Rtn4"
  182 ProGlyLeuLysArgLysAlaGlu 189
                            CCTGGATTGAAGCGCAAAGCAGAA 876
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/gene="Rtn4"
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TAASLESEDENGTYSTERREGYLGANGAAVSEGTIEETLUREAKELEERATUREPUND.

LAASLESEDENGTSPEKTHOTIENGAAVSEGTIEETLUREAKELEERATUREPUND.

LAEFSELESEDENGSPEKGEALIUSENTERETUREAKEDENGSALHSPORES

VGKEDRVVSPEKTHOTIENENGKSLGKOSEGRINEDAFREPERQAMEVKOTYEGSRUVLAAR

ANVESKVORKKLEEDLEDGKSLGKOSEGRINEDAFPEKPERQAMEVKOTYEGSRUVLAAR

ANVESKVORKKLEEDLEDGKSLGKOSEGRINEDAFPEKREPEVKOSERATITAAR

TOTILSKYTERAAVSINAPGGALTPOLVORACESELNBATOTYTATTVOLVOTSEBATOES

TOTILSKYTERAAVSINAPGATTAATTVOLOSTATIANSLESAGASVOTOSSVSPERAPPVSY

DSIKLEPENPP PYERAATTSENTULKALGTKEGIKEPESFNAAVOETEAPPYSI DIACOLIKET

KLEFTER SEDNENTALISANDELLSASKEDIKTESERDASPONLHSTATAAKSINIPTITK

KEKI SLOMEEFNTALISONDELLSASKEDIKTESEFORNIKTROAKSINIPTITK

KEKI SLOMEEFNTALISONDELLSASKEDIKTESETFORDSPREEDRSLASTINA

VOLMERSTITEVSERTATOLSASKEDIKTESETFORDSPREEDRSLASTING

KLAKRYTDLEVSDKSBI ANTOGADSLPCLELPCOLSFKNITYROEVHYSDBESERNRS

SVSRASI SPSNVSALBPOTEMGSIYVKSKITTKRABKKLJPSOTTERDRSLASTING

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KITSVVDLLYWROIKTGVVGALFROSTILLBLISLISTIVSTINGLANTSVKD
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                         SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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   US-09-830-972-29_COPY_990_1178 (1-189) x AX766046 (1-3489)

    3492
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/codon_start=1

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CQ829507
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                        21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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                        SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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.AX700396.1 GI:29536204
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LYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSY
DSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKET
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WIMMEKLITEVSETVAQVERELLAS-SPOELGKFYLESPOPNIHSTKDASANDIPTITK
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KLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRS
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SLKFAVLMWVFTYVGALFNGLTLILALISLFSIPVIYSRHQVQIDHYLGLANKSVKD
                        ROD 28-JAN-2000
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Van der Haar, M.B.
Direct Submission
Submitted (14-JUN-1999) Van der Haar M.B., Department of
Neuromorphology, Brain Research Institute, University of
Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND
Location/Qualifiers
                        linear
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Abtus norvegicus mRNA for Nogo-A protein. AJ242961 ALS4961.1 GI:6822246
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1. .4684
                                                                                                                                  Nogo-A protein.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Mammalia; Eutheria; Rodentia;
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253. .3744
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2782 183 4 2 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

3.5e-84 905.00 98.94% 96.83%

Percent Similarity: Best Local Similarity: Query Match: DB:

US-09-830-972-29 COPY 990 1178 (1-189) x RNO242961 (1-4684)

Scores:

Alignment Sc Pred. No.:

Score:

4684 184 3 0 0

Length:
Matches:
Conservative:
Mismatches:

3.23e-84 908.00 98.94% 97.35% 97.53%

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                                                                                 'note="Rtn4-B2; alternatively spliced"
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183
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701. 1840
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97.21%
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Oertle,T. and Schwab,M.E.
Direct Submission
Submitted (16-07-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
Zurich 8057, Switzerland
Location/Qualifiers
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGCGTGATCCAGGCT
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US-09-830-972-29_COPY_990_1178 (1-189) x AX700396 (1-2782)
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1. 7782
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ANNESCYDKKCFEDELEQKSHGKDSESRNENASFPSTPELVKDGSRAYITCDSFTSA
TESTRANIFPVLEDHTSENKTDEKI ERRKAQIITEKTSPKTSNFLVAIHDSEADYV
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TTDNLSKYTRAAVATWPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQE
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YDGIKLBPENPPPYEEAMSVALKTSDAKEEIKEPESFNAAAQEAEAPYISIACDLIKE
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AVMLMKESLTEVSETVTQHKKKERLSASPQEVGKPYLESFQPNLHITKDAASNEIPTL
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VSKVPLLLPNVSALESQIEMCNIVKPKVLTKEAEBKLPSDTEKEDRSLTAVLSAELNK
TSVVDLLYWRDIKKTCVVYFCASLFLLLSLTVFSIVSSIVSYTAYIALALLSVTISFRIYKG
                                                                                                                                                                       EDDEDLEELEVLERKPAAGLSAVPVPPAAAPILLDFSSDSVPPAPRGFLPAAPPTAPER
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KRRGSGSVDETLFALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAAS
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SVLEYSEMGSSFNGSPKGESAMLVENTKEEVIVRSKOKEDLVCSAALHNPQESPATLT
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                    rcagaggaarrggrrcagaaracagraarrcrgcrcrrggrcargrgaacagcacaara 1570
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                                                                                                                                                                                                                                                                                                                      161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Direct Submission
Submitted (17-MAY-2002) Institute of Neurosciences, 17 Chang Le Xi
Road, Xi'an, Shaanxi 710032, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (basea I to 3821)
Jin, W., Long, M., Li, R. and Ju, G.
                                                                                     LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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Mus musculus nogo-A mRNA, complete cds.
AY114152

    .3821
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    /mol_type="mRNA"
    /strain="BALB/c"

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247. .3738
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Mus musculus
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ORGANISM
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TITLE
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AY114152
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EEDEDELEERLERKERERAGSAAAVEPRAAARLIDESSDSVPPRREVEPLAAPPRAP
ERQESWERSPAASEPAAGSAAAVESKIPEDDEPPRAREPPPPAGASFLAEPAAPPAP
PAAPKRRGSGSVDETILFALPAASEPVIPSSAVVDILYWRDIKKTGVVFGASIFILISI
TYSTSYSVATYTALALISVTISFRIYKSVOJAJAGKSDEGHPFRAXLESEVAISBELVQ
KYSNSALGHVNSTIREIRIFLIVDILVDSVLKRAVLAWVFTVVGALFNGITLIIALIS
LESIPVIYERRQVQIDHYLGGLANKSVKOAMAKIQAKIFUGALFNGITLIILALIS
LESIPVIYERRQVQIDHYLGGLANKSVKOAMAKIQAKIFUGITLIILALIS
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ROD 18-MAY-1999
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                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      701. .. 1840
/note="member of reticulon gene family; alternate splice
                                                                                                                                                                                                                                                                                                                                                                                                              University of Washington, 1959
                                                                                                                                                                                                                                    1 (bases 1 to 2782)

Ito, T. and Schwartz, S.M.

Cloning of a member of the reticulon gene family in rat: One of minor splice variants
Unpublished
2 (bases 1 to 2782)

Ito, T. and Schwartz, S.M.

Direct Submission
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  AF132045 2782 bp mRNA linear ROD 18-
Rattus norvegicus foocen-m2 mRNA, alternate splice product,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="vascular smooth muscle"
/dev_stage="3 months old"
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Conservative:
Mismatches:
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar-Kyoto"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-FEB-1999) Pathology, L
Pacifice NE, Seattle, WA 98195, USA
Location/Qualifiers
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/protein_id="AAD31019.1"
                                                                                                                               rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="GI:4838513"
                                                                                                                               Rattus norvegicus (Norway Rattus norvegicus
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                                                                   AF132045
AF132045.1 GI:4838512
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96.83%
97.21%
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                                              complete cds.
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Best Local Similarity:
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DB:
                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  LOCUS
DEFINITION
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/translation="MOGOKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVPSIV
SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPPRAYLESEVAISEELVQKYSNSA
LGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 TTATTCCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 209
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Morris,N.J.
Direct Submission
Submitted (26-FEB-1998) Biochemistry, Dartmouth Medical School, Hanover, NH 03755, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                                                                                                                                 GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                              87. 107
/note="tyrosine kinase site; phosphorylation site"
/evidence=not_experimental
                                                                                                                                           IYERHOVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD"
                                                                                                                                                                                                                                                                                                                               produčt="GLUT4 vesicle 20kDa protein"
protein_id="AAF01564.1"
db_xref="GI:6016999"
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/evidence=not_experimental
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evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132. 194
/note="transmembrane-region site"
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/evidence=not_experimental
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Rattus norvegicus"
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97.34%
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                                                                                                                    source
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                 REFERENCE
AUTHORS
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Rattus norvegicus GLUT4 vesicle 20kDa protein mRNA, complete cds.
AF0S1335
VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELFRLFLVDDLVD
SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKD
AMAKIQAKIPGLKRKAE"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morris, N.J., Ross, S.A., Neveu, J.M., Lane, W.S. and Lienhard, G.E. Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family Biochim. Biophys. Acta 1450 (1), 68-76 (1999)
                                                                                                                                                                                                                                                                                                                                                                               40 IleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln
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                                                                                                                                Conservative:
Mismatches:
Indels:
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Matches:
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Rattus norvegicus
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98.95$
97.89$
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Best Local Similarity:
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Pred. No.:
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Oertle, T. and Schwab, M.E.
Direct Submission
Submitted (16-OCT-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
                                                                                                                                                                                                                                                     210
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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A reticular rhapsody: phylogenic evolution and nomenclature RTN/Nego gene family
FASEB J. 17 (10), 1238-1247 (2003)
                                                 Conservative:
Mismatches:
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Rattus norvegicus
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Query Match:
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AY164740.1
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Sciurognathi, Muridae, Murinae,
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                         MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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                                                                                                                                               ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT
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Submitted (14-UUN-1999) Van der Haar M.E., Department of
Neuromorphology, Brain Research Institute, University of
Winterthurestrasse 190, Zurich, CH-8057, SWITZERLAND
Related sequences: AJ242961-2.
Location/Qualifiers
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protein.
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/organism="Rattus norvegicus"
/mol_type="mRNA"
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Rattus norvegicus mRNA for Nogo-C
AJ242963
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Nogo-C protein.
Rattus norvegicus (Norway rat)
Rattus norvegicus (Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
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118. .717
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Van der Haar, M.E.
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RNO242963
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Alignment Scores:

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Submitted (14-JUN-1999) Van der Haar M.E., Department
Neuromorphology, Brain Research Institute, University
Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND
Related sequence: AJ242961.
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                                                                                                                                                               mRNA
protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
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/db_xref="taxon:10116"
1. 72156
                                                                                                                                                        Rattus norvegicus mRNA for Nogo-B ; AJ242962.1 GI:6822248 NOGO-B protein. Rattus norvegicus (Norway rat) Rattus norvegicus (Norway rat) Rattus norverian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                         function="unknown"
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89. .1271
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904.00
98.94%
97.34%
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Van der Haar, M.E.
                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                      Rattus.
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ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                     RNO242962
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
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ERQPSWERSPAAPAPSLPAAAVLPSKLPFAADELDFSSDSVPPARGGLSPAAPPAAP
ERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPAGASPLAEPAAPST
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TISFEL YKGYLQAIGKSDEGHPFAYLESEVALSEELVGCTVGKYSNSALGHVNSTIKELRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIle 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               705 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
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Matches:
Conservative:
Mismatches:
Indels:
                                            1. .2156
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                                                                                                                                                                             1. .188
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189. .1271
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/note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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1. 72156
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                         Location/Qualifiers
                                                                                                                                                                                                                                                                                             /codon_start=1
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904.00
98.94%
97.34%
Zurich 8057,
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Best Local Similarity:
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Pred. No.:
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DB:
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PAAPKRRGSGSVVVDDLYMRDIKKTGVVFGASLFLLLSLTVESIVSYTAYIALALLSV
TISFRIYKGYIQAIQKSDEGHPFRAYLESEVAISBELVQKYSNSALGHVNSTIKELRR
LFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYL
GLANKSVKDAMAKIQAKIPGLKRKAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 175 Row: a Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13029187 This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDB
EEDDEDLEELEVLERKPAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAP
ERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPST
                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Agele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Maduro,Q.L., Maskello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
Madvell,J., Pearson,R., Stantripop,S., Thomas,P.J., Tuchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Direct Submission
Submitted (17-M9-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Brown Norway)"
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                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="RGD:620989"
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Rlausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butfeard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC070879
Rattus norvegicus reticulon 4, mRNA (cDNA clone IMAGE:7096609), COMPONO 1970879
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                                                                                                              825 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 884
                                                                                                                                                                                                                                                                                                  82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                               165 TIATICCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC
                                                                                                                                                                                                                      CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA
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                                                                               LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Rattus norvegicus
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/translation="MEDIDQSSLVSSSADSPPRPPPRFKYQFYTEPEDEEDEEBEE
EDDEDLEELEVLERKPAAGLSAAPVPPAAAPLLDFSSDSVPPAPRGPLPAAPER
QPSWERSPAASAPSLPPAAAVLPSKLPEDDEPPRPPAAAGASPLAEPAAPSTPAAP
KRRGSCSVVDVDLLYWEDIKKTGVYYPGASLFLLLSLTVFSTVSVTAY TALALLSVTIS
FRIYKGVIQAIQKSBEGHPFRAYLESEVAISEELVQKYSNAALGHVNSTIKELFL
VDDLVDSLKFAVLAMVETYVGALFNGITLLILALISLFSIPVIYERHQAQIDHYLGLA
NKSVKDAMAKIQAKIPGLKRKAE"
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Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D., Treacy, M., Spaulding, V. and Agostino, M.J.
                                                                                                                                                                                                                                                          GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTATTTTGGTGCC
                                                                                                                                                                                                                                                                                                           AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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185
2
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Matches:
Conservative:
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BD190738
BD190738.1 GI:33000477
JP 2002515751-A/5.
Homo sapiens (human)
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900.50
98.94%
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                                                                                                                  Scores:
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BD190738
LOCTUS
DEFINITION
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                                                                                                                             TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGCGTGATCCAGGCTATC
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Corganism="Mus musculus"
/mol_type="mRNA"
/strain="BALBA"c"
/db_xref="taxon:10090"
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/protein_id="AAM77069.1"
/db_xref="G1:21898579"
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/note="RTN4; foocen"
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                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mismatches:
Indels:
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Matches:

    .2386
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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AX099401
AX099401.1 GI:13538524
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                                                                                         Homo sapiens (human)
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                                                                                                                                             PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC C12N15/12, C12NS/10, C07K14/47, C12Q1/68, A61K18/17 CC Strandedness: Double; CC Tropology: Linear; Et Key Location/Qualifiers.
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Secreted proteins and polynucleotides encoding them Patent: JP 2002515751-A 5 28-MAY-2002, GENETICS INSTITUTE INC PN JP 2002515751-A/5 PD 28-MAY-2002 PP 24-OCT-1997 JP 1998519738 PR 25-OCT-1997 JP 1998519738 PR 25-OCT-1997 UP 08/740274 PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, DAVID MRRBERG,
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                                                                                                                                                                                                                                                                                                                                                                                                                AX494005 2815 bp mRNA linear VRT 16-FEB-2004 Gallus gallus neurite outgrowth inhibitor NOGO-A (NOGO) mRNA, partial cds.
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IKETKVSGESASPSLTDYSTTPITEHLSQDVSEHKELAEKLSPQFGKCDLFSRQVMPD
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SEPPPRALITAKAEKI PLQMEELNALAYSTDVGVAMBERGGOSKGLSPSPSVSVEDDFV
MLUDPKTGTEFVAEKI PLQMEELNALAYSTDVGVAMBERGGOSKGLSPSPSVSVEDDFV
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                    545 TTGATGTGGGTGTTCACTTACGTTGTTGTTTTAATGGTCTGACATTACTGATACTG
                                                                                                                                           605 GCTTTGATTTCGCTGTTCAGTGTTCCTGTTATTTATGAGAGACATCAGGCCCAGATCGAC
                                                                                                                 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
                          LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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Caltharp, S.A., McNeill, D.S., Pira, C.U. and Oberg, K.C. Direct Submission
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1979. .2835
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 86
AY494005
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                          VRT 02-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 TCAGTIGITICACCTTTACTGGGGAGACATAAGAAGACAGGAGTGTTTGGTGC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 AGCTTGTTCCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACCGCTTACATT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCCAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTAGCTGTG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484
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                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
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                                                                                                                             Gallus gallus (chicken)
Gallus gallus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                             1 (bases 1 to 1591)
backdan, P. E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Tiklett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlalle 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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                     BX934715 1509 bp mRNA linear Gallus gallus finished cDNA, clone ChEST117m23.
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9031"
/clone="ChEST117m23"
/clone_lib="CSEQCHL24"
/dev_stage="16 days"
                                                                                       BX934715.1 GI:41635243
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889.00
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Pred. No.:
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                     LOCUS
DEFINITION
ACCESSION
VERSION
VERYORDS
SOURCE
ORGANISM
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AUTHORS
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VRT 11-MAR-2004
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                       536
                                                                                                                                               LeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus
Wararyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing project.
This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
from a library constructed by Blizabeth Bosch. cDNA was prepared
from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI
cut cDNA was then ligated into the vector. Vector: pBluescript II
KS(+); Site 1: BCORI; Site 2: NotI Host: Escherichia coli DH10B.
Location/Qualifiers
GAGCTGAGACGCCTCTTCCTCGTTGATGACTTGATTCTCTGAAGTTTGAGTTTGATTTG
                                                             MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                    537 Argregargrackarracerregaecerrerraaregaecerracrearacregecr
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Gallus gallus finished cDNA, clone ChEST12704.
CR353502
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Mismatches:
Indels:
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/mol type="mRNA"
/strain="Compton Line 151"
/db xref="taxon:9031"
/clone="ChEST12704"
/clone lib="CSEQCHL15"
/dev_stage="adult"
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/organism="Gallus gallus"
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885.00
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                     477
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KEYWORDS
SOURCE
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JOURNAL
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AUTHORS
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LOCUS
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Gallus gallus

Gallus gallus

Gallus gallus

Archosauria; Aves; Neognathae; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus

E (Dasses I to 1363)

S Boardman, P. E., Bonfield, J. K., Brown, W. R. A., Carder, C., Chalk, S. E., Croning, M. D. R., Davies, R. M., Francis, M. D., Grafham, D. V.,

Hubbard, S. J., Humphay, S. J., Hunt, P. J., Maddison, M., McLaren, S. R.,

Niblet, D., Overton, I. M., Rogers, J., Scott, C. E., Taylor, R. G.,

Tickle, C. and Wilson, S. A.

Direct Submission

L Submitted (102 FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,

CBLO 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk

BBSRC Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                   VRT 02-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGTTGACCTCCTTTACTGGCGAGACATTAAGAAGACAGGAGTGGTGTTTGGTGCCAGC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 Trescecreerrrergacearcacerrraggararacaaggagariarecaggeaare 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dequencing project.

This sequence is from the BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from cerebrum, and poly A-trimmed. BcoRI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI Host: Escherichia coli DH10B. Location/Qualifiers
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Gallus gallus finished cDNA, clone ChEST11g8.
BX933922
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Matches:
Conservative:
Mismatches:
Indels:
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/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="chEST11g8"
/clone_lib="CSEQCHL15"
/dev_stage="adult"
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  1288 CCTGGATTGAAGCGCAAAGCAGAT 1311
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Best Local Similarity:
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Xenopus laevis RTN4.1-A3 (RTN4) mRNA linear VRT 25-MAY-2004
spliced.
AY316195.1 GI:34809221
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17ERHQAQIDHYLGLVNKNVKDAMAKIQAKIPGLKRKTE"
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Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Mismatches:
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Matches:
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93.62%
94.74%
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Best Local Similarity:
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2 (bases 1 to 1597)
Dertle, T. and Schwab, M.E.
Derect Submission
Submisted (16-OCT-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
Zurich 8057, Switzerland
Location/Qualifiers
1. 1597
/organism="Gallus gallus"
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Gallus gallus
Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1597)
Oertle, T., Klinger, M., Stuermer, C.A. and Schwab, M.E.
A reticular rhapsody: phylogenic evolution and nomenclature of the FRNSUB 3. 17 (10), 1238-1247 (2003)
                                                             61
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         GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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Gallus gallus RTN4-C (RTN4) mRNA, complete cds.
AY164737
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/db_xref="taxon:9031"
1. .1597
/gene="RTN4"
                                                                                                                                                                                                                                                                                                                                                                                                                                   ProGlyLeuLysArgLysAlaGlu 189
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126. .725
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GLTTLLQEKPLQMEELDEGLSLEKIPCTKYSPVSESPERPRPSPVPEDLSSKLGDIQKE
YLIAKQPEDKYOKNRSNLDPYDENIETPAVQKPDDSGKAVSTPFGGLDTTTKGGSAV
HEVKVDKPKPPSKEDDGSKLPKESKASTVSSSDFMSVVDLIYWRDIKRSGVYFGAS
LFLLLSLSVFSIVSYLAXIAALALLSYTISLETYKGILQAIQKSEEGHPFRSILESNLA
VPEDLVQKYCNVALNHVNCTVKELRHLFLVEDLVDSLKRAVLMWVFTYIGALFNGLTL
LIVALISLFSIPVIYERHQTQVDHYLALVNKNLKSTSDLILSKVPGLKRKAE"
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DYPPRASKSGOVGYEVSDVARKPOVOKRALDESAVGHEERSSBEMET DISIDDISP
LITPELL-DOSTOYDMRATVOROVARLOVOVGKALDESAVGHEERSSBEMET DISIODISP
TVNPPYNESAQBESTYVTTHVATHVSTKPEGPTPDIVQEAYESBAYDTGIPKQKYESNI
PLOGYRAMSVÖEKVSPTAGAPRALESTDSVSSYLDDIVMEAPLASALTSTAKFDIS
PVGTKPPARVEKTKAEPEKPPSYEEAVTEVLONODLAAALGGSKQGAVWETFFPYIS
IACOLIKGTESVAGGTFEFSKLKQNEPESQFMBPSDBSSPDSSECSEPSYKQMDSBVVIG
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SSKEHAETVAPPTGLAATEALQEPTDNMYSVSRITSHLPLSDNLESKALDQVKEEVIF
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| A xreef="G1:34803222"
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| Kranalation="MBGS2D2"
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(bases 1 to 3967)

Klinger, W. Dickmann, H., Heinz, D., Hirsch, C., Hannbeck von Klinger, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A. Identification of two NOGO/RIN4 genes and analysis of Nogo-A expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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                                                                                                                                                                                                                             Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerValValAspLeuLeuTyrTrpArgAspIleLysLysLysThrGlyValValPheGlyAla
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Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and
Stuerner,C.A.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="RTN4"
note="reticulon-4; alternatively spliced"
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                                                                                                                                                                                                                                                                                                                                                          /tissue type="wholemount embryos"
/dev_stage="older than stage 50"
[..3967
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                        /organism="Xenopus laevis"
/organism="mRNA"
/mol_type="mRNA"
/db xref="taxon:8355"
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/gene="RTN4"
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/gene="RTN4"
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2616 TCAGTTGTCGACCTTATTTACTGGCGGACATTAAGAGATCCGGAGTGGTTGGGGCA 2675

SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

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2975
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Xenopus laevis RTN4.1-Al (RTN4) mRNA, complete cds; alternatively
AV316197
2676 AGCTTGTTCCTCCTGCTCTCTGAGTGTGTTCAGTATTGTCAGCGTGCTCGCTTATATT 2735
                                                                                                                         2736 GCCCTGGCCCTGCTCTCCGTCACCATCAGTTTAAGGATATACAAAGGGATTCTGCAGGCC 2795
                                                                                                                                                                                                                                       2796 ATCCAGAAGTCAGAGGAAGGACCACTTCAGATCCATCTTGGAGTCCAACCTGGCGGTG 2855
                                                                                                                                                                                                                                                                                                                                                           2856 CCAGAGGATCTGGTCCAGAAATACTGCCATGTGAACCATGTCAACTGCAGTC 2915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
"naiversitaetsstrasse 10, Konstanz 78457, Germany
                                                                                                                                                                                                         61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                             101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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1 (Dases i to 4024)

1 (Dases i to 4024)

1 (Dases i to 4024)

Hanwehr, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuermer Identification of two NOGO/RTN4 genes and analysis of Nogo-A expression in Xenopus laevis

Mol. Cell: Neurosci. 25 (2), 205-216 (2004)
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Kinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.O.
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/db_xref="taxon.8355"
/frsue_type="wholemount embryos"
/dev_stage="older than stage 50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog)
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Location/Qualifiers
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1. .110
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/gene="RTN4"
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variation 3337 / gene="RTN4" / replace="" variation 3348 / replace="RTN4" / replace="RTN4" / replace="RTN4" / replace="" / gene="RTN4" / replace="RTN4" / replace="RTN4" / replace="" / re	/replace="a" variation 3553 /gene="RTN4" /replace="c" variation 3631		on on ignal	Alignment Scores: Pred. No.: Scores: Scores: A.4e-71 Batches: Scores: Percent Similarity: 90.48 Mismatches: 151 Conservative: 90.48 Mismatches: 18 Best Local Similarity: 90.48 Mismatches: 18 Query Match: 83.89 10dels: 0 US-09-830-972-29 COPY_990_1178 (1-189) x AY316197 (1-4024) US-09-8310-972-29 COPY_1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 2673 TCAGTTGTCGACCTTATTACTGGCGGACATTAAGAGATCCGGAGTGGTGTTTGGGGCA 2732
/ gene="RTN4" / note="reticulon-4; alternatively spliced" / codon_start=1 / product="RTN4" / protein_id="AAQ82646.1" / protein_id="AAQ82646.1" / protein_id="MAD62646.1" / protein_id="MAD62646.1" / protein_id="MAD6264810.18SBHSGAREREPAQPGERKFWDDLDDVLDLFGGAGQ / translation="MAD62681DSSHSGAREREPAGPEEPGSIDSISPVSPHSPAVP SAPMEREPERPAGPTTELAPTLAPAGAHLMHASADANIMEPYSTAVSTGGEERA SVLLQSTASLSSLPSLESTDSSKERHATVAPPTGLAATALGEPTDNMYSVSRITSHIP LSDNLESKALDQVKEEVIPSEKGYVVDHPTSQQETISEEHAKLYSQSAKEMFSGALQS VAPPHEEPTDIKEVYPELLAPSTDSTDDNMYSVSRITSHIP EKSSEEMEIDSISDIPPELLAPSTSCASCATCHYGARALLESAWH ERKSSEEMEIDSISDIPPELPELLAPSTDYDMPATHVSTREPGPTPDIVQEA YESBAYDTGTP RQKYRSENIDLVQTAPANSVGRYSPRQAPARLEFTDSVSSPVLDDIV MRAPLASALETVALKPDISPYGIRPPARVSTRKAEPERPESYEERATTEUQNDLAAA LGGSKQGAVVEETETPY1SIACDLIKGTESVASGFTEFSKLKQNEFESQFMEPSDES PDSFSCEBERSVRQMDSBVQKEAPSTRTESVNAGSTIIPERGVYPEDSSESSEPP RSSPVPEDLSSKLGDIQKEVIIAKQPENKYRKAEPERSTEKESKASTL DSFQPEICVSKATSDLFAKGLTLLLGEKELQMEELDEGLSLEKIPCTKYSPVSEEPPR ANDDIFGALDTTTKGGAAVHHVVCTVKEERARLALSVTSSLEPNASV VDLIYWRDIKRSGVYPGASAHHVVCTVKFPRERSEDGSKLERINSVSTUAP IGKSEGGHPFRSILLSSNLAVPEDLVOKYCNVALNHVNCTVKELRHLFLVEDLVDSLKF ALMWRDIKRRSGVYPGASLFLLLSSLSVSSPVANSVENSPEN ILSKVARRERE	variation 206 // // // // // // // // // // // // //	variation //suce="g" / yelloce="g" / yelloce="g" / yelloce="g" / yelloce="g" / yelloce="c" / replace="c" / replace="a" / yelloce="a" / yelloce="a" / yelloce="RTN4" / yelloce="c" / yelloce="c" / yelloce="c" / yelloce="g" / yelloce="g" / replace="g" / yelloce="g" / yell	/gene="KIN4" /replace="a" 2286 gene="RTN4" /replace="t" /gene="RTN4" /gene="RTN4" /replace="t" /replace="t" /replace="t" /gene="RTN4" /replace="t"	

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FSQPFSGSHPARDIEEEEEDEEEERGAWKDSLEPSPVEEEPGSIDSISPVSPHSPAVP
SAPWEEPERPPAPCTAPSGSVAFTFLARRLPEEDENLFTLPAASAHLMHASADKIMEP
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                                                                                                         'note="reticulon-4; alternatively spliced"
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Matches:
Conservative:
Mismatches:
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db_xref="GI:34809224"
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/gene="RTN4"
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                                                   111. .3278
/gene="RTN4"
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/gene="RTN4"
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I. (bages I to 4060)
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A. Identification of two NOGO/RTN4 genes and analysis of Nogo-A Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Quallfiers
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                         SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von
Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and
Stuermer, C.A.O.
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                                                81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannber
Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.B. and
Stuermer, C.A.O.
  US-09-830-972-29_COPY_990_1178 (1-189) x AY316191 (1-1467)
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3189 CACTACCTGGCACTCGTAAACAAGAATCTCAAGAGCACATCAGACCTGATTCTCTCTAAAA 3248
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1. (bases I to 1467.)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A. Identification of two NOGO/RTN4 genes and analysis of Nogo-A expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
                                                                                                           161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
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Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.O.
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/tissue_type="wholemount embryos"
/dev_stage="older than stage 50"
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1.120
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121. .702
/gene="RTN4"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., More, T., Max, S.I., Wang, J., Haieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,

Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwant, F.L.,

McKernan, K.J., Malek, S.S., Loquellano, N.A., Peters, G.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinsk, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein, S. and Strausberg, R.
Direct Submission
Submitted (10-OCT-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4801, Rockville, MD 20892-7510, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 128 Row: c Column: 9
                                               BC059960 1512 bp mRNA linear VRT 03-FEB-2004 Xenopus laevis hypothetical protein MGC68489, mRNA (cDNA clone MGC:68489 IMAGE:4030449), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Rabkerr.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Klein, S.L., Strausberg, R.L., Wagner, L.,
and Richardson, P.
                                                                                                                                                                                                     Xenopus laevis (African clawed frog)
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12454917
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Contact: XGC help desk
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          664 CCAGAGGATCTGGTCCAGAAATACTGCAATGTGGCCCTGAACCATGTCAACTGCACAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 AGCTTGTTCCTCCTGCTCTCTGAGTGTGTTCAGTATTGTCAGCGTGCTCGCTTATATT
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                                                                                                                                                                                                                note="reticulon-4; alternatively spliced"
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/mol_type="mRNA"

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1. .1758
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Matches:
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Mismatches:
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/gene="RTN4"
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Xenopus laevis RTN4.1-C (RTN4) mRNA, complete cds; alternatively spliced.
AY316192.1 GI:34809215
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| product="kTN4 .1-C"
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| db xref="C1:34809216" |
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                                                                                        631
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Chopoda; Kanopus; Kenopus.

1 (Dases I to 1543)

Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.B. and Stuermer,C.A. Identification of two NOGO/KTN4 genes and analysis of Nogo-A expression in Xenopus laevis

MOIL Cell. Neurosci. 25 (2), 205-216 (2004)
                                              LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                  162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
    512 ATGTGGGTCTTCACCTATATTGGTGCCTTGTTCAATGGTCTCACCCTGCTCATTGTGGCA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
                                                                    2 (bases 1 to 1543)
Kilinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and
Stuermer,C.A.O.
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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                                                                                                                                                                                                                      182 ProGlyLeuLysArgLysAlaGlu 189
                                                                                                                                                                                                                                               692 CCCGGCTGAAACGCAAAGCTGAA 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="RTN4"
1. .194
/gene="RTN4"
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/gene="RTN4"
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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AUTHORS
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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                                                                                                                                                                                                                                                                                                          RESULT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
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[Agene="MGC68489"
| fogene="MGC68489"
| fogene="MGC68489"
| forte="Reticulon, Region: Reticulon, also know as neuroendocrine-specific protein (NSP), is a protein of unknown function which associates with the endoplasmic treticulum. This family represents the C-terminal domain of the three reticulon isoforms and their homologues" | db_xref="CDD:pfam02453"
                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAH59960.1"

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/db_xref="G1:37747787"

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LNHVNCTVKELRHLFLVEDLVDSLKFAVLMWVFTYIGALFNGLTLLIVALISLFSIPV
IYERHQTQVDHYLALVNKNLKSTSDLILSKVPGLKRKAE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGCCCTGCTCTCCGTCACCATCAGTTTAAGGATATACAAAGGGATTCTGCAGGCCATC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 GAGCTGCGGCACCTCTTCCTTGTAGAAGACCTGGTGGATTCCCTGAAGTTTGCAGTATTG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                        1. .1512

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="texon:8355"

/clone="MGC:68489 IMAGE:4030449"

/tissue type="Kidney, adult Xenopus"

/lab_host="NICHD_XGC_Kid1"

/lab_host="DH108"

/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-830-972-29_COPY_990_1178 (1-189) x BC059960 (1-1512)
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                  protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                      /gene="MGC68489"
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119-.718
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                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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/translation="MDEQSPDISSSHSGDERREPAQPGERKPWDDLDDVLDLTGGAGQ
FSQPFSGRIPARDIBEREBDBERERGAWKDSLRPSPVEREPGSIDSISPVSHSPAVP
SAPWEDEREPAPAPCTAPSGSVVVDLIYWRDIKGSGVVFGASLFLLLSLSVFSIVSVLA
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NCTVKELRHLFLVFDLVDSLKFAVLMWVFTYIGALFNGLTLLIVALISLFSIPVIYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGCCCTGCTCTCCGTCACCATCAGTTTAAGGATATACAAAGGGATTCTGCAGGCCATC 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   909
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937. .1701
/gene="RTN4"
                                           embryos"
age 50"
                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                       /dev stage="older than stage
1. .1701
  organism="Xenopus laevis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
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                                                                                                                                            codon_start=1
                                                                                   /gene="RTN4"
                                                                                                  1. .936
/gene="RTN4"
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777.00
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79.79%
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DB:
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spliced.
AY316194
AY316194.1 GI:34809219
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                                                                                                                           288 TIGITTCTCCTCCTGTCTCTCTGAGTGTGTTCAGTATTGTCAGGTGCTCGCTTATATTGCC 347
                                                                                                                                                                                                                                                          467
                                                                                                                                                                                                                                                                                                    GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
                                                                                                                                                                                                                                                                                                                                           GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                                                                                                                                                                                                                                                                                                                                                                                   MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEGATTTCCCTGTTCAGTATTCCTGTCATTTATGAAAGGCATCAGACTCAAGTGGATCAC 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

I (bases I to 1701)
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A. Expression of two NOGO/RTN4 genes and analysis of Nogo-A Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
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Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and
Stuermer,C.A.O.
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1 (bases 1 to 3886)

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1 (bases 2 to 3886)

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Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitetsstrasse 10, Konstanz 78457, Germany
Location/Qualifiers
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/note="reticulon-4; alternatively spliced"
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/mol_type="mcNA"
/db xref="taxon:8355"
/tisue_type="wholemount embryos"
/dev stage="older than stage 50"
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Alignment Scores:

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3943 bp mRNA linear VRT 25-WAY-2004 Xenopus laevis RTN4.2-Al (RTN4) mRNA, complete cds; alternatively AY316190
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1. (bases I to 3943)

Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A. Identification of two NOGO/RIN4 genes and analysis of Nogo-A Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuerner, C.A.O.
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Mismatches:
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YQYVDFKPFI SSNSRDI GYEVKDVAEKLHVGRLNI, BSTAKHEEKSSEEKEMDI SDDI S
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Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
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3128 CACTATCTGGGCTGATAAACAAGAACCTGAAAAATACTTCAGACCTGATTTTGGCTAAA 3187
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                      161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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148
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Conservative:
Mismatches:
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752.00
89.95%
78.31%
80.77%
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Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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141 AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp 160

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Add01174 Bovine ne Add01174 Bovine ne Add0550 Human Nog Aa209453 Human Nog Aa23454 CDNA enco Abv94680 Human pan Abx34563 Human pan Adr83534 Human nec Ab870449 Human nec Aa5032725 Human nec Aa72983 Human Nog Aax5659 Human Nog Aax5659 Human Nog Aax5688 Human Nog Aax5680 Human apo Adf11137 Full leng Abv94681 Human aut Abk90133 DNA enco Adx11137 Full leng Abv94681 Human neu Abx94408 Human neu Abx94408 Human neu Abx94408 Human neu Aax64406 Human neu Aax913137 Full leng Ady11337 Full leng Ady18854 Human neu Aax97587 Extended Ady18854 Human neu Aax97587 Extended Ady18854 Human neu Aax97587 Extended Ady185471 Ret NogoA
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Ado07888 Mouse pol
Aad01175 Rat neuri
Aav30920 Human sec
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Abn86600 Rat neuro
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ABN86600
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AAF90323
AAA72983
AAV23695
AAZ56888
AAZ56888
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Aaf90324 Human NOG
Abk90134 DNA encod
Abn86601 Human neu
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3160.540 Million cell updates/sec
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                                                                                                                                                 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189
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        version 5.1.6
- 2005 Compugen Ltd.
                                                      nucleic search, using frame_plus_p2n model
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The present sequence is that of cDNA encoding human NOGO-A (see AAB82349). NOGO-A is a previously known splice variant of the human NOGO gene on chromosome 2p21. NOGO-A CDNA was obtained by PCR amplification of human spinal cord CDNA. The invention relates to a novel splice variant, NOGO-C (see AAF90323). It provides NOGO-C polypeptides and polymuclectides, and methods for producing such polypeptides and polymuclectides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C impalance, and disposit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ServalvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
                                                                                                                                                                                                                                                                    NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuronal sorder; psychiatric disorder; developmental disorder; neuropsyctective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assays for detecting diseases associated with inappropriate NOGO-C
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                              3550 ATCCCTGGATTGAAGCGCAAAGCTGAA 3576
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181 IleProGlyLeuLysArgLysAlaGlu
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                                                                                                                     standard; cDNA; 3579
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24-JAN-2000; 2000GB-00001550.
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                                                                                                                                                                                                                                                                                           The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleotide is also useful for chromosome localization and for tissue expression studies. The present sequence represents a DNA encoding the human MAGI protein
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                                                                                                                                                                          Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
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                                          3070 AGCCTATTCCTGCTTCCTTCATAGACAGTATTCAGCATTGTGAGACGTAACAGCCTACATT
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(SMIK ) SMITHKLINE BEECHAM PLC.
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE polypeptides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating caute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neplastic (e.g. glioblastomas, cartenance), hyperproliferative or dysproliferative disorders (e.g. irrhobastomas), hyperproliferative or dysproliferative disorders (e.g. irrhobasis, psoriabis, keloid formation, fibrooystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may act as modulators or dand the polymucleotide encoding the BACE polypeptide are useful in anniation a medicament for the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a sasays, a probe, in recombinant protein synthesis, and in gene therapy econdition.
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Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
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                                                                                                                        Disclosure, Page 53-58; 68pp;
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protein of the invention
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                                                3489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt
                                                                         180
                                                                                                                                                                                                                                                                                                 Nerve regeneration, neuroprotection, neuronal degeneration, CNS, PNS, central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; neptrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; human; gene; ds.
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TTGATGTGGGTATTTACCTATGTTGGTGCCTTTGTTTAATGGTCTGACACTACTGATTTTG
                                                                         HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                  3490 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAA
                       AlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or
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                                                                                                                                                    ATCCCTGGATTGAAGCGCAAAGCTGAA 3576
                                                                                                                          IleProGlyLeuLysArgLysAlaGlu 189
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P-PSDB; ABB81078, ABB81080.
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/product= "Nogo"
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98WO-US014715.
98US-00218277.
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                                                                                                                                                                                                      ABN86601 standard; DNA; 3579
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damages caused by surgery such as rumour excision. In a disease is not an anticommune disease or neoplasm. The disease results in a degenerative autocimmune disease or neoplasm. The disease results in a degenerative disease, concurring in either gray or white matter or both. The disease is disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral neuropathies associated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute convemia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute amyolodosis, obstructive lung diseases, acromegaly, malabsorption amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-convented conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed converse conversed conversed conversed conversed conversed converse conversed conversed conversed conversed conversed converse converse conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed conversed converse
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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene in an expression of the gene in an expression of the gene in the agent, and identifying fat cell number or size in the subject. The agent comprises an antisense of ignouncleotide. The subject comprises a mammal, preferably a human. The method also comprises providing a polypeptide and an agent, exposing the polypeptide to the agent, detecting binding of the agent to the golypeptide or a change in an activity of the polypeptide, treating a subject with the agent and identifying fat cell number or size comprises an antibody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an agent the agent comprises providing a subject containing fat cells and an agent the agent and identifying a define the subject that changes the expression of a gene, and treating the subject and an expression of a gene, and treating the subject and an expression of a gene, and treating the subject and an expression of a gene, and treating the subject and an expression of a gene, and treating the subject and an expression of a gene, and treating the subject and an expression of a gene, and treating the subject and an expression of a gene, and treating the subject and an expression of a gene, and treating the subject and an expression of a gene, and an expression of a gene, and an expression of a gene, and an expression of a gene, and an expression of a gene, and an expression of a gene, and an expression of a gene, and an expression and an expression of a gene, and an expression and an expression and an expression and an expression and an expression and an expression and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents human cDNA used in the scope of the invention.
                                                                                                                                                                                                                                                                                     Human, gene, 88; fat cell number, fat cell size, obesity, diabetes, anorectic, antidiabetic.
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                                                         AD007886 standard; cDNA; 3579 BP
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Length:
Matches:
Conservative:
Mismatches:

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Similarity:

Percent Similarity: Best Local Similari

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Query Match: DB:

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US-09-830-972-29_COPY_990_1178 (1-189)

Gaps:

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                                                            3070 AGCCTATTCCTGCTTCCTTGACAGTATTCAGCATTGTGAGGTAACAGCCTACATT 3129
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                                                                                                                                                                      61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                                                  3250 TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATA
                                                                                                                                                                                                                                                                                                 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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                                                                                                                                    GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
                                                                                                        41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                 The invention relates to a myelin-associated glycoprotein (MAG) derivative comprising a mucation in or flanking MAG Ig-like domain 5 (Igd5), excluding the MAG derivative MAG (d1-3)-FC, where the mutation reduces or eliminates the ability of the derivative to regulate neurite outgrowth as compared to endogenous or soluble MAG without eliminating binding to neuronal surfaces. The inhibitors of MAG are useful for promoting neural growth and regeneration. They are also useful for treating neural degeneration associated with injuries, disorders, or diseases. The disorder, disease, or condition is associated with appoptosis or results from a demyelinating disease and includes amylotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease, kuru, multiple system atrophy, amylotrophic lateral sclerosis (Lougehrig's disease) or progressive supranuclear palsy. The present
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                                                                                                                                New myelin-associated glycoprotein (MAG) derivative comprises a mutation in or flanking MAG Ig-like domain 5 (Igd5), excluding the MAG derivative MAG (d1-3)-Fc, useful promoting neural growth and regeneration.
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Matches:
Conservative:
Mismatches:
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The present sequence is a cDNA encoding bovine Nogo protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The present sequence was obtained from bovine spinal cord white matter cDNA library. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharymgioma, ependyoma, pinemagioma, heemangioblastoma, acoustic neuroma, oligodendroglioma, pinemagiona, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative cor benjay dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or compensation of neurons or compensation of maintenance are deficient or desired. The animal models can be used in disquanceir and screening methods for predisposition or disorders and to screen for or test molecules which can treat or prevent disorders and screening methods for predisposition or provent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID No. 29 in disclosure of the
                                             3490 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAA 3549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS; central nervous system, neoplastic disease, antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; ss.
161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine neurite growth inhibitor Nogo cDNA
                                                                                                                                                                                                                                    3550 ATCCCTGGATTGAAGCGCAAAGCTGAA 3576
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09-DEC-2003; 2003WO-EP013960 10-DEC-2002; 2002GB-00028832

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nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder;
                                                                                                                                                                                                                                                                    2661 TIGATGTGGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAGTTTTG
                                                                                                                                   2301 TCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC
                                                                                                                                                                                  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysG1yValIleG1nAla
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                                                                                                                      SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
                                                                                                                                                                    SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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                                                                      Gaps:
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/product= "NogoA"
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3010 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 3069
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                                                                                                                                                                                                                                                                                                   New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.
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                                                                                                                                                                                                   Vitaliti A;
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P-PSDB; ADP45551.
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Zurini M;
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LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal

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3204 AGCCTATTCCTGCTTCATTGACAGTATTCAGCATTGTGAGGTAACAGCCTACATT 3263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy; axonal growth; central nervous system; CNS; Nogo; spinal cord injury; cratial trauma; spinal trauma; stroke; Krabbe; disease; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
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demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy,
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                                                                                                                                                                                                                                                                                                                                                                                                               1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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                                                                                                                                      Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;
                                                                                                                                                                                                          4053
189
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                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 IleProGlyLeuLysArgLysAlaGlu 189
                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                           viral infection and Krabbe's disease
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                                                                                                                                                                                                                                                                              Similarity:
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                                                                                                                                                                                     HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein; cranial trauma; cerebral trauma; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasis demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy; Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein, a 250kDa myelin-associated axon growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral traums, spinal cord injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence (Genbank accession number AB0202693) encodes the human Nogo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central nervous system disorders.
                                3370 TIGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG
                                                                                           AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
       LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                               3550 Arcccredarreaadcccaaagcreaa 3576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 95-100; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA encoding the Nogo protein.
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135. .3713
/*tag= a
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26-MAY-2000; 2000US-0207366P.
29-SEP-2000; 2000US-0236378P.
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3624 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAA 3683
                            3324 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3383
                                                                                                                                                                                                  3504 TIGATGIGGGTATTTACCTATGTIGGTGCCCTTGTTTAATGGTCTGACACTACTGATTTIG 3563
                                                                                                                           101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
                                                                                                                                                                                 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                                                                                                                                                                      AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
                                                                                                                                                                                                                                                                                             HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                           SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
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03-APR-2003; 2003US-0459782P.
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TWINE N C.
BURCZYNSKI M E)
TREPICCHIO W L
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(BURC/)
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (Pl, human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of Pl, in 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive residues. The nucleic acid of the invention has neuroprotective activity. The polymucleotide may have a use in gene therapy. The nucleic acid is useful for decreasing inhibition of axonal growth by a central nervous system (CNS) neuron. The NGR polypeptide or an agent inhibits the binding of Nogo to NgR or NgR capinal transduction in the central nervous system disease, disorder or injury, e.g. used in treating central nervous system disease, disorder or injury, e.g. thibition of axonal regeneration following cranial, cerebral or spinal complaint displayment and intiple solarization, encephalopathy, panencephalopathy, panencephalopathy, panencephalopathion of the invention continued the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3204 AGCCTATTCCTGCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3264 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                 New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system neuron, or in treating central nervous system disease, disorder or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                             /product= "Human NogoA"
                                                   Location/Qualifiers
135. .3713
                                                                                                                                                                                                                                                                                                                                                                              injury, e.g. spinal cord injury.
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931.00
100.00%
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Query Match:
DB:
                                                                                                                                                                                                                                                               Strittmatter SM;
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                           Homo sapiens.
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ds, diagnosis, non-blood disease, solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stover JA;
Renal cell carcinoma differentially expressed gene #310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dorner A,
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照.

AAA23454 standard; cDNA; 4093

(first entry)

19-JUN-2000

AAA23454;

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cuch as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes; where each of the genes is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample (claimed). (Mn) is useful for identifying genes that are differentially expressed in peripheral blood samples is and/or other solid tumors. This sequence corresponds to a gene that is differentially expressed and detected by the method of the invention. (Note: this sequence is not given as part of the printed specification to the was obtained from WIPO in electronic format at the invention of the wipo./pub/published_pot_sequences).
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invention relate to a method of diagnosing (M1) non-blood disease
                                                                                                                                                                                                                                                                                                                                                                   Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;
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3684 ATCCCTGGATTGAAGCGCAAAGCTGAA 3710

AAA23454

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The invention relates to 40 human secreted proteins (AAY94981-Y95020),
and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
CC of the invention include those that are thought to be only partially
secreted, i.e., transmembrane proteins. The proteins of the invention may
CC exhibit one or more activities selected from the following: cytokine
exhibit one or more activities selected from the following: cytokine
cativity; cell proliferation; differentiation; immune modulation;
cativity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
activity; anti-inflammatory activity; and tumour inhibition and thrombolytic
activity; anti-inflammatory activity; and tumour inhibition activity. The
proteins may be administered to patients as vaccines, and the nucleotides
CC autoimmune diseases; genetic disorders; haemophila; cardiovascular
Cd seases; cancer; bacterial, fungal and viral infections, especially HIV;
Cd iseases; cancer; bacterial, fungal and viral infections, especially HIV;
Cd diseases; rheumatoid arthritis; pulmonary inflammation;
Cd iseases, nathem and anaemia. They may also be used for
treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
CC diseases, Altheimer's disease, Parkinson's disease,
and amyotrophic lateral sclerosis (ALS): Proteins with activin/inhibin
cativity may additionally be useful as contraceptives. Nucleic acid
sequences of the invention may be used in chromosome mapping, and as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune diseases and
                                                                                                                                   Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; hammophilia; autoimmune disease; diabetes; inflammation; infection; fungal; bacterial; viral; HIV; allergy; arthritis; neurodegenerative disease; asthma; contraceptive; ss.
                                                                                                  cDNA encoding human secreted protein vb22_1, SEQ ID NO:63,
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source of diagnostic primers and probes. The present sequence represents CDNA encoding one of the 40 proteins of the invention
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                                                                                                                                                 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
cytostatic; tumour; gene; ss.
                              Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 U; 0 Other;
                                                                                                                                x AAA23454 (1-4093)
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                                                          Length:
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Conservative:
Mismatches:
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                                                Alignment Scores:
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-ABF68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, tusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating parcreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 ATCCAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and pancreatic tumor polypeptides, useful idiagnosing, preventing and/or treating cancer, particularly pancreatic
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                                                                                                                                                                                                                                                                                                                                                                                                                          Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English
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                                                     2001US-0265305P.
2001US-0265682P.
2001US-0267568P.
2001US-0278651P.
2001US-0287112P.
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2002WO-US002781
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Best Local Similarity:
Query Match:
DB:
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                                                  30-JAN-2001; 2
31-JAN-2001; 2
09-FEB-2001; 2
21-MAR-2001; 2
8-APR-2001; 2
16-MAY-2001; 2
12-JUL-2001; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                          Benson DR,
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ankylosing spondylitis, ulcerative colitis, primary sclerosing cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis. This polynuclectide is a DNA sequence representing human mRNA that is differentially expressed in patients with SLE, used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 IleProGlyLeuLysArgLysAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3691 ATCCCTGGATTGAAGCGCAAAGCTGAA
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                                                                                                Sequence 4632 BP; 1398 A; 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to novel methods for diagnosing and monitoring autoimmune and chronic inflammatory diseases. Specifically, it refers to the identification of genes that have a clinical utility as diagnostic tools for the management of, in particular, patients with systemic lupus erythematosis (SLE) or rheumatoid arthritis (RA). Accordingly, the present invention describes a method for determining the levels of multiple differentially expressed genes of a patient, in a concerted manner, in order to achieve an improved diagnostic assay with sensitivity and specificity for the disease in question. As such, these genes are useful for the diagnosis of various other inflammatory disorders including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
                                                                                                                   140
                                                                                                                                                                                AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp 160
                                                                                                                                                                                                                                            HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uman; ds; autoimmune; chronic inflammatory disease; SLE; yetemic lupus erythematosis; rheumatoid arthritis; cholecystitis; oggren's disease; CREST syndrome; scleroderma; ankylosing spondylitis; lcerative colitis; primary sclerosing cholangitis; appendicitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing or monitoring autoimmune and chronic inflammatory diseases, such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, psoriasis and asthma by detecting the expression level of one
                                                                                   AAGGAACTCAGGCGCCTCTTCTTAGTTGATGTTTAGTTGATTCTCTGAAGTTTGCAGTG
                          TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATA
                                                                                                                   LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
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                                                     LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
        Human DNA differentially expressed in patients with SLE SeqID96
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C; 1011 G; 1210 T; 0 U; 0 Other;
                                                   4632
189
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Matches:
Conservative:
Mismatches:
Indels:
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SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle

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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polynucleotides are particularly useful for diagnosing, treating or preventing cell particularise disorders (e.g. cancers including adenocaricinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's disease, acquired immunodeficiency syndrome (ADDS), Goodpasture's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis, ABX34410-ABX34835 encode the MDDT polypeptides represented i ABU11450-ABU11485, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpaature's syndrome; inflammation; osteoporosis; thrombocytopaenia; psoriasis; hepatitis; gene; ss.
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, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
, Daw TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
H, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME;
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                                                                                                                                                                                                                                                       28-MAR-2001; 2001US-0279619P.
29-MAR-2001; 2001US-0280067P.
29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-029180P.
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20-JUN-2001; 2001US-0299776P.
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Peralta CH, David MH,
Flores V, Marwaha R,
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P-PSDB; ABU11573.
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                                                                                              Homo sapiens
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3155 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 3214

SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla

US-09-830-972-29_COPY_990_1178 (1-189) x ABX34563 (1-4698)

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Indels:

Length: Matches: Conservative: Mismatches:

1.49e-102

Alignment Scores:

931.00 100.00% 100.00%

> Percent Similarity: Best Local Similarity: Query Match: DB:

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3215 AGCCTATTCCTGCTTCGTTGACAGTATTCAGCATTGTGAGGCGTAACAGCCTACATT 3274
                                                                            3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3635 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 3694
                                                                                                                                                                                               3395 TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATA 3454
                                                                                                                                                                                                                                                                      3455 AAGGAACTCAGGCGCCTCTTTTTTGTTGATTTTAGTTGATTCTCTGAAGTTTGCAGTG 3514
                                                                                                                                                                                                                                                                                                                        3515 TTGATGTGGGTATTTACCTATGTTGGTGCCCTTGTTTAATGGTCTGACACTACTTTTG 3574
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                                                                                                                                                                                                                                                                                                                                                                                                                                    161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating expression of a target gene in a cell, for treating cancer, an immune disease, or a nerve disorder, comprises introducing into the cell a polynucleotide that forms a duplex region with an mRNA transcribed from the target gene.
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                                                                                                         IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                          SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
                                              AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                               1275 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT
                                                                                                                             3335 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA
                                                                                                                                                                                                                                        LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu
                                                                                                                                                                                                                                                                                                                                                                     AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human, ds; miRNA, microRNA; ontogenesis; cell therapy; cancer; immune disease; nerve disorder; amyotrophic lateral sclerosis; Parkinson's disease; Alzheimer's disease; inflammatory disease; alzhening precursor; cytostatic; immunosuppressive; nootropic; neuroprotective; antiinflammatory; immunotherapy; reticulon 4.
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This invention relates to a novel method for modulating the expression of a target gene in a cell. Specifically, it refers to the introduction into a call of a polynucleotide that forms a duplex region with an mRNA transcribed from the target gene, where the duplex region with an mRNA transcribed from the target region i.e. a non-coding microRNA (miRNA) that regulates mRNA at a post-transcriptional level. The present invention describes a method for controlling ontogenesis of a mammalian cell, differentiation of a mammalian cell or viability of a mammalian cell, differentiation of a mammalian cell or viability of a mammalian cell in the post-transcriptional phase, which comprises introducing a plasmid vector comprising a promoter and nucleic acid collecule expressing an miRNA or siRNA silencing precursor to the miRNA. Accordingly, it provides a cell therapy method for treating cancer, mammalian disease, nerve disorder (e.g. amyotrophic lateral sclerosis, parkinson's disease, or Alzheimer's such, they can be developed into pharmaceutical compositions that exhibit cytostatic, immunosuppressive, noctropic, neuroprotective and antihinflammatory activities and hence can be used for immunotherapy. This polynucleotide sequence is a human target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene whose expression is modulated by miRNAs of the invention.
SEQ ID NO 436; 865pp; English.
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0000 Length:
Matches:
Conservative:
Mismatches:
Indels: 1.53e-102 931.00 100.00% 100.00% Alignment Scores:

Sequence 4789 BP; 1422 A; 1052 C; 1075 G; 1240 T; 0 U; 0 Other;

3313 3373 3433 3493 3553 3613 3673 3733 3793 140 160 180 100 120 80 40 09 AGCCTATTCCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCTACATT ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle TCTGAGGGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATA 3554 AAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTTTGAAGTTTGCAGTG LeumetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG 141 AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 3254 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTCC AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 3374 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal US-09-830-972-29_COPY_990_1178 (1-189) x ADR83534 (1-4789) Percent Similarity: Best Local Similarity: 3314 3434 3494 121 3614 3674 3734 21 41 19 101 191 81 Query Match: DB: 8 셤 ò 셤 ઠે 셤 ð a ò 임 ઠે 유 8 ď ò g 8 임

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3445 AICCAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGCTATA 3504

61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle

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IleProGlyLeuLysArgLysAlaGlu 189

181

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3325 AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATT 3384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a combination comprising a number of substantially purified and isolated polynuclectides which are coexpressed with genes known to be involved in bone remodelling and osteoporosis. The invention is used to diagnose disorders associated with bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone
                                                                                                                                                                                                                                                                                                                                                                                                                                               A combination of polynucleotides which are co-expressed with genes known to be involved in bone remodeling and osteoporosis are useful in an array for the diagnosis of bone remodeling and osteoporosis associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3265 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAAGAAGACTGGAGTGGTGTTTGGTGCC
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Mismatches:
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Matches:
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Claim 1; Col 283-288; 206pp; English.
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                                                                      BP,
                                                                                                                                                            Human bone remodelling gene #106
                                                                      ABS70449 standard; cDNA; 4822
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931.00
100.00%
100.00%
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                                                                                                                              (first entry)
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Best Local Similarity:
                                                                                                                               27-NOV-2002
                                                                                                                                                                                                                   Homo sapiens.
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DB:
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                                                                                                                                                                                                                                                   HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; infection; angiogenesis; nervous system disorder; Alzheimer's disease; skin aging; coular disorder; corneal infection; wound healing; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, secreted protein, diagnosis, immunosuppressive, antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiant, vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial, virucide,
                                                                                                                                          TIGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG
                                                                                                                                                                                                                                                                             CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAA
                           rcreaggagrreagaagracagraarrcrecrcrregreargreaacrecacgara
                                                              LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                             LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                                     AlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
                                                                                                                                                                                                          polynucleotide sequences given in AAF32699 to AAF32747 encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a human secreted protein a medical condition.
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Cycostant; datalant, wasotropic; cerebiroprotective; notitopic; cerebiroprotective; antibacterial; virucide; fungicide; and ophthalmological. The polymucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders infections caused by bacterial, viruses and fungi and ocular disorders infections. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAR32690 to AAR32698 and AAB64421 represent sequences used in the exemplification of the present
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Matches:
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CTATTCCTGCTTTTCATTGACAGTATTCAGCATTGTGAGGGGTAACAGCCTACATTGCC 153
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                                                                                                                                                                                                                                                                                          334 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 393
                                                                                                                                                                                                                                                                                                                                                MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCTAGGACTTGCAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 573
                                                                          154 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                                    LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                          GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThr11eLys
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                                                                                                                                                                                                                                                                                                                                                                        ATGTGGGTATTTACCTATGTTGCTTGTTTTAATGGTCTGACACTACTGATTTTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein of human neuroendocrine, coding sequence and
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1 NSPH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGATTGAAGCGCAAAGCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of cDNA encoding human NOGO-C (see AAB82348). NOGO-C is a novel splice variants of the human NOGO-G one chromosome 22pl. 2 Other splice variants. NOGO-A and NOGO-B, have previously been identified. The invention provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury. brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic
                                                                                                                                                                                      NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuropyrotective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide designated NOGO-C is a splice variant of the human NOC gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GITGITGACCICCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assays for detecting diseases associated with inappropriate NOGO-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 161 A; 113 C; 144 G; 182 T; 0 U; 0 Other;
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                                    AAF90323 standard; cDNA; 600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 25; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM PLC.
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24-JAN-2000; 2000GB-00001550.
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P-PSDB; AAB82348.
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                                                                                                                                                    Human NOGO-C cDNA.
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408 GAACTCAGGCGCCTCTTTAGTTGATTTAGTTTGATTCTCTGAAGTTTGCAGTGTTG
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                                               (INCY-) INCYTE PHARM INC
                                                                Au-Young J,
                                                                                WPI; 1998-159533/14.
                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                            593
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                                                                                                                                                                        Trescenterererereacearcaserrrassararassassererearecrasserare 293
                                                                                                                                                                                                                                                                                           141
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                                                                                     LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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                                                                                                                                                                                                                                    GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAACTGCACGATAAAG
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                                                                                                                                                                                                                                                                                                                                    LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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                                                                                                                                                                                                                         GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                                                                                                                                                                           414 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
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                               Conservative:
Mismatches:
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Matches:
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sclerosis. Also antisense nucleic acids and artagonists of NSPLP can be used to inhibit activity of the NSPLP proteins. Antibodies specific for used to inhibit activity of the NSPLP proteins. Antibodies specific for NSPLP are used for diagnosis and monitoring treatment of diseases associated with NSPLP expression, in usual immunoassays, and to isolate NSPLP from natural sources. The NSPLP proteins, or their fragments can also be used in drug screening to identify NSPLP antagonists. The nucleic acid can be used diagnostically and for monitoring treatment (in hybridisation or amplification assays); to isolate closely related sequences; in gene therapy for both sense and antisense applications (including use of ribozymes) and for mapping the natural genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes a human neuroendocrine-specific protein-like protein (NSPLP) of the invention. Recombinant cells transformed with the DNA are used to express the NSPLP proteins, which are used to treat cancer and neurodegenerative diseases such as amyotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 TIGGCCCTGCTCTGTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGCTATATCT
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                                                                                                                                                                                                                                                                           Human neuro-endocrine-specific protein-like proteins - useful for diagnosis, monitoring and treatment of cancer and neuro-degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 799 BP; 218 A; 141 C; 196 G; 242 T; 0 U; 2 Other;
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Mismatches:

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                                                                                                                                                              616 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
                                                                                                                                                                                                                                                                                                                                                  GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          796 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        916 AIGIGGGRATITACCTAIGTIGGGGCCTIGTITAAIGGICTGACACTACTGAITIGGCT
                                                                                                                                      ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                             LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  856 GAACTCAGGCGCCTCTTCTTAGTTGATTTAGTTGATTCTCTGAAGTTTGCAGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                   GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleoited is also useful for chromosome localization and for tissue expression studies. The present sequence represents a DNA encoding the human MAGI protein variant
                          LeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis
                                                       TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle
                                                                                                                                                                588 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; stroke; cytostatic; cerebroprotective; neuroprotective; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides related to neuroendocrine-specific proteins ar polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
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/*tag= a
/product= "MAGI polypeptide"
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Matches:
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                                                                                                                                                                                                                                                            CCTGGATTGAAGCGCAAAGCTGAA
                                                                                                                                                                                                                                                                                                                                                     BP
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99GB-00016898
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P-PSDB; AAY56969.
                                                                                                                                                                                                                                                                                                                                                     AAZ56888 standard;
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spinal inium.
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Conservative:

Percent Similarity:

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1036 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1095
                                                                                                                                                                                                                                                                             Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obsity; osteoclast; thynus; osteoporosis; arthitis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes and the secreted polypeptides they encode
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, Greene JM, Ferrie AM,
                                                                                                                                                                                                                                                 Human secreted protein gene 69 clone HAGFT48.
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                                                   ProGlyLeuLysArgLysAlaGlu 189
                                                                                                                                                  BP.
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97US-0049548P.
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97US-0061059P.
                                                                                                                                                  AAX04379 standard; DNA; 1213
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Brewer LA,
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13-JUN-1997;
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                                                                                                                                                                                                          The present sequence is that of cDNA encoding human NOGO-B (see AAB82350). NOGO-B is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel NOGO gene splice variant, NOGO-C (see AAF90323). It provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury. brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular for example Alzheimer's disease and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assersys for detecting diseases associated with inappropriate NOGO-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                              polypeptide designated NOGO-C is a splice variant of the human NOGO and may be useful in the treatment of neural disorders including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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Mismatches:
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Alzheimer's and Parkinson's diseases.
                                                                                                                                                                                 Disclosure; Page 27; 25pp; English.
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 (SMIK ) SMITHKLINE BEECHAM
                                Michalovich D, Prinjha R;
                                                                2001-343822/36
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Best Local Similarity:
Query Match:
DB:
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P-PSDB; AAB82350.
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin for portion (e.g. AAX04302) for increasing the stability of the fused protein as genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed
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useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                                                                                                                                                                                                                                      Sequence 1213 BP; 335 A; 222 C; 297 G; 355 T; 0 U; 4 Other;
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Mismatches:
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Matches:
                                                 Claim 1; Page 235-236; 380pp; English.
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The invention relates to human RTN4B protein and coding sequence, useful for providing a cDNA sequence of human RTN4B. The protein is an isomer of RTN4 with RTN family members. The present invention also refers to polypeptide encoded by a nucleotide sequence and manufacturing method and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGluLeuValGlnLygTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
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                                                                                                                                                                                                                                                                                                                                                  preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1216 BP; 256 A; 354 C; 341 G; 265 T; 0 U; 0 Other;
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Indels:
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                                                               Human RTN4B encoding cDNA SEQ ID NO
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ABA05903 standard;
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Best Local Similarity:
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                                                                                     Human; RTN4B;
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                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis, cell death; cytostatic, neuroprotective; immunosuppressive; antirheumatic; antiarthritic; dermatological; antiinflammatory; hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian; vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour; autoimmune disease; degenerative disease; viral infection; leukaemia; carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes; lupus; hepatitis; influenza viruses; Alzhaimer's disease; Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;
                                                             GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                860 GAACTCAGGCGCCTCTTCTTAGTTGATTTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
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therapy. The polynucleotides also related vectors, hosts (or their extracts), encoded polypeptide (or their receptors) and/or agents that inhibit their activity (including antisense sequences) are used for treatment or prevention of tumours, autoimmune or degenerative disease and viral infections, specifically leukaemia, carcinoma, sarcoma, multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection with hepatitis or influenza viruses, Alzheimer's, Huntington's or Parkinson's disease, reperfusion injury, stroke and alcoholic liver disease. Detection of the polynucleotides and derived polypeptides can also be used for diagnosis of these diseases. This sequence encodes an apoptosis-associated protein described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
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AAZ3628-49 encode bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell lines, to regulate hematopoiesis, and to treat myeloid cell lines, to proliferation of erythroid progenitor cells, and to treat various an emakas. They can have colony simulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo.

Suppression, to support the growth and proliferation of megakaryocytes and platelers, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and coliferation of megakaryocytes and platelers, thereby allowing prevention or treatment of platelet disorders, such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and the remain and replacement, and in the treatment of burner incorpination or the content of burner, in the content of burner, and an order or the content of the content or the content or the content of the content or the content or the content or the content or the content or the content or the content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use in fracture
                                            Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoiesis; anaemia; mweloid cell deficiency; lymphoid cell deficiency; myeloid cell; erythroid progenic cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; bone fracture; cartilage damage; artificial joint; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations.
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reduction and also in the improved fixation of artificial joints
cDNA encoding a bone marrow secreted protein designated BMS112
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product= "bone marrow secreted protein"
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98US-0101603P.
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Alignment Scores: Pred. No.:

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987 GAACTCAGGGCGCCTCTTCTTAGTTGATTTAGTTGATTCTTCTGTAAGTTTGCAGTGTTTG 1046
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                                                                                                                                                                 687 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
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787 CCTGGATTGAAGCGCAAAGCTGAA 810

ABK90133 standard; DNA; 2052

RESULT 29

ABK90133;

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The invention relates to a method of detecting an autoimmune disorder in a subject comprising obtaining a biological sample, preferably a peripheral blood mononuclear cell, from a subject, determining expression levels of at least two genes in the biological sample, and comparing the expression level of each gene determined with a standard, where the comparison detects the presence of an autoimmune disorder in the subject. The method is useful for detecting or diagnosing an autoimmune disorder, e.g. rheumatoid arthritis, systemic lupus erythematosus, multiple selenosis, or type 1 (insulin-dependent) diabetes. The present sequence represents one of seventy genes used to detect autoimmune disorders with the described method.
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                                                                                        Detecting an autoimmune disorder in a subject comprising comparing the expression level of each gene determined with a standard, where the comparing detects the presence of an autoimmune disorder in the subject.
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                                                                                                                                                                                      Claim 10; SEQ ID NO 62; 86pp; English
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE by peptides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating caute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas), hyperproliferative or dysproliferative disorders (e.g. cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may be useful in treating Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polymuclectide encoding the EACE polypeptide are useful in cemponal and medicament for the treatment or prevention of disorders captomative to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading a season a proche in accer. The polypulant properties and in generation of a season and in generation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                                                                                                Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoB; Nogo-associated disease; metastasis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assays, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present nucleic acid sequence encodes the human NogoB protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Human NogoB protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blackstock WP, Hale RS, Prinjha R, Rowley A;
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                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                         DNA encoding human NogoB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD.
(SMIK ) SMITHKLINE BEECHAM PLC.
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                                                              21-OCT-2002 (first entry)
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TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181 TATCTAGGACTTGCAAATAAGAATGTTAAAGGATGCTATGGCTAAAATCCAAGCAAAAATC 786

ProGlyLeuLysArgLysAlaGlu 189

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LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis

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Alignment Scores:
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The invention relates to an isolated polymucleotide (I) comprising: (a)

any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)

complements of (a); (c) sequences consisting of at least 20 contiguous

residues of (a); (d) sequences that hybridize to (a), under moderately

stringent conditions; (e) sequences having at least 75% or 90% identity

con (a); or (f) degenerate variants of (a). Polymeptides (ABP68556-

ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer

in a patient and compositions comprising polymeptides, polymucleotides,

antibodies, fusion proteins, T cell populations and antigen presenting

colls expressing the polymeptide are useful in treating parcreatic cancer

and stimulating an immune response. The polymucleotides can be used as

probes or primers for nucleic acid hybridisation, in the design and

preparation of ribozyme molecules for inhibiting expression of the tumour

polymeptides and proteins in the tumour cells, in vaccines and for gene

therapy. Note: The sequence date for this patent did not form part of the

printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                             New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
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21-MAX-2001; 2001US-0218651P.
28-ARR-2001; 2001US-0287112P.
16-MAX-2001; 2001US-0291631P.
12-UUJ-2001; 2001US-033954P.
27-NOV-2001; 2001US-0333626P.
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P-PSDB; ABP68601.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour; stress-phosphorylated endoplasmic reticulum protein; cytostatic; gene therapy; cell growth; cellular stress response; neuron growth; regulator of oxidative stress; inhibitor of neurite outgrowth; axon regeneration; diagnosis; cancer; identification; ss.
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GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                              MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                                                                                                              CTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAATCAT
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                                                                                                                                                                                       LeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, and slycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuPheLeuLeuLeuSerLeuThrValPheSerlleValSerValThrAlaTyrlleAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligonucleotide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
                                                                                                                                                                                                                                                                                      human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
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T, Koga l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ai T, Hayashi K, Ishii S,
Nagai K, Kojima S, Otsuk:
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Mismatches:
Indels:
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02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
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                                                                                                                                                                                                                                                                       clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the the printed specification, but was obtained in CD-ROM format directly from EPO.
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                                                                                                                                                                   synthesizing full length cDNA clones and their use
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                                                                                                                                                                                                                                                            The invention relates to primers for synthesising full length cDNA
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                                                       Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                        Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;
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 neuroblastoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to nucleic acids (AAI98058-AAI98161) or their monologues expressed by human neuroblastomas useful for detecting genes expressed by neuroblastoma and for analysing their structure and function. The nucleic acids are useful for the diagnosis and prognosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids for prognosis of human neuroblastoma comprise nucleic acids expressed by human neuroblastomas.
848 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGC 907
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                  LeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle
                             908 TIGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                                                        GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                          ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
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                                                                                                                                                                                                                                                                           TATCTAGGACTTGCAAATAAGAATGTTAAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC
                                                                                                GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                                        GlubeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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                                                                                                                                                                               MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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12-MAY-2000; 2000JP-00140387.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; neuroblastoma; ss
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T; 0 U; 0 Other;
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                                                                      Length:
Matches:
Conservative:
Mismatches:
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128 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
                           LeuileSerLeuPheSerValProValileTyrGluArgHisGlnAlaGlnIleAspHis
                                                Human; secreted protein; gene; ss; genetic disease.
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                                                                                                                               ProGlyLeuLysArgLysAlaGlu 189
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09-FBB-1999; 99WO-IB000282.
21-UJM-2000; 2000WO-IB000951.
15-SEP-2000; 2000US-00663600.
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P-PSDB; ADP19259.
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                                                                                                                                                                                                                                                                                   sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DMAS can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify individuals to the extended collaboral expression of the genes corresponding to the extended collaboral also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases
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                                                                                                                                                                                                                                                                          represents an extended human secreted protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 280 A; 175 C; 232 G; 304 T; 0 U; 0 Other;
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                                                                                                                                                                                                                        New isolated human secreted proteins.
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                                                              97US-0069957P.
98US-0074121P.
98US-0081563P.
98US-0096116P.
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13-APR-1998
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The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and amethod of binding the polypeptide to an antibody. The polymucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing human tissues and cells, and for distinguishing between human tissues and cells, and for the polymucleotides comprising the cDNAs. The polymucleotides and polymer special in forensic procedures or diagnostic procedures to individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence taptesents a human secreted polymucleotide of the invention.

Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
New isolated polynucleotide encoding secreted polypeptide, useful for gene therapy, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia; antiinflammatory; antiasthmatic; antiulcer;
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Crohn's disease; asthma; ulcerative colitis; hypereesinophilia;
irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
acute monocytic leukaemia; antiinflammatorv; antiasthmatir: anti
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Length:
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The invention relates to a composition comprising a plurality of CDNAs CC for detecting the altered expression of genes in an immunological cordetecting the altered expression of genes in an immunological cordetecting the invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of CDNAs under conditions to form one or more hybridisation complexes and comparing the levels of the detected in a non-diseased sample, where an altered level of the detected hybridisation complexes with the level of hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a comprising a microarray and a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray can be used in the expression of target polynucleotides. The microarray can be used in drug discovery and development, toxicological and carcinogenicity studies, formerics or pharmacogenomics. The composition carcinogenicity studies, formerics or pharmacogenomics. The composition carcinogenic fragments. This sequence cate for this patent did not form part of the prome and the prome and the prome and the printed specification by was obtained and prome the printed specification by we septements the lettronic format directly formed the printed specification by we see the printed specification by we see the printed specification of a subpopulation of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of
                                                                                                                                                                                           A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
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                                            (INCY-) INCYTE CORP.
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US-09-830-972-29_COPY_990_1178 (1-189)

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LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl

aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLy8GlyValIleGlnAlaIl

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1551 TGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAA 1610
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                                                                uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAl
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05-JUN-2002; 2002US-0386481P.
05-JUN-2002; 2002US-0386481P.
05-JUN-2002; 2002US-0386513P.
05-JUN-2002; 2002US-0386513P.
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06-JUN-2002; 2002US-0387017P.
06-JUN-2002; 2002US-0387026P.
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The present invention describes a method for identifying an agent for treating a diabetic or pre-diabetic individual. The method comprises contacting an agent to a mixture comprising a polypeptide encoded by a nucleic acid that hybridises under stringent conditions to a nucleic acid that hybridises under stringent conditions to a nucleic acid conceding any of the 23 fully defined amino acid sequences given in the specification, and selecting an agent that modulates the expression or activity of the polypeptide. Also described: (1) a method of treating a diabetic or pre-diabetic animal, comprising administering to the animal acid therefore the animal acid amount of an agent identified by the method described above; (2) a method of introducing an expression cassette into a cell, comprising introducing into the cell an expression cassette comprising a promoter operably linked to a polynucleotide encoding a polypeptide, where the polynucleotide hybridises under stringent conditions to a uncleic acid encoding the above amino acid sequences; and (3) a method of diagnosing an individual who has Type 2 diabetes or is pre-diabetic, comprising detecting in a sample from the individual the level of the polypeptide or the level of the above-mentioned polynucleotide encoding the above-mentioned polynucleotide in the sample compared to a level of the polypeptide or comprising or the level of the above-mentioned polynucleotide in either a lean individual is diabetic or pre-diabetic. The method is useful in diagnosing and treating diabetes, insulin resistance or related metabolic diseases in human subjects or pre-diabetic. The method is useful in diagnosing and treating diabete; insulin my also be used in identifying agents for treating diabetic or pre-diabetic or pre-diabetic insulvalual. Identifying an agent for treating diabetic or pre-diabetic individuals comprises contacting an agent with a polypeptide, e.g., human ceramidase, and selecting an agent that modulates the expression or activity of the Disclosure; SEQ ID NO 87; 209pp; English present invention

Sequence 734 BP; 202 A; 138 C; 179 G; 215 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder;
LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis
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(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
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P-PSDB; ADP45572.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rat; gene; ss.
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Zurini M;
142
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3342

3402

140

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120

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Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; ss.
                                                                                                                neurite growth inhibitor Nogo A cDNA.
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
253. .3744
                 BP
               AAD01173 standard; cDNA; 4684
                                                                                  02-NOV-2000 (first entry)
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Sequence 3492 BP; 1031 A; 804 C; 822 G; 835 T; 0 U; 0 Other;

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120

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3535 TTGATGAGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTA 3594
                                                                                                                                                                                                                                                                                                                                                                        3655 CATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAA 3714
                                                                                                                                                                                                                                                                                                                                           HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nerve regeneration, neuroprotection, neuronal degeneration, CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; neptropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; rat; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Promoting nerve regeneration and preventing neuronal degeneration in the
                                                                                                                                                                                                                                                                                              3355 Arccagaaarcagargaaggccacccarrcagggcararraagaarcrgaagrrgcrara
                                                                                                              3415 TCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATA
                                                                                                                                                                              3475 AAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTG
                                                                                                                                                                                                                                                                             141 AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp
                61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                               SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
                                                                                                                                               LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurotransmitter receptor protein Nogo encoding DNA.
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253. .3744
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/product= "Nogo-A"
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98US-00218277.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-607255/65.
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21-JUL-1998;
22-DEC-1998;
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ABN86600
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                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a cDNA encoding rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The present sequence was generated by fusing NO18U37-3, R1-3U21 cDNA sequences isolated from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte clibrary. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharymgioma, ependyoma, cpinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, cpinealoma, haemangioblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative disorders e.g. psoriasis and tissue cor bromote structural plasticity of the CNS in disorders where neurite cromote structural plasticity of the CNS in disorders where neurite cromodels can be used in disquestic and screening methods for predisposition cor maintenance are deficient or desired. The animal cord provent disorders and to screen for or test molecules which can treat or cord cord cromoders or test molecules which can treat or referred in claim 32 and SEO ID NOS. Notes DID numbers 35-42 are creferred in claim 32 and SEO ID NOS. 29 in disclosure of the
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                                                                                                                                                                                                                                                                                                                            yo proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 U; 0 Other;
/*tag= a
/product= "Nogo A"
/transl_except= (pos:1462. .1464, aa:Ile)
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184
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Matches:
Conservative:
Mismatches:
Indels:
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908.00
98.94%
97.35%
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                                                                                                                                                                                                                                              Chen MS;
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                                                                                                                                                                                             SCHWAB M E. CHEN M S.
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                                                                                                                                                                                                                                                                                               P-PSDB; AAY71310
                                                                  WO200031235-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                             Claim 26; Fig
                                                                                                                                05-NOV-1999;
                                                                                                                                                                06-NOV-1998;
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                                                                                                02-JUN-2000
                                                                                                                                                                                                                                              Schwab ME,
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                                                                                                                                                                                               (SCHM/)
                                                                                                                                                                                                                CHEN/)
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DB:
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central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, analogs/peptides.
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Disclosure; Page 40-44; 93pp; English.

The invention relates to promoting nerve regeneration or conferring central/peripheral nervous system (NS). The method involves administering central/peripheral nervous system (NS). The method involves administering (NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt frauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not autoimmune disease or neoplasm. The disease results in a degenerative contournating in either gray or white matter or both. The disease is disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral dise hernialiton, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral to uremia, porphyria, hypoglycemia, Sjorgren Lareson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstractive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobula, in [19]A and 1gG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia atelangectasia, Friedreich's ataxia, amyloid polyneuropathies, adrenomyloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents a DNA encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B and Nogo-C), an example of NS-specific antigen

Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 U; 0 Other;

3354 3415 TCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATA 3474 3475 AAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTG 3534 3235 AGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATT 3294 3355 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATA 3414 120 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140 40 9 80 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 3175 TCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 3295 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCT 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla US-09-830-972-29_COPY_990_1178 (1-189) x ABN86600 (1-4684) Conservative: Mismatches: Indels: Length: Matches: Gaps: 9.47e-100 908.00 98.94**%** 97.35**%** Best Local Similarity: Percent Similarity: Alignment Scores: 101 81 Query Match: DB: g 셤 ò ద 셤 ò ò ð 셤 ò 셤 ઠ

2782

1.06e-99

Alignment Scores: Pred. No.:

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3655 CATTATCTAGGACTTGCAAAGAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGGAAAA 3714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of gene sequence that is down-regulated in response to streptozocin-induced diabetes, vector, host cell, animal, polypeptide and antibody, in screening of compounds for treating or diagnosing pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated gene sequence that is down-regulated in the spinal cord in response to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence identity to a sequence whose expression products are kinases, phosphatases, ion channel proteins, receptors, transporters, G-protein coupled receptor proteins, DNA-binding proteins, proteases or enzymes, given in the specification. A gene of the invention has analgesic activity, and may have a use in gene therapy. The gene sequences, vector, host cell, animal, polypeptide and antibody are useful for screening of compounds for diagnosing or treating pain. The kits are useful for simultaneous, separate or sequencial detecting and/or quantifying downsubulation of a gene sequence in the spinal cord of a mammal in response to streptozocin-induced diabetes. The compound or pharmaceutical composition is useful as a medicament for treating or diagnosing pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat; streptozocin; kinase; phosphatase; ion channel protein; receptor; transporter; G-protein coupled receptor; GPCR; DNA-binding proteins; protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.
3535 TIGATGIGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTA
                                                                                                                                  HisTyrLeuGlyLeuAlaAsnLygAsnValLygAspAlaMetAlaLygIleGlnAlaLyg
                                                                                            Sequence 2782 BP; 635 A; 728 C; 765 G; 654 T; 0 U; 0 Other;
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                                                                                                                                                                                                                              3715 ATCCCTGGATTGAAGCGCAAAGCAGAT 3741
                                                                                                                                                                                                             IleProGlyLeuLysArgLysAlaGlu 189
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                                                                                                                                                                                                                                                                                                                           ADB85284 standard; DNA; 2782 BP
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                             | IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                                                      AAAGAACTGAAGGGGGCTTTTCTTAGTTGATGATTTAGTTGATTGCTTGAAGTTTGCAGTG
                                                                                                                                                                                                                                                           LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                                                                                                                     TIGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTA
                                                                                                                                                                                                                                                                                                    HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                                             SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle
                                                                                                                                                                                                                             LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                           AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
                                                                                               SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                              AlaleuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      number; fat cell size; obesity; diabetes;
183
2
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                                               x ADB85284 (1-2782)
       Conservative:
Mismatches:
Indels:
 Matches:
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                                               US-09-830-972-29_COPY_990_1178 (1-189)
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905.00
98.94%
96.83%
97.21%
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     Percent Similarity:
Best Local Similarity:
Query Match:
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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the cells not expression of the gene in an expression of the gene crelative to expression of the gene in an expression vector not exposed to the agent, treating a subject with the agent comprises an antisense coligonucleotide. The subject to comprises a mammal, preferably a human. The method also comprises providing a polypeptide and an agent, exposing the olypeptide or a change in an activity of the polypeptide, treating a subject that the agent comprises an antibody. A method of requising fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the agent that cell number or size of number or size of number or size or number in the conditions of the fat cell size or number in the agent that cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents
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                                                                                                                Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
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186
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Conservative:
Mismatches:
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WPI; 2004-328526/30.
P-PSDB; AD008105.
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3220 ATAAAAGAATTGAGGGGGTCTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCA 3279

120 ValLeuMetTrpValPheThrTyzValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle

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151 GITGITGACCICCICTACTGGAGACATTAAGAAGACTGGAGTGGTGGTTGGTGCCAGC 210
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Best Local Similarity:
WO200031235-A2
                                                                                                                         06-NOV-1998;
                                                                                   05-NOV-1999;
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3280 GTGTTGATGTGGGTATTTACTTACGTTGCTGCCTTGTTCAATGGTTTGACACTACTGATT 3339
                                                                                                                                            3400 GATCATTATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAGCA 3459
                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antieense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Nogo C protein (residues 40-238) flanked by 1-39 residues at the N-terminal and 239-522 residues at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ept= (pos:1537. .1539, aa:Xaa)
corresponds to in-frame stop codon; the CDS
                                      140 LeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIle
                                                                                                                       160 AspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla
                                                                              3340 Traccretearcretrerererererererarandaacecarcaeecagara
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/*tag= b
/note= "Start codon of Nogo C coding region"
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/note= "Stop codon of Nogo C coding region"
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(pos:1264. 1266, aa:Xaa)
(pos:1297. 1299, aa:Xaa)
(pos:1318. 1320, aa:Xaa)
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(pos:1216. .1218, aa:Xaa)
(pos:1222. .1224, aa:Xaa)
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(pos:883. .885, aa:Xaa)
(pos:889. .891, aa:Xaa)
(pos:940. .942, aa:Xaa)
(pos:952. .954, aa:Xaa)
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(pos:1111. .1113, aa:Xaa)
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(pos:787. .789, aa:Xaa)
(pos:826. .828, aa:Xaa)
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                                                                                                                                                                                                                                              3460 AAAATĆĊĊTGGATTGAAĞCĞCAAAĞCAĞAA 3489
                                                                                                                                                                                                      180 LysileProGlyLeuLysArgLysAlaGlu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pos:1120.
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note= "Xaa corresponds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat neurite growth inhibitor Nogo C cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .1566
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Matches: Conservative: Mismatches: Length:

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Indels:

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potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, campioblastoma, acoustic neuroma, oligodendrogalioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo crivity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy.

Ribozymes or antisense Nogo nucleic acids can be used to inhibit con production of Nogo protein to induce regeneration of neurons or to production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal codels can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or treat in classification of the CNS. Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disolosure of the creating or referred in claim 32 and SEQ ID NO: 29 in disolosure of the creating or the contraction of the creating method in claim 20 and SEQ ID NO: 29 in disolosure of the creating or the contraction of the creating method in claim 20 and SEQ ID NO: 29 in disolosure of the creating or the contraction of the creating method in claim 20 and SEQ ID NO: 29 in disolosure of the creating or the contraction of the creating method in claim 20 and SEQ ID NO: 29 in disolosure of the creating contraction or contraction or contraction or contraction or contraction or contraction or contraction or contraction or contraction or contraction or contraction or contraction or contraction or contraction or contraction or contraction or contract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
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99WO-US026160
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P-PSDB; AAY71312.
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secreted proteins. Novel cDNA clauses (see AAV39916-32) coding for human secreted proteins (see AAW58580-90) are claimed. These can be used for recombinant production of the secreted proteins for analysis, characterisation, diagnostic or therapeutic use. They can also be used as tissue or mol.wt. markers, for chromosome identification, to identify genetic disorders, to isolate new related DNA, as sources of primers for PCR, to generate antibodies, and in interaction trap assays. The secreted immunomodulator, haematopoiesis regulating activity, tissue growth activity, activity nor inhibin activity, chemotactic or chemokinetic activity, activity or inhibin activity, chemotactic or chemokinetic activity, antiinflammatory, cabherin and tumour invasion suppressor activity, and tumour inhibition activity. The proteins can be expressed in vivo from DNA, introduced in gene therapy vectors
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to neuroendocrine
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894.50
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predicted AT415
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GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA
                                                                                                                                                                                                                                                                                  TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAAATCCAAGGAAAAATC
                                                                                                           MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLleLeuAla
                                                                                                                                                CTGATCTCACTCTTCAGTATTTCCTGTTATTTATGAACGGCATCAGGTGCAGATAATAGATCAT
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                                     GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                        GAACTGAGGGGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "putative leader/signal peptide"
1900...2027
/*tag= c
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102. .2030
/*tag= a
1863. .1899
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97US-00740274
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V, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEMY ) GENETICS INST INC.
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Spaulding V,
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24-OCT-1997;
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE properties and control other interaction between these polypeptides, and determining if the test agent interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating content in the neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas).

Controlastomas), hyperproliferative or dysproliferative disorders (e.g. cirrhosis, progriasis, psoriasis, psoriasis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators (c.g. baCE activity and in particular agents that may be useful in treating to Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polymucleotide encoding the BACE polypeptide are useful in cresponsive to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polymucleotide may also be an essential component in cassays, a probe, in recombinant protein synthesis, and in gene therapy control of the invariance of the human NogoC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                                                       Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoC; Nogo-associated disease; metastasis; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                               /product= "Human NogoC protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 62-64; 68pp; English.
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                             DNA encoding human NogoC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLAX ) GLAXO GROUP LTD.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002; 2002WO-GB000228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2001; 2001GB-00001312.
                      (first entry)
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P-PSDB; ABG30939.
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                                                                                                                                                                                                                                                                   Homo sapiens
                    21-OCT-2002
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Length:
Matches:
Conservative:
Mismatches:
Indels:

1.19e-97 886.00 98.94% 98.94% 95.17%

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Query Match: DB:

Alignment Scores:

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                                                        248 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 307
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                                                                                                                                               LeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValIleGlnAlaile
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                                                                                                                                                                                                                                                                                        GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
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                                                                                      LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                          ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collins-Racie LA, Evans C; Spaulding V, Agostino MJ;
US-09-830-972-29_COPY_990_1178 (1-189) x ABK90135 (1-1798)
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Treacy M, Bowman MR,
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Merberg D;
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                                                                                                                                           Human cDNA clones represented in AAF98374 - AAF98489 encode secreted proteins AAB90667 - AAB90750. The cDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The polypeptides and nucleic acids may be used as nutrients or to modulate cytokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The cDNA sequences, proteins, their agonists and/or antagonists exhibit haematopoiesis regulating activity; tassue growth activity; activin/inhibin activity; chemokinetic activity; haemostatic and thrombolytic activity; ceceptor/ligand activity; anti-inflammatory activity; haematopoiesis activity cadherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98872 which are specific for the CDNA clones encoding the secreted
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                                                Isolated nucleic acids encoding polypeptides, useful for modulating e.g. cytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1476 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCC
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2001-244801/25
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The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell canisodies that bind to the proteins encoded by the polynucleotides, and the proteins and identification of modulators of the proteins or the expression of the polynucleotide. The polynucleotides can be used as probes for the identification and isolation of full length contains and genomic DMA. The polynucleotides and proteins can also be used as nutritional supplements. The protein is useful in the treatment of various immune deficiencies and disorders such as viral infections, carious immune deficiencies and disorders such as viral infections, carious immune deficiencies and disorders (e.g. asthma). They are also useful for treating neutodegenerative diseases (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease), liver fibrosis, coagulation disorders (e.g. haemophila), inflammatory disorders (e.g. crohn's disease) and disorders (e.g. haemophila), inflammatory disorders (e.g. crohn's disease) and disorders (e.g. haemophila), inflammatory disorders (e.g. crohn's disease) and districtions (e.g. when the contains and conditions (e.g. crohn's disease) and disorders (e.g. crohn's disease) and disorders (e.g. crohn's disease) and disorders (e.g. crohn's disease) and disorders (e.g. crohn's disease) and disorders (e.g. crohn's disease) and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders described and disorders d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ss; gene; secreted protein; immune deficiency; viral infection; bacterial infection; fungal infection; autoimmune disorder; burn; theumatoid arthritis; multiple sclarosis; autoimmune thyroiditis; diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; tissue regeneration disorder; haemophilia; inflammatory disorder; ulcer; tissue regeneration; wound healing; haematopolesis; myeloid deficiency; lymphoid cell deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopoiesis, for treating myeloid or lymphoid cell deficiencies. The present sequence is one of the 625 CDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA for novel secreted protein, SEQ ID 349.
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181 IleProGlyLeuLysArgLysAlaGlu
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K, Graham JR;
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Gulukota K,
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/product= "Mature human secreted protein"

830. .898 /*tag= b 899. .1189 /*tag= c partial

g,

Komatsoulis

99US-0138629P

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788 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTTTTGGTGCCAGC 847
                                                                                                                                        01-JUN-2000; 2000WO-US015136
                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                  Rosen CA, Ruben SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemotaxis; food additive; gene therapy; binding partner identification;
                                                                                                                                                                      63 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG
                                                                                                                                                                                                                                                                    TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT
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                                                                                                  13 LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSer
                                                                                                                            AAGACTGGAGTGGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC
                                                                                                                                                  33 IleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArg
                                                                                                                                                                                                    53 IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla
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/note= "CDS does not include start codon"
                                                                          x ABK34580 (1-1514)
             Conservative:
Mismatches:
Indels:
                                                Gaps:
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                                                                          US-09-830-972-29_COPY_990_1178 (1-189)
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ARD08345-AAD08394 represent cDNAs corresponding to 50 human secreted

protein genes and AAE03898-AAE03947 represent the proteins they encode.

AAE03948-AAE03996 represent human secreted protein fragments or variants.

CT he genes and their secreted proteins are useful for preventing, treating

cr ameliorating medical conditions, e.g., by protein or gene therapy.

CT pased on the tissues in which they are most highly expressed, and include

CT based on the tissues in which they are most highly expressed, and include

CT che new genes. Specific uses are described for each of the 50 genes,

CT che new genes. Specific uses are described for each of the 50 genes,

CT che new genes. Specific uses are described for each of the 50 genes,

CT check cancer, tumours, foetal and developmental abnormalities,

CT developing products for the diagnosis or treatment of proliferative

CT developing products for the diagnosis or treatment of proliferative

CT disorders, cancer, tumours, foetal and developmental abnormalities,

CT disorders, cancer, tumours, foetal and developmental abnormalities,

CT disorders, cancer, tumours, for schizophrenia, asthma, sith disorders, and include

CT cognitive disorders, genizophrenia, asthma, sith disorders,

CT cognitive disorders, chilabetes, atherosclerosis, cardiovascular disorders,

CT cognitive disorders, diabetes, atherosclerosis, cardiovascular disorders,

CT creamers, and in chemotaxis, atherosclerosis, cardiovascular colors

CT preservative to modify storage properties. Antibodies specific for a

CT preservative to modify storage properties. Antibodies specific for a

CT preservative to modify storage properties. Antibodies specific for a

CT preservative to modify storage properties. Antibodies specific formance with the disorders mentioned above, and in diagnostic immunosassay or environment and properties and in diagnostic immunosassay or environment and properties and in diagnostic immunosassay or environment and properties are allowed to an environment and an environment and an 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ValValAspLeuLeuTyrTrpArgAsplleLysLhrGlyValValValPheGlyAlaSer
Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;
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Mismatches:
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                                                                                                                                                                                                            Claim 1; Page 520; 614pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                         GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                                                                                                                                                                                           122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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                                                                                                                62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                        LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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11-JAN-2000; 2000US-00480902.
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(WARR/) WARREN W C.
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences.

Complements as ABX34836-ABX4937, or complements of them. Also included are interested acid molecule comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and comprising a level or pattern of a molecule acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the complementary nucleic acid permits the detection of the molecule.

Complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for clevel or pattern of the molecule. The LMFD nucleic acid is used for the section of the molecule. The present sequence is one of the complement sequence is one of the present sequence is one of the present sequence acid in the sequence in the part of the present sequence is not and analysis. 116 121 96 181 9/ 61 present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: 62 GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCT 2 Acesectacarrecerresererererereserareaserrrassarararasser 97 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 37 ThralaTyrileAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 122 GAAGTIGCTATATCIGAGGAGTIGGTICAGAAGTACAGCAATICIGCTCTIGGTCAIGTT 57 ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer Sequence 422 BP; 109 A; 79 C; 94 G; 140 T; 0 U; 0 Other; 44 00 00 00 00 breeding, or for genetically improving cattle US-09-830-972-29_COPY_990_1178 (1-189) x ABX43312 (1-422) segdata.uspto.gov/sequence.html?DocID=20020137139 Matches: Conservative: Mismatches: Indels: Length: Claim 2; SEQ ID NO 8477; 245pp; English 3.14e-75 695.00 100.00% 100.00% 74.65% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Score: g ð 셤 g Š ð ò

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LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 136

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242 AAGTITGCAGIGITGAIGIGGGGIATITACCIAIGITGGIGCCTIGITCAAIGGICTGACA LeuLeulleLeuAlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGln

AlaGlnileAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 176

302 157 362

RESULT 51 ADJ56527

137

475 122 535

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TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
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anorectic, antidiabetic.
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P-PSDB; ADO08104.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to movel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polynucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protononcogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic well as for screening assays by identifying molecules or compounds that acids (or complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       printed specification but has been obtained in electronic format from US Patent Office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                     rat; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss; MYCN activated cell.
                                                                                                                                        Rat cDNA differentially expressed in MYCN activated cells SegID 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1520 BP; 398 A; 354 C; 336 G; 432 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009.
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Matches:
Conservative:
Mismatches:
Indels:
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  BP
ADJ56527 standard; cDNA; 1520
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85.03%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (STUA,) STUART S G.
(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
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Best Local Similarity:
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                                                                                            06-MAY-2004
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DB:
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Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
                                                                                                                                                                                                                                                                                                                    The invention relates to a method of identifying compounds that influence
                                                                    fat cell number; fat cell size; obesity; diabetes;
                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 213; 275pp; English
                                                                                                                                                                                                                                                                                 agent.
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235

PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42

23

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ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu

US-09-830-972-29_COPY_990_1178 (1-189) x ADJ56527 (1-1520)

AAX75770 standard; DNA; 3202 BP.

22-JUL-1999

AAX75770;

and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, The method comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene contains a subject with the agent ovector not exposed to relative to expression of the gene in an expression of the gene comprises an autisense comparises an autisense coligonucleotide. The subject comprises a mammal, preferably a human. The method also comprises providing a polypeptide and a agent, exposing the polypeptide to the agent, detecting binding of the agent to the collypeptide or a change in an activity of the polypeptide, treating a subject with the agent and identifying fat cell number or size in the subject with the agent comprises an antibody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject configured the agent conditions so that fat cell size or number in the subject conditions so that fat cell size or number in the capities or conditions so that fat cell size or number or size in the capities or size, for preparing a composition for the condition or preventing or preventing or preventing or preventing compounds that the coll number or size, for preparing a composition for the coll of the co treating or preventing obesity or diabetes. The human cDNA used in the scope of the invention. DDDDDDDDDDDDDDDDDDDDDXX

Sequence 2331 BP; 552 A; 698 C; 649 G; 432 T; 0 U; 0 Other;

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Alignment S Pred. No.: Score: Percent Sim Best Local Query Match DB:	a :	cores: ilarity: Similarity: ::	1.33e-72 682.00 85.03 68.45 73.25	Length: Matches: Conservative: Mismatches: Indels:	2331 128 31 28 0
-08-60-SD	972	-29_COPY_9	990_1178 (1-189)	x ADO07887 (1	-2331)
ò	m	ValAspLeuL	LeuTyrTrpArgAspI]	eLysLysThrGl	yvalvalPheGlyAlaSerLeu 22
qq	1768	ATTGACCTG	STIGTATIGGCGGGAC	CATCAAGCAGACGGGC	:::
δ	23	PheLeuLeu	eLeuLeuLeuSerLeuThrValPhe	SerlleValSer	ValThrAlaTyrIleAlaLeu 42
eg Q	1828	CTGCTGCTC	rrcrccrcaccac	CTTCTCCCTGACCCAGTTCAGCGTGGTGAGCGT	Gregeetaceregecerg 1887
ò	43	AlaLeuLeuSerVal	Thriles	erPheArglleTyrLys(sGlyValIleGlnAlaIleGln 62
qq	1888	GCCGCACTC	GCCGCACTCTCAGCCACCATCAGTTT	CCGCAT	CTACAAGTCTGTTTTACAAGCAGTGCAG 1947
ò	63	LysSerAspG	uGlyHisProPh	eArgAlaTyrLeuGlu	uSerGluValAlaIleSerGlu 82
Q	1948	AAAACCGAC	GAAGGCCACCTTT	TCAAGGCCTACTTGGAGG	CTACTTGGAGCTTGAGATCACCCTTTCTCAG 2007
ò	83	GluLeuValGlnLy	8TY	rSerAsnSerAlaLeuGlyHisValAsnCy	ValAsnCysThrIleLysGlu 102
අධ	2008	GAGCAGATT	CAGAAGTACACGGAC	CTGCCTGCAGTTCTACC	
ò	103	LeuArgArgL	LeuPheLeuValAspAspLeuValA	Sgs	erLeuLysPheAlaValLeuMet 122
qa	2068	CTGAGGAGG	CTCTTCCTTGTCCAC	GACCTGGTGGATTCC	CICTICCTIGICCAGGACCIGGIGGATICCTIAAAATITGCAGTCCIGAIG 2127
ò	123	TrpValPheThrT	YrValGlyAl	aLeuPheAsnGlyLeu	VLeuThrLeuLeulleLeuAlaLeu 142
ą	2128	TGGCTCCTG	ACCTACGTTGGCGC	rcrcrrcaarggccrg	CATGGCT
ò	143	IleSerLeu	PheSerValProVa	eSerLeuPheSerValProValIleTyrGluArgHisGlnAl	GlnAlaGlnIleAspHisTyr 162
q _Q	2188	GTTTCAATG	TTACTCTACCTGT	AGTGTATGTTAAGCAC	GTTTCAATGTTTACTCTACCTGTGTGTGTTAAGCACCAGGCACAGATTGACCAATAT 2247
ò	163	LeuGlyLeu	AlaAsnLysAsnVa	etAl	aLysileGlnAlaLysilePro 182
qq	2248	CTGGGACTT	GTGAGGACTCACATA		AAGATTCAGGCTAAAATCCCA 2307
ò	183	GlyLeuLys	SArgLysAlaGlu 16	189	
qq	2308	GGCGCTAAG	 GCGCTAAGAGCCACGCTGAG 2:	2328	-

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Alzheimer's disease, Down's syndrome; myotonic dystrophy, neuronal; Huntington's disease, Down's syndrome; myotonic dystrophy, neuronal; diabetes mallitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-N; neurofilament-P; presenilin I; presenilin II; callular tumour antigen; glial fibrillary acidic protein; GRAP; ps3; semaphorin III; HUPF-I; bcl-2; B-cell leukemia/lymphoma 2 prote-oncogene; HWGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA.
                                                                                           Human, beta-amyloid precursor protein, beta-APP, diagnosis, cancer, frameshift mutation, age-related disease, neurodegenerative disorder;
                                                                 Human neuroendocrine-specific protein NSP-A DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Burbach JPH;
                                                                                                                                                                                                                                                                                                                                                                               (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI. (UYRO-) UNIV ROTTERDAM ERASMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 19; 258pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  Grosveld FG,
                                                                                                                                                                                                                                                                                                                           98WO-IB000705,
                                                                                                                                                                                                                                                                                                                                                      97US-0043163P
                                                                                                                                                                                                                                                                                                                                                                                                           (UYUT-) RIJKSUNIV UTRECHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-609901/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Leeuwen FW,
                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                           02-APR-1998;
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This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift cancer and a wide range of neurodegenerative diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, allown's syndrome, myotonic dystrophy, Huntington's disease, alcoholic liver disease, diabetes mellitus type II cand many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated protein Z (MAP2), neurofilament-L, microtubule associated protein Z (MAP2), neurofilament-L, meurofilament-F, presenllin I, presenlin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma CC 2 (bcl-2) prote-oncogene, semaphorin III, HUFF-1, high mobility group croces cencedes the wild type and mutant protein fragments represented in AAV21434-Y21520

Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

Alignment Scores: Pred. No.:

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Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;
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                                                                                                                                                                                           GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLysGlu 102
                                                                                                                                                                                                                                                             TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
                                                                                            42
                                                                                                                            62
                                                           22
                                                                                                                                                           LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                      2070 AAAACCGACGAAGGCCACCTTTCAAGGCCTACTTGGAGCTTGAGATCACCCTTTCTCAG
                                                                                                                          2010 GCCGCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTCTGTTTTACAAGCAGTGCAG
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                                                          3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu
                                                                                            23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu
                                                                                                                                                                                                                             LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet
                                                                                                                                                                                                                                                                                             IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr
                                                                                                                                                                                                                                                                                                                            LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro
                                          US-09-830-972-29_COPY_990_1178 (1-189) x AAX75770 (1-3202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung cancer related gene sequence SEQ ID NO:3237
    Conservative:
           Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                             GlyLeuLysArgLysAlaGlu 189
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2000US-0209531P.
2000US-0233133P.
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  85.03%
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Percent Similarity:
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Query Match:
DB:
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05-JUN-2000; 2
18-SEP-2000; 2
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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent cobe tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 of ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity, (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is cantinoplastic activity and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carter KC, Ebner R, (Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 3237; 44pp; English
                                                                                                                                                   2000US-0235280P.
2000US-0235637P.
2000US-0235638P.
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2000US-0236032P.
2000US-0236033P.
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2000US-0237172P.
2000US-0237173P.
2000US-0237278P.
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2000US-0237295P.
2000US-0237316P.
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Weaver Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-188264/24.
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02-OCT-2000;
03-OCT-2000;
22-SEP-2000;
25-SEP-2000;
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27-SEP-2000;
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Soppet DR,
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(PROT-) PROTEIN DESIGN LABS INC.

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1949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
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                                                                                                               1950 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGAGCGTCGTGGCCTACCTGGCCCTG
                                                                                                                                                                                   AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln
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                                                                                                  ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu
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                                                                                                                                                                                                                                                                                                             LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human soft tissue sarcoma-upregulated DNA - SEQ ID 1480
      3202
128
31
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                                                                              (1-3202)
                           Conservative:
Mismatches:
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Matches:
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                                                                              US-09-830-972-29_COPY_990_1178 (1-189)
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Alignment Scores
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                                                                                                                                                                                                 The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the
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                                                                                         Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                                                                                                                  specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                C; 825 G; 702 T; 0 U; 0 Other;
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Matches:
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                            Zlotnik A
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                            Ginsburg WM,
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                                                                                                                                        LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu
                                                                                                                      GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu
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14-MAY-2003; 2003DE-01022134.
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Staub E;
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ROSENTHAL A.
HERMANN K.
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DAHL E.
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Xinzhong L,
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2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAAGATTCAGGCTAAAATCCCA 2429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
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                                                                                                                                                                                                                                                                            ds; breast cancer; prognosis; gene expression; diagnosis.
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                                                                                                                                                                                                                                           Breast cancer prognosis marker #386.
                                                                  2430 GECECTAAGAGECACECTGAG 2450
                                GlyLeuLysArgLysAlaGlu 189
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                                                                                                                                 ADR24525 standard; DNA; 3202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding
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mann H, Roepcke S;
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f T, Kinnemann H,
#1.
Human prostatic carcinoma derived DNA SEQ ID 10
                                                     human; cytostatic; diagnosis; prostatic cancer; differential expression analysis; ds.
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G, Bruemmendorf T,
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This invention describes moved cytoseratic polymucleotide and polypoptice sequences which can be used in a method for diagnosing prostatic cancer. Diagnosis is based on the trisk of developing prostatic cancer. Diagnosis is based on prostatic tissue. Screening for inhibitors of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interferring RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an organic molecule of molecular aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; a monoclonal) antibody (Ab) against the polypeptide; a monoclonal antibody affected against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that compactatic cancer patients, or subjects at risk, were incubated from prostatic cancer patients, or subjects at risk, were incubated between the diaminobenzidine as collure former (brown). The sequentially but normaliand with hemalum (blue). Malignant cells stained surfaced second antibody; streptavidin-conjugated horseradish cannon manaland with hemalum (blue) of samples were counterstained with member of samples of strongly and prostations and then diaminobenzidine as colour formaliances. adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the This invention describes novel cytostatic polynucleotide and polypeptide nvention.

Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142 2130 GAGCAGATTCAGAAGTACAGGACTGCCTGCAGTTCTACGTGAACAGCACACTTAAAGGAA AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln GlubeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu CTGAGGAGGCTCTTCCTTGTCCAGGACCTGGTGGATTCCTTAAAATTTGCAGTCCTGATG TGGCTCCTGACCTACGTTGGCGCTCTCTTCAATGGCCTGACCCTGCTGCTGCTCATGGCTGTG 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet US-09-830-972-29_COPY_990_1178 (1-189) x ADR65814 (1-3202) Conservative: Mismatches: Indels: Length: Matches: 2.08e-72 682.00 85.03% 68.45% Best Local Similarity: Percent Similarity: Alignment Scores: 23 43 103 2190 123 63 83 Query Match: DB: ઠે 셤 8 ద ò 셤 ò 요 g ò 음 8 g ò ò

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This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection constant the broad are brinding assay, any compounds that bind are substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular which below 5000, preferably 300, that binds to the polypeptide; an expanser against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polypucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated
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Bruemmendorf T, Kinnemann H, Roepcke S;
LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro
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HERMANN K.
PILARSKY C.
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(DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
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sequentially with anti-human CD4 murine monoclonal antibodies; blotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counteretained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR6954 represent the polymucleotide and polypeptide sequences used in the method of the
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2010 GCCGCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTCTGTTTTACAAGCAGTGCAG 2069

43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln

1949

3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu

US-09-830-972-29_COPY_990_1178 (1-189) x ADQ23106 (1-3305)

3305 128 31 28 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

2.17e-72 682.00 85.03% 68.45% 73.25%

Best Local Similarity:

Query Match: DB:

Percent Similarity

Alignment Scores:

PheleuleuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu

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2009

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LeuargargLeuPheLeuValaspaspLeuValaspSerLeuLysPheAlaValLeuMet

GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu

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2070 AAAACCGACGACGCTTTTCAAGGCCTACTTGAAGCTTGAGATCACCCTTTCTCAG

LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu

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The invention relates to a novel method for detecting soft tissue sarcom which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples, where a higher level of protein expression in the first soft tissue sample, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                  Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 828 A; 913 C; 843 G; 721 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 5926; 210pp; English.
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                                                                                                                                                                                                                         LABS INC.
                                                                                                                                                                                  26-NOV-2002; 2002US-0429739P
                                                                                                                                              26-NOV-2003; 2003WO-US038193
                                                                                                                                                                                                                       (PROT-) PROTEIN DESIGN
                                                                                                                                                                                                                                                            Ginsburg WM,
                                                                                                                                                                                                                                                                                                 WPI; 2004-441208/41.
                                                                      WO2004048938-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3305
                                 Homo sapiens.
                                                                                                         10-JUN-2004
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2309
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2190 CTGAGGAGGCTCTTCCTTGTCCAGGACCTGGTGGATTCCTTAAAATTTGCAGTCCTGATG 2249
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                              142
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                             TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu
                                                2310 GTTTCAATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATAT
                                                                                                                                                                      143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr
                                                                                                                                                    LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; gene; Bisulphite; metastasis; cancer; cytostatic; DNA methylation; matrix-assisted laser desorption/ionisation; MALDI; electrospray; mass spectrometry; CpG dinucleotide; solid tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid derived from chemically treated metastasis genes, diagnosis of cancers by analysis of cytosine methylation, also
                                                                                                                                                                                                                                                                                                                                                                                                       Human reticulon 1 (RTN1), transcript variant 1, cDNA.
                                                                                                                                                                                                                                               2430 GGCGCTAAGAGGCACGCTGAG 2450
                                                                                                                                                                                                                  GlyLeuLysArgLysAlaGlu 189
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2000DE-01019173.
2000DE-01032529.
2000DE-01043826.
2001WO-EP003970.
                                                                                                                                                                                                                                                                                                              ADS99925 standard; cDNA; 3327
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                                                                                                                                                                                                                                                                                                                                                                        02-DEC-2004 (first entry)
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PIEPENBROCK C.
BERLIN K.
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01-SEP-2000;
06-APR-2001;
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07-APR-2000;
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(PIEP/)
(BERL/)
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method of above 5-unmethylated cytosines in a genomic DNA sample are converted chemically to uracil, or another base with hybridisation to properties different from those of cytosine, then fragments of the treated DNA amplified (particularly by polymerase chain reaction) using the oligomers and a polymerase (preferably heat stable) to produce the oligomers and any hybridisation detected. The amplicons are labelled with fluorescent or radioactive markers, or with a detachable mass marker to allow their detection by mass spectrometry, specifically using the matrix cassisted laser desorption/ionisation (MALDI) or electrospray techniques. To improve detection in the mass spectrometer, fragments formed in the complement have only a single net charge (positive or neggative). The embedded tissue sample. Oligonucleotides or peptide-nucleic acids that care complementary to (or identical with) parks of the nucleic acids that care complements, and for determining cytosine methylation status and/or single nucleotide polymorphisms in metastasis-related genes. They can be used for analysis of diseases.associated with methylation of CRG and/or therapy of disease.sasociated with methylation of CRG and/or therapy of disease.sasociated with methylation of an analysis and the parks of solid tumours and cancer. The recomplements is human que frament or CDNA associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is human gene fragment or cDNA associated with metastasis. Note: The sequence was not displayed in the specification but was obtained by the indexer from Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3327 BP; 829 A; 907 C; 877 G; 714 T; 0 U; 0 Other;
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128
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85.03%
68.45%
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LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro

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143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162

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fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene in an expression of the gene that expression vector not exposed to the agent, treating a subject with the agent and identifying fat cell number or size in the subject. The agent comprises an antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
                                                                                                                                                                                                                                                                    IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of identifying compounds that influence
                                                                                                                                                                               CTACGGAGGCTCTTCCTGGTCCAGGACCTGGTGGATTCCTTAAAATTTGCAGTCCTCATG
                                                                                                                                                                                                                                             TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu
GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu
                                                                                                                                                        LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fat cell number; fat cell size; obesity; diabetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLeuLysArgLysAlaGlu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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anorectic; antidiabetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to nucleotide sequences which are useful the screening of compounds for the treatment of pain, or for the diagnosis of pain. The nucleotide sequences are up-regulated in the spinal cord in response to streptozocin-induced diabetes. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValIleGlnAlaIleGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of isolated gene sequences and encoded polypeptides that are upregulated in the spinal cord in response to streptozocin-induced diabetes for screening compounds for the treatment of pain, or for
                                                                                                                                                                                                                                                                                                                               Analgesic; pain; streptozocin-induced diabetes; rat; gene; ds
                                                                                                                                                                                                                                                                                    Rat rS-Rex-s human NSP C homolog coding sequence, SEQ ID 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1502 BP; 348 A; 392 C; 363 G; 399 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                         183 GlyLeuLysArgLysAlaGlu 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is one such nucleotide
                                                                                                                                                    ADB79854 standard; DNA; 1502 BP
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07-FEB-2002; 2002GB-00002910.
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P-PSDB; ADB79853.
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Best Local Similarity:
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Bovine EST associated with lactation/muscle/fat deposition #11567

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                     method also comprises providing a polypeptide and an agent, exposing the polypeptide to the agent, detecting binding of the agent to the polypeptide or a change in an activity of the polypeptide, treating a subject with the agent and identifying fat cell number or size in the subject. The agent comprises an antibody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents mouse cDNA used in the scope of the invention.
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preferably a human.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2343 BP; 536 A; 710 C; 646 G; 451 T; 0 U; 0 Other;
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21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle 40
                                                                                                                                                                                                                           New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                            muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence was not shown in the specification but was obtained in
                       Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
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(MATH/) MATHIALAGA
(TAON/) TAO N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of gene sequence that is down-regulated in response to streptozocin-
induced diabetes, vector, host cell, animal, polypeptide and antibody, in
screening of compounds for treating or diagnosing pain.
                                                                                                                                                                                                           AAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTG 303
                                                                                                                                                                                                                                               LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                                                                                                                                                                                             TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated gene sequence that is down-regulated in the spinal cord in response to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence identity to a sequence whose expression products are kinases, phosphatases, ion channel proteins, receptors, transporters, G-protein coupled receptor proteins, DNA-binding proteins, proteases or enzymes, given in the specification. A gene of the invention has analgesic activity, and may have a use in gene therapy. The gene sequences, vector,
                                                                                                                                           SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
                                                                                                                                                                    TCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATA 243
                                                                                                                                                                                            LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
                                                               GCCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCT 123
                                                                                                                124 ATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATA 183
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                                                                                                                                                                                                                                                                                                AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIle 159
                                                                                                                                                                                                                                                                                                              364 GCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rat; streptozocin; kinase; phosphatase; ion channel protein; receptor; transporter; G-protein coupled receptor; GPCR; DNA-binding proteins; protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.
11eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                       AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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07-FEB-2002; 2002GB-00002880.
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host cell, animal, polypeptide and antibody are useful for screening of compounds for diagnosing or treating pain. The kits are useful for simultaneous, separate or sequential detecting and/or quantifying downregulation of a gene sequence in the spinal cord of a mammal in response to streptozocin-induced diabetes. The compound or pharmaceutical composition is useful as a medicament for treating or diagnosing pain. The present sequence represents a gene of the invention.
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Matches:
Conservative:
Mismatches:
Indels:
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665.00
85.03%
67.91%
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Best Local Similarity:
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No.:
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                                                                                                                                                                                                                                                           rleuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Full length human cDNA useful for treating neurological disease Seq 471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; ss; human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                                  2294 FGGCTCCTGACCTTGGCGCTCTTGCAATGGCCTGACCCTGCTGCTGCTGTGT
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                                                                          TrpValPheThrTyrValGlyAlaLeuPhe-AsnGlyLeuThrLeuLeuIleLeuAlaLe
                                                                                                                                                                                             2354 GGTTTCAATGTTTACTCTACCTGTAGTGTATGTTAAGCACCCAGGCACAGATTGACCAATA
                                                                                                                                                                                                                                                                                        2414 TCTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGGCAAAGATTCAGGCTAAAATCCC
                                                                                                                                                                   142 ulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTy
Sugiyama T,
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Irie R;
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Nagai K, I
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A, Ishii S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in some therapy. (I) and sasays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for disgnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology
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    neuroprotective; gene therapy; cancer; immunopathology; neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1994 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGGTGAGCGTCGTGGCCTACCTGGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                New cell and tissue specific polynuclectides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3279 BP; 814 A; 905 C; 850 G; 710 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 312-313; 327pp; English.
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84.04%
67.55%
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                                                                                                                                                                                                                                                                               GENOMICS
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                                                  Homo sapiens.
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they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polynucleotide is a full length human CDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained
                                                                                                                                                                                                                                             61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HP02061; transmembrane domain; Saos-2; homology;
heuroendoorine-specific protein C; antibody; assay reagent;
diagnostic marker; primer; probe; antisense; gene therapy; agonist;
antagonist; ligand; therapeutic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human transmembrane protein cDNA clone HP02061 coding sequence
                                                              Sequence 4607 BP; 1428 A; 944 C; 945 G; 1290 T; 0 U; 0 Other;
                                         from the European Patent Office, Vienna Sub-office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 ACGCTGATCATGCTGCTTTCCCTGCCTTTCAGTGTCATCAGTGTGTCTTCTTACCTC 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human proteins with transmembrane domains, involved in control of c
proliferation and differentiation, useful for treating e.g. cancer
                                                    /*tag= a
/product= "Human transmembrane protein HP02061"
/note= "No stop codon given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 708 BP; 158 A; 195 C; 169 G; 186 T; 0 U; 0 Other;
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                                                                                                                                                               41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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                                              x ADK67496 (1-711)
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Mismatches:
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                                              US-09-830-972-29_COPY_990_1178 (1-189)
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CACTATGTIGGCATCGCCCGAGATCAGACCAAGTCAATTGTIGAAAAGATCCAAGCAAAA 678
                                                                                                                   AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp 160
                                                                                                                                                                HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide having BACE1 activity, useful in preparing a composition for treating amyloidosis or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polypeptide having BACE1 activity. The protein is RTM4 or RTM3 protein. The polypeptide is useful in preparing a composition for treating amyloidosis or Alzheimer's disease. This sequence corresponds to the RTM'3 gene.
                                    379 TCCTCAGAAGCTTTCCATAATTACATGATGCTGCCATGGTGCACATCAACAGGGCCCTG
                        LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                         ds; neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3; amyloidosis; Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                    Human RTN-3 cDNA sequence.
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P-PSDB; ADK67497.
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AAX60810 standard; DNA; 1656 BP.
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98US-00197886.
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Treacy №
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Query Match:
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Merberg D,
Fechtel K;
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                                                                                                         Cancer-associated nucleic acid molecules (N) and proteins (P), where the cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P carcinomas and cancers. Additionally and Additionals. N and P carcinomas and cancers. Additional colorectal sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at the color of the process are present for SEQ ID NO:1027
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                                               4277 human colon cancer-associated polypeptides, diagnosing and/or treating colorectal cancers.
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                                               Nucleic acids encoding 4277 human colon cancer-associated
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                                                                                     Claim 1; Page 3443; 9803pp; English.
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                                                             useful for preventing,
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           2001-235357/24.
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           WPI; 2001-235357/
P-PSDB; AAG75448.
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30-MAR-2000; 2000US-00539330. 04-DEC-2000; 2000US-00729674. 22-MAR-2001; 2001WO-US009369

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AAACTCATTATTCGTCTCTTTCTCGGTAGAAGATCTGGTTGACTCCTTGAAGCTGCTGTTTC 524
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                                                                                   41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                        285 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or centarion of other cytokines cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune suppressing activity, which is useful for the treatment of various immune components and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus exthematosia arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders combined in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, disease, Huntington's disease, amylotrophic lateral contral nervous system vessel e.g. stroke, sepsis, inflammatory bowel central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or contral nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as four supplements. The proteins and nucleic acids are also received any and activity of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of the invarion of 
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                                                                                                                                                                                                                                                                                                                                                Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke).
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Agostino MJ, Steininger RJ, Spaulding V, Wong GG,
Merberg D;
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Fechtel K,
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Treacy M.
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New secreted proteins and encoding polynucleotides, useful in gene therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or

Claim 13; Page 191-192; 349pp; English

inflammations.

Collins-Racie LA, Evans C; Steininger RJ, Spaulding V;

Lavallie ER, 4, Agostino MJ, Fechtel K;

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(AGOS/)

AGOSTINO M J. STEININGER R J SPAULDING V. WONG G G.

FECHTEL K.

(SPAU/) (WONG/) (CLAR/) (FECH/))

Jacobs K, Mccoy um, Merberg D, Treacy M,

WPI; 2002-040725/05.

P-PSDB; ABB55707

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                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; crohn's disease; chactic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.
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                                                                                                                                                                                                     HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlle 100
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               121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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97US-0067454P.
97US-0068379P.
98US-0070643P.
98US-007055P.
98US-0072134P.
                                                                                                                                                                                                                                                                                                                                   ABA90885 standard; cDNA; 1656
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20-DEC-1997;
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The invention relates to isolated polymucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB55800), especially composed by the polymucleotides SEQ ID NO 16 (ABA908707) contained in proteins SEQ ID NO 16 (ABB55707) contained in cromes bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 care deposited with the American Type Culture Collection (ArCO with accession number 98599. The polymucleotides and encoded polypeptides have cycostatic, anti-inflammatory, immunomodulator, vulnerary, cultiammatory activity and acting as cytokine modulators, cand anti-inflammatory activity and acting as cytokine modulators, cand anti-inflammatory activity and acting as cytokine modulators, cand anti-inflammatory fissue growth modulators and/or cadherin guppressors. The polypeptides and polymucleotides are useful in gene therapies, particularly for preventing, treating or ameliorating and corting or fungal infections, autoimmune disorders, cancer, systemic lupus corting infections, autoimmune disorders, cancer, systemic lupus deficiencies; wound, burns, incisions and ulcers, osteoporosis or costeoarthritis; central and peripheral nervous system diseases and controphic lateral sclerosis or systemic inflammations, shock, sepsis corting and controphic lateral sclerosis or stroke; inflammations, shock, sepsis corting and peripheral cardiac infarction or stroke; inflammations, shock, sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease; or tumours or cancers, pemphigus vulgaris or pemphigus foliaceus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endotoxin lethality, arthritis, inflammatory bowel disease or Crohn'
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98US-00197886 2000US-00539330

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COLLINS-RACIE MCCOY J M. LAVALLIE E

JACOBS K.

(JACO/) (MCCO/) (LAVA/)

30-MAR-2000;

EVANS C. MERBERG D. TREACY M.

(COLL/) (EVAN/) (MERB/) (TREA/)

other cytokines in certain cell populations

production of

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SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
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                525 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTTAACGGAATCACCCTTCTAATTCTT
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                                                                                                                                                                                                               HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                             Bone marrow secreted protein, bone marrow stromal cell; cytokine, cell proliferation; cell differentiation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; erythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; bone fracture; cartilage damage; artificial joint; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding a bone marrow secreted protein designated BMS240.
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/product= "bone marrow secreted protein"
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98US-0101603P.
98US-0102540P.
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New isolated human polynucleotide and secreted proteins can induce

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AAZ36228-49 encode bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell lines, to reficiencies. In addition, they may be used to support the growth and proliferation of erythroid progenitor cells, and to treat various anemias. They can have colony stimulating factor (GSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo.

Cyproliferation of bematoportic stem cells, either in place of or in conjunction with platelet transfusions, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet conjunction with platelet transfusions, to treatment of platelet conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anaemia and paroxysmal nocturnal hemoglobinutia, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions confunction eartilage and/or bone growth in circumstances where the confunction or confunction or called the anaemia and paroxysmal prophylactic use in fracture and cartilage canding some an application in healing bone fractures and cartilage was enaemial and publication or prophylactic use in fracture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the improved fixation of artificial joints
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 435 A; 414 C; 349 G; 470 T; 0 U; 0 Other;
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                                        Claim 11; Page 98-100; 120pp; English.
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Gaps:

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US-09-830-972-29_COPY_990_1178 (1-189) x AAZ38319 (1-1759)
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                         776
HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human proteins with transmembrane domains, involved in control of cell proliferation and differentiation, useful for treating e.g. cancer or
             neuroendocrine-specific protein C; antibody; diagnostic marker; primer; probe; antisense; gene therapy; agonist; antagonist; ligand; therapeutic; ds.
                                                                                                                                                                                                                                                                                                                                         /product= "Human transmembrane protein HP02061"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                            Human transmembrane protein cDNA clone HP02061.
                                              181 IleProglyLeu---LysArgLysAlaglu 189
                                                             Claim 4; Page 92-94; 114pp; English.
                                                                                                                                                                                                                                                                                                     location/Qualifiers
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                                                                                                                                                                                SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                                41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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This sequence represents a nucleic acid molecule designated Gene 92 from the human cDNA clone HAUBLS7 (deposited as clone ATCC 97897 and ATCC 909043) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW7731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in a sample or by generating the presence of mutations in the new polynucleotides. Based on which tissues are described for each of the 186 polynucleotides, based on which hissues they are most highly expressed in (see AAV59511 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 473-474; 721pp; English.
                                          970S-0056819P-
970S-0056881P-
970S-0056881P-
970S-0056884P-
970S-0056886P-
970S-0056889P-
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97US-0056911P.
97US-0057650P.
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97US-0056878P
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97US-0061060P
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P-PSDB; AAW74963.
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12-SEP-1997;
02-OCT-1997;
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Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

1766 115 39 35 Conservative: Mismatches: Indels: Length: Matches: Gaps: 9.34e-66 624.50 81.05\$ 60.53\$ 67.08\$ Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: .. Q

x AAV59748 (1-1766) US-09-830-972-29_COPY_990_1178 (1-189)

1 ServalvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

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9705-0043671P-
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                      SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
                                                                                                                                                                                                                                                                                                                                    41 AlaLeuAlaLeuLeuSerValThrIleSerPheArglleTyrIysGlyValIleGlnAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn; nervous system disorders, Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional.
                                                                                                            LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                                                                                                              647 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTTAACGGAATCACCCTTCTAATTCTT
                                                                407 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT
                                                                                                                                                                                                           HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
        21 SerteuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA #2 for novel secreted protein gene 92.
                                                                                                                                                                                                                                                                                                                                                                     181 IleProGlyLeu---LysArgLysAlaGlu 189
                                                                                                                                                                                                                                                                                                                                                                                  827 CTCCCTGGAATCGCCAAAAAAAAAGGCAGAA 856
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97US-0040161P.
97US-0040163P.
97US-0040333P.
97US-0040334P.
97US-0040336P.
97US-0040336P.
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07-MAR-1997;
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347 ACGCTGATCATGCTGCTTTCCTGCCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCTC 406

21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification, encoded by one of 309 cDNA condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. Contromerase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a cDNA derived from a gene encoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was contend in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                      Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * isolated human secreted protein for diagnosing, preventing, treating ameliorating medical conditions and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                   Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Gr Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 254; 129pp; English.
             97US - 0056887P
97US - 0056887P
97US - 0056889P
97US - 0056892P
97US - 0056913P
97US - 0056913P
97US - 0056910P
97US - 0056911P
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97US-0058785P.
97US-0061060P.
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                                                              22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
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SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

39 35

Matches: Conservative: Mismatches:

Indels:

Length:

9.34e-66 624.50 81.05% 60.53% 67.08%

Percent Similarity: Best Local Similarity:

Best Local S Query Match:

US-09-830-972-29_COPY_990_1178 (1-189) x ABS73741 (1-1766)

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Human, secreted protein; hyperproliferative disorder; leukaemia;

Whereast cancer; wound; reproductive disorder; blood-related disorder;

When peophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;

Whiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;

When infection; bacterial infection; fungal infection; AIDS; sepsis;

When infection; bacterial infection; congenital heart defect;

Respiratory disorder; neurological disorder; Alzheimer's disease;

Mangina pectoris; cerebral ischaemia; congenital heart defect;

Respiratory disorder; neurological disorder; Alzheimer's disease;

Mantinosuppressive; antibacterial; haemostatic; thrombolytic;

Manticoagulant; neuroprotective; thyromimetic; antiallergic;

Mantiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;

Mantischaemian;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA sequence #244 containing coding region of a human secreted protein.
                              61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                      467 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 AlaLeulleSerLeuPheSerValProVall1eTyrGluArgHisGlnAlaGlnIleAsp
41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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970S-0038621P
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22-AUG-1997
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New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral
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Greene JM, Ferrie AM;
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'Yu G, Ni J, Feng P, Young PE, Greene JM,
Hu J, Florence KA, Olsen HS, Fischer CL, Ebne
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z,
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Brewer LA, Moore PA,
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NI J.
FENG P.
YOUNG P E.
GREENE J M.
FERRIE A M.
DUAN D R.
HU J.
FLICCHER C A.
OLSEN H S.
EISCHER C L.
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ROSEN C A.
SOPPET D R.
CARTER K C.
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P-PSDB; ABO34617.
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SHI Y.
LAFLEUR D W
LI Y.
ZENG Z.
KYAW H.
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Endress GA, Yu G
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08-SEP-1998;
17-MAR-2000; 2
22-AUG-1997;
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The present invention relates to the isolation of novel human secreted proteins and the polynucleotide sequences encoding them. The invention

Claim 4; SEQ ID NO 254; 260pp; English.

schemia.

ADI22969 standard; cDNA; 1766 BP.

ADI22969

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also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polynucleotide sequences for the secreted proteins are useful for preventing, treating, sequences for the secreted proteins are useful for preventing, treating, disorders (e.g. leukaemia or breast cancers), wounds, reproductive disorders (e.g. leukaemia or breast cancers), wounds, reproductive disorders, blood-related disorders (e.g. wiskott-Aldrich syndrome or thrombocytopaenia), immunodeficiencies (e.g. wiskott-Aldrich syndrome or thrombocytopaenia), immunodeficiencies (e.g. wiskott-Aldrich syndrome or thrombocytopaenia), incumune disorders (e.g. graft-versus-host disease, within or fungal infections (e.g. AIDS or sepsis), renal disorders (e.g. kidney failure), cardiovaecular disorders (e.g. Angina pectoris, cerebral ischaemia or congenital heart defects), respiratory disorders, unuclogical disorders (e.g. Alzheimer's disease). The polynucleotide or polypeptide may also be used as vaccine adjuvants. ACDB2641-ACDB2950 encode human secreted proteins or their fragments.

ACDB2641-ACDB2950 encode human secreted proteins or their fragments.

C.C. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USDFTO web site at seqdata.uspto.gov/psipsDIDEntry.html
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RESULT

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cytostatic; gene therapy; cancer; human; secreted protein; gene;
                                           cDNA encoding novel human secreted protein seq id 254.
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9705-0043670E

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                            (first entry)
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                                                                          Homo sapiens.
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YOUNG P E.
GREENE J M.
FERRIE A M.
DUAN D R.
HU J.
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FISCHER C L.
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BREWER L A.
MOORE P A.
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SOPPET D R.
CARTER K C.
BEDNARIK D P.
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NI J.
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08.-UL-1997;
16.-UL-1997;
18.-AUG-1997;
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(SHIY/)
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The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the CDNA sequence; a polynucleotide sequence encoding a polynpeptide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of polynucleotide that hybridises under stringent conditions to any one of medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer. The sequence encodes a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCAAGCT
                                            Rosen CA, Soppet DR, Carter KC, Bednarik DP; , Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM, Hu J, Florence K, Olsen Mozee PA, Shi Y, Laffeur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                      New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition
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81.05%
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P-PSDB; ADI23278.
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Best Local Similarity:
                                            Ruben SM, Rosen
Endress GA, Yu C
Duan DR, Hu J,
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
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161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180

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Isolated nucleic acid molecules encoding human secreted proteins, useful for preventing, diagnosing and treating disorders associated with aberrant expression and activity.
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Endress GA, Yu G, Ni J, Feng P, Young PB. Greene JM, Ferrie AM;
Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Enber R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                 97US - 0047599P - 97US - 0047601P - 97US - 0047601P - 97US - 0047613P - 97US - 0047614P - 97US - 0047611P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047613P - 97US - 0047632P - 97US - 0047632P - 97US - 0047632P - 97US - 0047633P - 97US - 0047633P - 97US - 0047633P - 97US - 0047633P - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 97US - 
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P-PSDB; ADH74280.
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      human; secreted protein; cancer; haematopoietic disorder; endocrine disorder; immune system disease; inflammatory disorder; ss;
                                             181 IleProGlyLeu---Ly8ArgLy8AlaGlu 189 :::|||||||||| 827 CTCCTGGAATCGCCAAAAAAAGGCAGAA 856
                                                                                                                                                                                                                                 Human secreted protein cDNA #244.
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970S-0040161P-
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ADM36177 standard; DNA; 1911 BP.

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RESULT 80
ADM36177
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                               The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPB) they encode. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haemacopoietic disorders, endocrine disorders, diseases of the immune system, inflammatory disorders and many others. Full details of disorders than may be prevented, diagnosed and/or treated by the above methods are given in the specification. The nucleic acid molecules may be used to produce their proteins. The nucleic acid and it's complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patients may be in need of restorative therapy. The SPs may also be used as antigons in the production of antibodies against the proteins and in assays to identify modulators of SP expression and activity. The anti-SP antibodies and antagonists may also be used to down regulate expression and activity. The anti-SP antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 ATCCTGGCTCTTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-830-972-29_COPY_990_1178 (1-189) x ADH73971 (1-1766)
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents a human secreted protein cDNA.
Claim 3; SEQ ID NO 254; 142pp; English.
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67.08%
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Query Match:
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The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (1) of the RTW (reticulon)3 gene. Differential expression of RTM3 is a specific marker of meuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular disorders, specifically amyotrophic lateral sclerosis (Abs) and myopathy. Also (1) antibodies specific for isoforms of RTM3 or oligonucleotides (antisense sequences or small interfering RMA) that can block/reduce expression of these isoforms are useful for treating neuromuscular diseases and (ii) cells that express RTM3 are useful in screening for therapeutic agents. The present sequence is a RTM3 DNA sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing, prognosing and monitoring neuromuscular disease, particularly amyotrophic lateral sclerosis, comprises detecting modulation of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loeffler J;
C, Rene F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1911 BP; 488 A; 463 C; 406 G; 554 T; 0 U; 0 Other;
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                                                                                                              Human RTN3 isoform VI coding sequence, SEQ ID 60.
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/product= "RTN3 isoform VI"
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Boutillier AL,
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                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                     03-JUN-2004 (first entry)
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Gonzales De Aguilar J,
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P-PSDB; ADM36178.
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ADM36177;
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Human; cytokine; cell proliferation; cell differentiation; growth factor; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastesis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastesis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; athritis; chronic inflammatory condition; proliferative retinopath; atherosclerosis; coronary heart disease; arterial ischemia; bone disorder; osteoporosis; vascular growth disorder; tissue respeneration; wound healing; infection; immune disorder; etll culture; drug screening; gene therapy; antiaflammatory; antiasthmatic; antiaxthritic; haemostatic; antiaxteriosclerotic;
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                 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
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21 SerbeupheLeuleuleuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
                                                                                                                            61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                              382 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT
                                                             41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLygGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                               TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCTT
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27-APR-2000; 2000US-00560875.
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB10981-ABA09574 represent nucleic acids encoding them. The current on also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides of the invention, methods of detecting the nucleotides controlled to a sample, and methods of detecting the nucleotides or polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence to polypeptides of the invention by probable biological activities, and hence to potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activity; activity; issue growth activity; memucopoleists regulatory activity; tissue growth activity; immunoulatory activity; activities, or inhibin-related activities; chemotactic or chemokinetic activities; neeptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Comparing on their biological activities; polypeptides and nucleotides of the invention are useful for preventing, treating or amaliorating medical conditions, e.g., by protein or gene therapy. Such conditions include disorders, heamatopoletic disorders (e.g., myebiol or 1 ymmhol, cell or proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, conditions, e.g., by protein or gene therapy. Such conditions include disorders, changed encoding and ulcers), while those which healing (e.g., of burns, incisions and ulcers), while those with immunomedulatory activities may be used in the treatment of viral, metaling (e.g., of burns, incisions and ulcers), while those when the anipulate stem cells in culture to give rise to neuroepithelia or properties or aucoimmune disease or accidental damage. The polypeptides may be used in the disapones. The p
                                                                                                                                    nan proteins and DNA encoding sequences useful for preventing, treating ameliorating a medical condition in a mammalian subject e.g. arthritis
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                                                                                                                                                                                                                                     Claim 1; Page 838; 1963pp; English.
                      Liu C, Drmanac RT;
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                                                                2001-457740/49.
                                                                                                                                         Human proteins and
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Sequence 1915 BP; 492 A; 463 C; 411 G; 549 T; 0 U; 0 Other; 1915 115 39 35 Length: Matches: 1.05e-65 624.50 81.05% 60.53% 67.08% Alignment Scores:

Conservative: Mismatches:

Indels:

US-09-830-972-29_COPY_990_1178 (1-189) x ABA09204 (1-1915) Query Match:

Best Local Similarity:

Percent Similarity:

21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla ठ 셤 ò

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 80
             LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                    TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCTT
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                                                SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlle
                                                                LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                  AlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
                                                                                                                                                                                                                                                          HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                                                                                                                                   CACTATIGTTIGGCATCGCCGAGATCAGACCAAGTCAAATTGTTGAAAAGATCCAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding secretory proteins/membrane proteins, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding a membrane or secretory protein clone PSEC0103.
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                                                                                                                                                                                                                                                                                                           IleProGlyLeu---LysArgLysAlaGlu 189
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11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
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therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (BLISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                   HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
                                                                                                                                                                                                                                                                                      101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu
                                                                                                                                                    141 AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp
                                                                                                                                                                                                                    Human secreted protein gene 92 clone HAUBL57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene NSPL1 with expression difference in human normal neuroglia cell and neuroglia cell tumor.
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                                                                                                 ss; gene; human; neuroencocrine specific protein linked gene; hNSPL1; glia cell; tumour; nervous system disease.
                                                                Human neuroencocrine specific protein linked gene, hNSPL1, cDNA.
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                                                                                                                                                                                   Location/Qualifiers
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/product= "hNSPL1"
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Greene JM;
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                                                                                                                                                                                                                                                             New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                            Rosen CA, Fischer CL, Soppet DR, Carter KC;
DP, Bndress GA, Yu G, Ni J, Feng P, Young PE, Gr
4, Duan R, Hu J, Florence KA, Olsen HS, Ebner R,
Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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                                                                                                (HUMA-) HUMAN GENOME SCI INC.
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Ferrie AM, Duan R,
Moore PA, Shi Y,
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501

TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTG

SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThr1le

81

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502

LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal

382 ATCCTGGCTCTTCTCTCTGTCACCTTCAGGATCTACAAGTCCGTCATCCAAGCT

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41 AlabeuAlaLeuLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAla

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  HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
            121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
                                                                                                           801
                                                                                                                                                                                                                                                                 Human; ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional.
                                                                                                 622 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTTAACGGAATCACCCTTCTAATTCTT
                                                                                                                                                                                                                                                 Human cDNA #3 for novel secreted protein gene 92
                                                                                                                             IleProGlyLeu---LysArgLysAlaGlu 189
                                                                                                                                        ABS73742 standard; cDNA; 2664 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0038621P.
97US-0040161P.
97US-0040163P.
97US-004033P.
97US-0040331P.
97US-0040331P.
97US-00403312P.
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                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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11-APR-1997;
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                                                                                        161
                                                                                                                                                                    RESULT 85
                                                                                                                                                                            ABS73742
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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a pharmaceutical composition used to prevent, treat or ameliorate a medical pharmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, or the polypeptides can also be used to aid wound healthelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. The carbohydrate, vitamins, minerals, cofactors and other nutritional concents of the present sequence represents a cDNA derived from a gene encoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was concent and the concent are concent.
                                                                               Greene JM;
, Brewer LA;
                                                                                                                                                                                                                                                                      New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or
                                                Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Gr Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    segdata.uspto.gov/sequence.html?DocID=6420526B1
                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 255; 129pp; English
(HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                         2002-634796/68.
                                                                                  Bedhar Perrie AM, Duam Perrie AM, Shi Y,
                                                                                                                                                                                      WPI; 2002-634796/
P-PSDB; ABG95424.
                                                                                                                                                                                                                                                                                                                                  preservative.
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Alignment Scores

Alignment Scores: Pred. No.:	Scores:	1.668-65	Length:	2664	
Score:		624.50	Matches:	115	
Percent S	Percent Similarity:	81.05%	Conservative:	39	
Best Loca	Best Local Similarity:	60.53%	Mismatches:	35	
Query Match:	ch:	67.08%	Indels:	ਜਜ	
		D	Gapa:	4	
US-09-830	-972-29_COPY_9	US-09-830-972-29_COPY_990_1178 (1-189) x ABS73742 (1-2664)	x ABS73742 (1-;	2664)	
ò	1 Servalval	AspleuleuTyrTrpA	rgAspileLysLys	ServalvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValvalPheGlyAla 20	
qa	262 GCGGTGCAC	 GATCTGATTTTCTGGA	 GAGATGTGAAGAAG	::: ::::::	
δ	21 SerLeuPhe	leuleuleuSerleuT	hrValPheSerIle	ValTh	
Ωp	322 ACGCTGATC	:::			
È	41 AlaLeuAla	LeuLeuSerValThrI	leSerPheArgile	AlaLeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAla 60	
qq	382 ATCCTGGCT	CTTCTCTCTGTCACCA	TCAGCTTCAGGATC	ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 441	
È	61 IleGlnLys	SerAspGluGlyHisP	ropheArgAlaTyri	IleGinLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80	
Ор	442 GTACAGAAG	:::	CATTCAAAGCCTAC		
ò	81 SerGluGlu	LeuValGlnLysTyrS	erAsnSerAlaLeu	Æ	
qq	502 TCCTCAGAA	 AGCTTTCCATAATTACA	::: ::: TGAATGCTGCCATGGT		
È	101 LysGluLeu	uArgArgLeuPheLeuV	alAspAspLeuVal <i>i</i>	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120	

11-APR-1997

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Human; secreted protein; hyperproliferative disorder; leukaemia; breast cancer; wound; reproductive disorder; blood-related disorder; haemophilia; thrombocytopeania; immunodeficiency; thymic hypoplasia; wiskott-Aldrich syndrome; autoimune disorder; multiple sclerosis; wiskott-Aldrich syndrome; autoimune disorder; multiple sclerosis; wiral infection; hand infection; hand infection; hand infection; hall special infection; hand infection; hall special infection; hand special infection; and sorder; wind disorder; kidney failure; cardiovascular disorder; cytostatic; angina pectoris; cerebral ischaemia; congenital heart defect; respiratory disorder; neurological disorder; Alzheimer's disease; randionistatory disorder; hardological disorder; Alzheimer's disease; will amunosuppressive; antibacterial; haemostatic; thrombolytic; antianglant; neuroprotective; thyromimetic; antianlergic; antianglami; cerebroprotective; antianginal; cerebroprotective; antianginal; antiinflammatory; gene; ss.
140
                                                        160
                                                                                                              161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                 cDNA sequence #245 containing coding region of a human secreted protein.
                                          121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeu
                                                                                              141 AlaLeuileSerLeuPheSerValProValileTyrGluArqHisGlnAlaGlnIleAsp
                                                                                                                                                                                                       181 IleProGlyLeu---LysArgLysAlaGlu 189
                                                                                                                                                                                                                       802 CTCCCTGGAATCGCCAAAAAAAAAAGGCAGAA 831
                                                                                                                                                                                                                                                                                       ACD82885 standard; cDNA; 2664
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97US-0043670P.
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97US-0061660P.
98WO-US004493.
98US-00149476.
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
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FLORENCE K A.
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FISCHER C L.
EBNER R.
BREWER L A.
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NI J.
FENG P.
YOUNG P E.
GREENE J M.
FERRIE A M.
DUAN D R.
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LAFLEUR I
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ZENG Z.
KYAW H.
22-AUG-1997;
05-SEP-1997;
05-SEP-1997;
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09-OCT-1997;
06-MAR-1998;
17-MAR-1998;
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Bednarik DP; Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP; Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie Al Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R; Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;

WPI; 2003-521800/49. P-PSDB; AB034618

New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral ischemia.

Claim 4; SEQ ID NO 255; 260pp; English.

The present invention relates to the isolation of novel human secreted proteins and the polynucleotide sequences encoding them. The invention also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polynucleotide for producing human secreted proteins are useful for preventing, treating, ameliorating or disgnosing medical conditions such as hyperproliferative disorders (e.g. leukaemia or breast cancers), wounds, reproductive clisorders (e.g. haemophilia or thrombocytopaenia) immunodeficiencies (e.g. haemophilia or thrombocytopaenia), autoimmune disorders (e.g. wiskott-Aldrich syndrome or thymic hypoplasia), autoimmuned disorders (e.g. wiskott-Aldrich syndrome or thymic hypoplasia), autoimmuned of thyroiditis), allergies (e.g. sathma), autoimmune of thyroiditis), allergies (e.g. sathma), autoimmune or thyroiditis), allergies (e.g. sathma), critical or bacterial or fungal infections (e.g. AIDS or sepsis), renal disorders (e.g. Aidsorders (e.g. widney failure), cardiovascular disorders (e.g. angina pectoris, cerebral ischaemia or congenital heart defects), respiratory disorders, neurological disorders (e.g. Alzheimer's disease). The parkinson's disease), and inflammations (e.g. Crohn's disease). The colymucleotide or polympeptide may also be used as vaccine adjuvants.

CRACHS2641-ACD82950 encode human secreted proteins or their fragments.

CRACHS2641-ACD82950 encode human secreted proteins or their fragments.

CRACHS2641-ACD82950 encode human secreted proteins or their fragments.

CRACHS2641-ACD82950 encode human secreted proteins or their fragments.

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SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
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                                                                                                                                                                                           cytostatic; gene therapy; cancer; human; secreted protein; gene; ss
Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;
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                                                                             US-09-830-972-29_COPY_990_1178 (1-189) x ACD82885 (1-2664)
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Matches:
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Mismatches:
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fragment of the cDNA sequence, a polynucleotide sequence encoding a polypeptide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(a). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer. The sequence encodes a novel human secreted
                                                                                                                                                                                                                                                                                      322 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGATGTGTTTTCTTACCTC 381
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                                                                                          Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;
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 97US-0056876P.
97US-0056878P.
97US-0056880P.
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GREENE J M.
FERRIE A M.
DUAN D R.
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OLSEN H S.
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ROSEN C A.
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       Homo sapiens.
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970S-0056877P.
970S-0056877P.
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97US-0056862P.
97US-0056864P.
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97US-0056881P.
97US-0056882P.
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97US-0056892P.
97US-0056893P.
97US-0056994P.
97US-0056908P.
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970S-0056911P.
970S-0057659P.
970S-005761P.
970S-0058781P.
              97US-0056662P
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22-AUG-1997;
22-AUG-1997;
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02-OCT-1997
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(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP; Endress CA, Yu G, Ni J, Fenng P, Young PE, Greene JM, Ferrie AM, Duan R, Hu J, Florence KR, Olsen HS, Fischer CL, Enber R; Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;

WPI; 2004-131264/13. P-PSDB; ADH74281.

Isolated nucleic acid molecules encoding human secreted proteins, useful for preventing, diagnosing and treating disorders associated with aberrant expression and activity.

Claim 3; SEQ ID NO 255; 142pp; English.

The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPB) they encode. The proteins and nucleic acids may be used in the prevention, disgnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoletic disorders, cancer, haematopoletic disorders, cancer, haematopoletic disorders, cancer, haematopoletic disorders, cancer, haematopoletic disorders, cancer, disorders, and many others. Full details of disorders that may be be concerned, disorders and many others. Full details of disorders that may be proteins. The nucleic acid molecules may be used to produce their specification. The nucleic acid molecules may be used to produce their capacities. The nucleic acid molecules may be used to proteins. The nucleic acid molecules may be used to produce their capacities may be in need of restorative therapy. The SPB may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of SP expression and activity. The anti-SP antibodies may also be used as disgnostic and activity. The anti-SP antibodies may also be used as disgnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELSA)). The present sequence

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                                                                                                                                                                                   41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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                 U; 7 Other;
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Matches:
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                 566 G; 779
 protein cDNA
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcome amples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcome. The method of the invention has cytostatic and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
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                                                    (PROT-) PROTEIN DESIGN LABS INC.
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26-NOV-2002; 2002US-0429739P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing, prognosing and monitoring neuromuscular disease, particularly amyotrophic lateral sclerosis, comprises detecting modulation of the reticulon 3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            small interfering RNA) that can bloc \bar{k}/reduce expression of these isoforms are useful for treating neuromuscular diseases and (ii) cells that express RTN3 are useful in screening for therapeutic agents. The present sequence is a RTN3 DNA sequence used to illustrate the invention.
740 GCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 799
                                         HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                       800 CACTATGTTGGCATCGCCCGAGATCAGACCCAAGTCGAATGTTGAAAAGATCCAAGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3; amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.
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C, Rene F;
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Boutillier AL, Gaiddon
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/product= "RTN3 isoform III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                             ADM36171 standard; DNA; 1968 BP
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Gonzales De Aguilar J,
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P-PSDB; ADM36172.
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Length: Matches: Conservative:

1.44e-65 623.50 80.95%

Percent Similarity:

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621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 LeuileSerLeuPheSerValProValileTyrGluArgHisGlnAlaGlnileAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 802 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAACTC 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human, tumour-associated antigenic target, TAT; cytostatic, gene therapy, cancer, cell proliferative disorder, gene; ss.
                                                                                                                                                                                                                                                                                                             82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLys 101
                                                                                 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
                                                                                                                                         LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
                                                                                                                                                                                              42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLygGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                             62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tumour-associated antigenic target (TAT) cDNA sequence #1279.
                                                         x ADM36171 (1-1968)
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-830-972-29_COPY_990_1178 (1-189)
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60.85%
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WU T D.
ZHOU Y.
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WWITD, Zhou Y;

WW TD, Zhou Y;

WW TD, 2004-534300/51.

WE WILL 2004-534300/51.

WE WILL 2004-534300/51.

WE WILL 2004-534300/51.

WE WE WILL SEQ ID NO 1279; 5504pp; English.

The present invention describes an isolated tumour-associated antigenic target (TAX) muclaci acid comprising: (a) any of 4622 nucleotide compensation to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that which disse to (a)-(c). Also described: (1) an expression vector comprising the above expression vector comprising the above expression vector; (3) approcess for producing a polypeptide; (b) an isolated polypeptide comprising the above expression vector; (3) a process for producing a polypeptide; (b) an amino acid sequence encoded by any of the above comprising the above expression vector; (a) an expression of the above expression vector; (b) an amino acid sequence encoded by any of the above comprising the above polypeptide; (b) an amino acid sequence encoded by any of the above comprising the above polypeptide; (a) an isolated polypeptide; (b) an amino acid sequence encoded by the full-comparising the above polypeptide; (a) an isolated polypeptide; (b) an amino acid sequence encoded by the full-comparising the above polypeptide; (b) an amino acid sequence encoded by the full-comparising the above polypeptide; (b) an isolated oligopeptide or (TAY binding organic molecule that binds to the above (mineric polypeptide; (d) an isolated oligopeptide; (d) an isolated oligopeptide or TAY binding organic molecule, in combination of matter compaining the composition of matter contained within the container; (l1) an article of manination organic molecule, in composition of matter contained within the container; (l2) amethod of composition of matter contained within the container; (l2) amethod of composition of matter contained within the container; (l2) amethod of containing a maning an amend of the cell is at least in part dependent upon a growth of the cell is at least in part dependent upon a
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Alignment Scores:

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2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer ||| |||||||||||| 1 GIGCACGATCTGATTTTCTGGAGATGTGAAGAACACTGGGTTTGTCTTTGGCACCGG LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

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62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla1leSer 81

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a) -(c); or (e) a sequence that hybridises to (a) -(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101 102 GlubeuargargbeuPhebeuValaspaspleuValaspSerbeuLysPheAlaValbeu 121 141 161 GAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGATCAC 480 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181 human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss. MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 361 Argregergargaccrarerregregregrerrrrraacceaarcacccrrcraarrerrecr 142 LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis Human tumour-associated antigenic target (TAT) cDNA sequence #3281 New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer Claim 1; SEQ ID NO 3281; 5504pp; English. ProGlyLeu---LysArgLysAlaGlu 189 ccrecaaraaaaaadecadaa 567 ADQ86409 standard; cDNA; 2250 BP. 15-OCT-2003; 2003WO-US029126. 18-OCT-2002; 2002US-0418988P. (first entry) (GETH) GENENTECH INC. WPI; 2004-534300/51. WO2004060270-A2. (WUTD/) WU T D. (ZHOU/) ZHOU Y. Zhou Y; Homo sapiens. 07-0CT-2004 22-JUL-2004. 421 541 ADQ86409; 181 122 182 162 Wu TD, RESULT 92 ADQ86409 ð a ò ద ò 셤 ò d ò g ò 셤

TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

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length coding region of the above nucleotide sequences; or (c) a sequence comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to binding organic molecule that binds to the above polypeptide; (7) a composition of matter comprising the above (chimeric) polypeptide; (7) a composition of matter comprising the above (chimeric) polypeptide; (7) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of the composition of matter contained within the container; (12) methods of the composition of matter contained within the container; (12) methods of the growth of a cell that expresses the above protein; where the growth of the cell is at least in part dependent upon a growth contraining effect of the above protein; (13) a method of determining the protein contraining the protein and sample suspected of containing the protein containing the protein containing the protein and mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expresses the protein described above corganic molecule to a cell that expresses the protein described above corganic molecule to a cell that expresses the protein described above corganic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic and city for a cell that composition is a nethod of the protein for described above. The TAT sequences have cytostatic and city for a cell that expresses the protein described above. The TAT sequences have cytostatic and city is and on the described above. The presence of a protein method are useful for dispositing the protein and in gene containing the protein described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human TAT cDNA sequence from the present invention.
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Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

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241 TCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTGAAA 300
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                                                                                                                       ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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The present invention describes an isolated tundur-associated antigenic target (TAT) nucleic acid comprishing: (a) any of 4622 nucleotide acromptement of (a) or (b); (d) a sequence that has 80% sequence that those 80% or (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a) -(c); or (e) a sequence that hybridises to (a) -(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprishing: (a) an amino acid sequence encoded by any of the above comprishing: (a) an amino acid sequence encoded by the full-clength coding region of the above nucleotide sequences; or (c) a sequence comprishing the above polypeptide; (d) an amino acid sequence of a process or (c) a sequence comprishing the above polypeptide fused to a heterologous polypeptide; (d) a process or producing the antibody; (8) an isolated antigenic target (TAT) a process for producing the antibody; (8) a tumour-associated antigenic target (TAT) a composition of matter comprising to the above polypeptide; (1) a process or producing the antibody; (8) an isolated antigenic target (TAT) a composition of matter comprising the above polypeptide; (1) a matter comprising the above polypeptide; (1) a matter comprising the above protein; (1) an article of manufacture comprising a container of the cell is at least in part dependent upon a growth che composition of matter contained within the container; (12) methods of the cell is at least in part dependent upon a growth che composition of matter contained within the containing the protein of a cell that above protein; (11) a method of determining the protein in a sample suspected of containing the protein in a sample suspected of containing the protein in a sample suspected of containing the fundamental general part or presence of a protein in a sample suspected of containing the fundamental part or presence of a protein in a semple
human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
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                                                                                                                                                                                                                                                                                                                           Human tumour-associated antigenic target (TAT) cDNA sequence #2076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2076; 5504pp; English.
                                                                                      ProGlyLeu---LysArgLysAlaGlu
                                                                                                                                                                                           BP.
                                                                                                                                                                                           ADQ85262 standard; cDNA; 2250
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WU T D.
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cancer; cell proliferative disorder; gene; ss.

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                                                                                          preparing
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disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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                                                                                                                                       human TAT cDNA sequence from the present invention.
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DB:
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The present live for an describes an isolated cumour associated antigenic target (TAT) nucleic acid comprising; (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% equence complement of (a). Or (b) a sequence that has 80% of comprising the above expression vector; (a) a notice or a process for producing a polypeptide; (4) an isolated polypeptide comprising; (a) an amino acid sequence encoded by any of the above comprising; (a) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence comprising the above polypeptide; (b) an amino acid sequence encoded by the full-comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated onlypeptide; (7) a process for producing the antibody; (8) an isolated onlypeptide; (7) a process for producing the antibody; (8) an isolated onlypeptide; (10) a composition of matter comprising to the above polypeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein; (13) a method of cells that express the above protein; (14) a method of cells that expresses the above protein; (14) a method of cells that express the above protein; (14) a method of cells that express the above protein; (14) a method of containing the protein in a sample suspected of containing the protein as ample suspected of containing the protein in a sample surpression or method of containing a container.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
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Best Local Similarity:
                                                                                         WO2004060270-A2
                                                                                                                                                                                                                                                                                              (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                Wu TD, Zhou Y;
                                            Homo sapiens.
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                              LeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle
                                                                                                                          GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                                                          MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAla
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TATGTTGGCATCGCCCGAGATCAGACCAATTGTTGAAAGATCCAAGCAAAGTC
                     ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                   LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                    ene expression profile, hepatotoxicity, liver, toxicity assay; ds.
      US-09-830-972-29_COPY_990_1178 (1-189) x ADQ83313 (1-2250)
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2002US-0364055P.
2002US-0436643P.
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screening; tox
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15-MAR-2002;
15-MAR-2002;
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The present invention relates to a method for predicting a toxic effect
of a compound. The method comprises preparing a gene expression profile
of a tissue or cell sample exposed to the compound, and comparing the
differential expression of the gene indicates at least one toxic effect.

The method is useful for predicting at least one toxic effect of a compound, identifying an agent that modulates the onset or
progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed profile to the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of t
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Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
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                                                                                                                                                                            Claim 1; SEQ ID NO 3915; 1156pp; English
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1705 CTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCTGTA 1764
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2065 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAACTC 2124
                                                                                                                                                                                                                                                                                                                                                                                                                                        102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                                                                                                                                             82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                                                                                                                                                                                                                   2 ValvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                  22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                                                                                  142 LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis
                                                                                                                                                                                                 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                              62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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US-09-830-972-29_COPY_990_1178 (1-189) x ADM36175 (1-3231)
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124. .2211
/*tag= a
/product= "RTN3 isoform II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Tapia M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM36169 standard; DNA; 3288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prognosing and monitoring neuromuscular disease, particularly lateral sclerosis, comprises detecting modulation of the
747 CACTATGTTGGGGATTGCCCGGGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAG 806
                                                                                                                                                                                                                                                                                                                        Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3; amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.
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Boutillier AL, Gaiddon C, Rene F;
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                  SEQ ID 58.
                                       181 Ileprodlyteu---tysArgtysAlaglu 189
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Matches:
                                                                            807 cricciccaarccccaaaaaacccagaa 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "RTN3 isoform V"
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                                                                                                                                                                                                                                                                                Human RTN3 isoform V coding sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
124. .2154
/*tag= a
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                                                                                                                                                              ADM36175 standard; DNA; 3231
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80.95%
60.85%
66.97%
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Gonzales De Aguilar J,
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P-PSDB; ADM36176.
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Best Local Similarity:
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Query Match:
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141

182 ProGlyLeu---LysArgLysAlaGlu 189

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The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (1) of the RTN (reticulon)3 gene. Differential expression of RTN3 is a specific marker of method is allowing early diagnosis from readily available meucle biopsies. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular disorders, specifically comportension or therapy of) neuromuscular disorders, specifically specific for isoforms of RTN3 or oligonucleotides (antisense sequences or small interfering RNA) that can block/reduce expression of these isoforms is mail interfering neuromuscular diseases and (ii) cells that express RTN3 are useful in screening for therapeutic agents. The present sequence is a RTN3 DNA sequence used to illustrate the invention.
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                                                                             Diagnosing, prognosing and monitoring neuromuscular disease, particularly amyotrophic lateral sclerosis, comprises detecting modulation of the reticulon 3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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   Rene F;
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115
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 Gaiddon C,
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Matches:
Conservative:
Mismatches:
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 Boutillier AL,
                                                                                                                                           Claim 35; SEQ ID NO 52; 116pp; French.
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623.50
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Gonzales De Aguilar J,
                            WPI; 2004-071743/07.
P-PSDB; ADM36170.
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Best Local Similarity:
Query Match:
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The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (1) of the RTM (reticulon)3 gene. Differential expression of RTM3 is a specific marker of neuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular disorders, specifically amyotrophic lateral sclerosis (ADS) and myopathy. Also (1) antibodies specific for isoforms of RTM3 or oligonucleotides (antisense sequences or small interfering RTM3) that can block/reduce expression of these isoforms small interfering neuromuscular diseases and (ii) cells that express RTM3 are useful in screening for therapeutic agents. The present sequence is a RTM3 DNA sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing, prognosing and monitoring neuromuscular disease, particularly amyotrophic lateral sclerosis, comprises detecting modulation of the reticulon 3 gene.
                                                                                                                                                                                                            Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3; amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.
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C, Rene F;
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115
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                                                                                                                                                                             Human RTN3 isoform VII coding sequence, SEQ ID 62.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Boutillier AL, Gaiddon
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/product= "RTN3 isoform VII"
2182 CCTGGAATCGCCAAAAAAGGCAGAA 2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 35; SEQ ID NO 62; 116pp; French.
                                                                                                                                                                                                                                                                                       Location/Qualifiers
163. .3015
                                                                          ADM36179 standard; DNA; 4092
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Gonzales De Aguilar J,
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                                                                                                            ADM36179;
                                             RESULT 98
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Best Local Similarity:

Query Match:

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2004-071743/07
                                           P-PSDB; ADM36174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 LeulleSerVelProValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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                                              LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                            LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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                       ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                             82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                                                                                                                                                                                          GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human RTN3 isoform IV coding sequence, SEQ ID 56.
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/product= "RTN3 isoform IV"
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|CCTGGAATCGCCAAAAAAAGGCAGAA 3012
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124. .3162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2653 CTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTTGTGGTTTCTTACCTCATC 2712
                                                                                                                                                                                         The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (I) of the RTN (reticulon)3 gane. Differential expression of RTN3 is a specific marker of neuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular diseases, specifically amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies specific for isoforms of RTN3 or oligonucleotides (antisense sequences or small interfering RNA) that can block/reduce expression of these isoforms are useful for treating neuromuscular diseases and (ii) cells that express RTN3 are useful in screening for therapoutic agents. The present sequence is a RTN3 DNA sequence used to illustrate the invention.
Diagnosing, prognosing and monitoring neuromuscular disease, particularly amyotrophic lateral sclerosis, comprises detecting modulation of the reticulon 3 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4239 BP; 1282 A; 925 C; 890 G; 1142 T; 0 U; 0 Other;
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The present invention relates to a method for diagnosing, or evaluating progression of, a neuromuscular disease. The method comprises detecting modulation of the expression of a product (1) of the RTN (reticulon)3 gene. Differential expression of RTN3 is a specific marker of neuromuscular disease, allowing early diagnosis from readily available muscle biopsies. The method is also useful for determining the efficacy of treatment. The method is used to diagnose (also to evaluate progression or therapy of) neuromuscular disorders, specifically amportory isoforms of RTN3 or oligonucleotides (antisense sequences or small interfering RNA) that can block/reduce expression of these isoforms are useful for treating neuromuscular diseases and (ii) cells that express RTN3 are useful in screening for therapeutic agents. The present sequence is a RTN3 bNA sequence used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De Tapia M, Larmet Y, Loeffler J;
Boutillier AL, Gaiddon C, Rene F;
                                                                                                                                                                                                      Human RTN3 isoform I coding sequence, SEQ ID 50
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/product= "RTN3 isoform I"
                 3133 CCTGGAATCGCCAAAAAAAGGCAGAA 3159
ProGlyLeu---LysArgLysAlaGlu 189
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Gonzales De Aguilar J,
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P-PSDB; ADM36168.
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Search completed: June 19, 2005, 07:21:13 Job time : 412 secs

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Conservative:
Mismatches:
Indels:
           Length:
Matches:
           4.31e-65
                  623.50
80.95%
60.85%
66.97%
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                               Percent Similarity:
Alignment Scores:
                                                    Query Match:
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US-09-830-972-29_COPY_990_1178 (1-189) x ADM36167 (1-4296)

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2890 TCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTGAAA 2949
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             CTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCTGTA 2829
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2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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                                                 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                  42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                     GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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OTHER INFORMATION: a, t, c, g, or other
  102, App
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
                    US-09-949-016-1419

US-09-949-016-11788

US-09-949-016-11788

US-09-949-016-11589

US-09-949-016-15651

US-09-949-016-15651

US-09-949-016-12869

US-09-949-016-12869

US-09-949-016-119335

US-09-949-016-14730

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US-09-949-016-119336

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Sequence 106, Application US/09484970B

Sequence 106, Application US/09484970B

Parent No. 6426186

GENERAL INFORMATION:

APPLICANT: Volkmuth, Wayne

APPLICANT: Walker, Michael G

TILE REFERENCE: PB-0014 US

CURRENT APPLICATION WHERE: US/09/484, 970B

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 172
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Sequence 2. Appli
Sequence 325, Ap
Sequence 382, Ap
Sequence 1127, Ap
Sequence 2988, Ap
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13561, A
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12: /cgn2 6/ptodatcal/ina/5B_COMB.seq:*
31: /cgn2 6/ptodatcal/ina/6A_COMB.seq:*
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US-08-700-607-2
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US-09-949-016-3309
US-09-949-016-3309
US-09-949-016-1127
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Length

Query Match

Score

Result

799 1669 2069 3206 3202 2262 1766 3517 1095

931 927 927 914 682 627 627 624 526 536 518

99.6 99.6 98.2 73.3 73.3 67.4

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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
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Mismatches:
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Matches:
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                 SEQUENCE CHARACTERISTICS:
LENGTH: 799 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO:
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LIBRARY:
Consensus
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Best Local Similarity:
                                                                                                 TOPOLOGY: lines
MOLECULE TYPE: CI
IMMEDIATE SOURCE:
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                                                                                21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle
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SerValvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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Patent No. 5858708
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE INVENTION: TWO NOVEL HUMAN NSP-LIKE INVENTION: TWO NOVEL HUMAN NSP-LIKE INVENTION: TWO NOVEL HUMAN NSP-LIKE INVENTION: TWO NOVEL HUMAN NSP-LIKE INVENTION: TWO NOVEL HUMAN NSP-LIKE INVENTION:
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ZIP: 943.04.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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Patent No. 6607879
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Cocke, Benjamin G.
APPLICANT: Jeffrey J. Sailhamer
APPLICANT: Jeffrey J. Sailhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
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Matches:
Conservative:
Mismatches:
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FLIME DATE: 2000-10-20
PRIOR PLIME DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3253
LENGTH: 1669
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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
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                                                                                                STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
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Matches:
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TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: HEREWITH
CLASSIFICATION:
PRICA PELICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: 97,071
REFERENCE/DOCKET NUMBER: 97,071
REFERENCE/DOCKET NUMBER: 97,071
REFERENCE/DOCKET NUMBER: 97,071
REFERENCE/DOCKET NUMBER: 98-05
TELEPHONE: (650) 855-055
INFORMATION FOR SEQ ID NO: 382:
SEQUENCE CHARACTERISTICS:
LENGTH: 2610 base pairs
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99.47%
99.47%
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STRANDEDNESS: singl
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CLONE: 1508778
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; Sequence 1127, Application US/09949016
; Patent No. 681233
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE REFERENCE: CLOOL3307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFFWARE: PRESECT FOR Windows Version 4.0
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                                                                       TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu
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US-09-949-016-1127
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general information;
patent Venter, J. Craig et al. |
patent Venter, J. Craig et al. |
patent Pille Reference: CLO01307 |
general application NUMBER: Us/09/949,016 |
general application NUMBER: 60/241,755 |
patent Pille Date: 2000-10-20 |
prior Application NUMBER: 60/231,768 |
patent Pille Date: 2000-10-03 |
patent Pille Date: 2000-09-08 |
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ORGANISM: Human
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367 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCCTTCTAATTCTT 426
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                                                                                                                                                                                                                                                                           HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                        LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal
                                                                                                                                                             LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                        181 IleproGlyLeu---LysArgLysAlaGlu 189
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CURRENT PELLING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: US/09/149,476

CURRENT FILING DATE: 1998-03-06

EARLIER APPLICATION NUMBER: 60/040,162

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER PILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,163

EARLIER PILING DATE: 1997-03-07

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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,584
FILING DATE: 1997-05-23
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Patent No. 6420526
GENERAL INFORMATION:
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US-09-149-476-254
; Sequence 254, Apr
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Fatent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR PELING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESEQ for Windows Version 4.0

SEQ ID NO 2988
LENGTH: 2262
                                                                                                                                        2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAAGATTCAGGCTAAAATCCCA 2429
                                                                                                                  142
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                                                  2190 CTGAGGAGGCTCTTCCTTGTCCAGGACCTGGTGGATTCCTTAAAATTTGCAGTCCTGATG
                                                                                                                TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu
                                                                                                                                                                                                                                  TCAGTGCACGATCTGATTTTCTGGAGAGAGAGAAGAAGACTGGGTTTGTCTTTGGCACC
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                     LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet
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Matches:
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Pred. No.:
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ORGANISM: 1
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APPLICATION NUMBER: 60/043,313
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Matches:
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Mismatches:
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Fatent No. 6420526
GREERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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Best Local Similarity:
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US-09-149-476-255
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FILING DATE: 1997-03-07
APPLICATION WUMBER: 60/040,336
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/043,312
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
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APPLICATION NUMBER: 60/047,583
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APPLICATION NUMBER: 60/047,617
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APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/047,492
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APPLICATION NUMBER: 60/047,632
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APPLICATION NUMBER: 60/047,601
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APPLICATION NUMBER: 60/043,671
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APPLICATION NUMBER: 60
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APPLICATION NUMBER:
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1997-04-11 NUMBER: 60/043,67 1997-04-11 1997-04-11 1997-04-11 NUMBER: 60/048,97 1997-06-06 NUMBER: 60/056,88 1997-08-22 NUMBER: 60/056,87 1997-08-22 NUMBER: 60/056,87	1997-08-22 NUMBER: 60/056 NUMBER: 60/056 NUMBER: 60/056 NUMBER: 60/056 NUMBER: 60/056 NUMBER: 60/056 NUMBER: 60/056 NUMBER: 60/056 NUMBER: 60/056 NUMBER: 60/056	NUMBER: 60/056,63 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-23 1997-08-23 1997-05-33 1997-05-33 1997-05-33 1997-05-33 1997-05-33 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,59
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3266 ATGTGGCTGATGACCTATGTTGGTGGTGTTTTTAACGGAATCACCCTTCTAATTCTTGCT 3325
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 966 CTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCAGTGTGGTTTCTTACCTCATC 3025
                                                                     3026 cricicriticricricricaccarcacerricacearcracaagrecercarceaaccrera 3085
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                                                                                                                                                                                82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLys 101
                                                                                                                                                                                                                                                     102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                  142 LeulleSerLeuPheSerValProVallleTyrGluArgHisGln---AlaGlnIle--- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- AspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAla 173
                                     42 LeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle 61
                                                                                                                                                                                                                                                                                                                             122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                         62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillan, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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TELEPHONE: 415-855-0555
TELEPAX: 415-8454166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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3506 GTTGAAAG 3514
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OPERATING SYSTEM:
SOFTWARE: FABESEQ
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                                                                       681
                                                                                                       AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
                                                                                                                           HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                     LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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                                                                     622 TTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCTT
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TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPERBNCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: DL_Genes Version 2.0
SEQ ID NO 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                   181 IleProGlyLeu---LysArgLysAlaGlu 189
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                                                                                                                                                                                                                                                                                                                                                         Sequence 111, Application US/09799451
Patent No. 6783969
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Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
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543.00
69.46%
51.23%
58.32%
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Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
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Wang, Jian-Rui
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Xue, Aidong J
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (196)..(654)
US-09-799-451-111
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Best Local Similarity:
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US-09-149-476-102
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 LENGTH: 2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AAGGTTCCAAGCAAA 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FITLE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REPERENCE: FILE REPERENCE: FILE REPERENCE: FILE REPERENCE: FILE REPERENCE: FILE REPERENCE: FILE REPERENCE: FILE REPERENCE: PACENTY NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PACENTIN VEr. 2.0

SEQ ID NO 13561
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                                                                                                                                                                                                                                                                                                                                                                                                             41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
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                                                                                                                                                                                                                                                                US-09-830-972-29_COPY_990_1178 (1-189) x US-08-700-607-4 (1-1095)
                                                                                                                                                          1095
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Mismatches:
Indels:
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Matches:
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Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                            1.19e-63
526.50
72.77%
54.45%
56.55%
1095 base pairs
             TYPE: nucleic acid
STRANDEDRES: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: THPINOBOL
CLONE: 31870
                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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224 CTGGCGGCCATCTCCGGTGATCAGCGTGTTCGCCTACTTGTCGCTCCTAACC 283
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILLING DATE: 1998-09-08
EARLIER PILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
                                                                                                                                     Conservative:
Mismatches:
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                                                                                                                                                                                                                                     US-09-830-972-29_COPY_990_1178 (1-189)
TYPE: DNA; CRGANISM: Drosophila melanogaster
US-09-270-767-13561
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704 AACAAGAAGCCCGAG 718
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518.00
74.05%
51.35%
55.64%
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Best Local Similarity:
Query Match:
DB:
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/040,6 /040,3 /040,3 /040,1 /047,6 /047,6 /047,5	05-23 05	NUMBER: 60/043,314 NUMBER: 60/043,569 1997-04-11 NUMBER: 60/043,311 1997-04-11 NUMBER: 60/043,671 1997-04-11 NUMBER: 60/043,669 1997-04-11 NUMBER: 60/043,669 1997-04-11 NUMBER: 60/043,312 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,313
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RESULT 14
US-09-949-016-1419
i Sequence 419, Application US/09949016
sequence 419, Application US/09949016
sequence 419, Application US/09949016
general incommation:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOL1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PELING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTHARE: PSESEX for Windows Version 4.0
SEG ID NO 1419
LENGTH: 2181
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                           612 TCTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTC
                                                                                                                                LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL
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ER APPLICATION NUMBER: 60/056,908
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/048,964
ER FILING DATE: 1997-06-05
ER APPLICATION NUMBER: 60/057,650
ER PILING DATE: 1997-09-05
ER PILING DATE: 1997-09-05
ER PILING DATE: 1997-09-05
ER APPLICATION NUMBER: 60/057,650
ER APPLICATION NUMBER: 60/057,650
ER APPLICATION NUMBER: 60/049,610
ER FILING DATE: 1997-06-13
ER APPLICATION NUMBER: 60/049,610
ER FILING DATE: 1997-06-13
ER RELING DATE: 1997-06-13
                R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,576
R APPLICATION NUMBER: 60/047,501
R FILING DATE: 1997-04-11
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R RFLING DATE: 1997-05-23
R RPLICATION NUMBER: 60/043,670
R APPLICATION NUMBER: 60/056,632
R RPLING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,876
R FILING DATE: 1997-08-22
R RFLING DATE: 1997-08-22
R RPLICATION NUMBER: 60/056,881
R FILING DATE: 1997-08-22
R RPLICATION NUMBER: 60/056,881
R FILING DATE: 1997-08-22
R RELICATION NUMBER: 60/056,989
R FILING DATE: 1997-08-22
R RELICATION NUMBER: 60/056,909
R FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,862
FILING DATE: 1997-08-22
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Sequence 117589, Application US/09949016

Sequence 117589, Application US/09949016

Retent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 117589

LENGTHREE FASTESEQ for Windows Version 4.0

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Sequence 14995, Application US/09949016

Betent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOD1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FBELSEQ for Windows Version 4.0

LENGTH: 42075
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US-09-949-016-117589
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Sequence 117588, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION UNMBER: 60/241,755
PRIOR PELLING DATE: 2000-00-20
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: PRESE PRESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 117588
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ORGANISM: Human
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Sequence 15051, Application US/09949016
; Sequence 15051, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLOOU.307
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR PILING DATE: 2000-04-14
; PRIOR PILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2007012
; SOFTHARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 15051
; LENTH: 135667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 CTGCTCTTCTCCCTGACCCAGTTCAGCGTGAGCGTCGTGGCCTACCTGGCCTG 278
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                                                                                                                                                                                                                                                                                                                                                                                                 3 ValAspieuLeuTyrTrpArgAspileLysLysThrGlyValValPheGlyAlaSerLeu
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Best Local Similarity:
Query Match:
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                                                                                                                        LOCATION: 41
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity:
                                NAME/KEY: UNSURE LOCATION: 22
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NAME/KEY: UNSURE
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ORGANISM: Human
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APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PILE REPERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SEQ ID NO 3784
LENGTH: 443
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LOCATION: 96..239
OTHER INFORMATION: score 4.6
OTHER INFORMATION: seq VFGSFLLLLFSLT/QF
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; Sequence 3784, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: 305
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NAME/KEY: misc_feature
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LOCATION: 360
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LOCATION: 96..437
, ORGANISM: Human
US-09-949-016-14995
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RESULT 21
US-09-949-016-40169/C

Sequence 40169, Application US/09949016

Bettent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FORENET FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: PSECSO for Windows Version 4.0

LENGTH: 601
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                                                                                                                         SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla
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                                                                         US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-12869
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: uS/09/949, u16

CURRENT PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-00-09-08
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                    US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-15051 (1-135667)
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12869
LENGTH: 122486
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US-09-949-016-12869
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ORGANISM: Human
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                             461
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      23
55
40
      Conservative:
                  Mismatches:
Indels:
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Patent No. 6812339
GENERAL INFORMATION:
   50.00%
37.89%
29.70%
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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280 GTTTCTCTGAGACCCAACAGACCTCTTAGAGTCTCCCCTAACACCCTGTCTTTGAATATC 221
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; Sequence 9, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
601
72
23
55
40
  Length:
Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER FRADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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Length: Matches: Conservative:

Mismatches: Indels:

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2127 ATCCTGGCTCTTCTCTCTCTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 2186
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                     4.87e-26
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87.32%
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Best Local Similarity:
Query Match:
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US-09-949-016-13161
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US-09-949-016-14730

j Sequence 14730, Application US/09949016

j Patent No. 6812339

j GENERAL INFORMATION:

j TILLE OF INVENTION: POLYMOREHISMS IN KNOWN GENES ASSOCIATED

j TILLE OF INVENTION: POLYMOREHISMS IN KNOWN GENES ASSOCIATED

j TILLE OF INVENTION: POLYMOREHISMS IN KNOWN GENES ASSOCIATED

j TILLE OF INVENTION: POLYMOREHISMS IN KNOWN GENES ASSOCIATED

j TILLE OF INVENTION: POLYMOREH: US/09/949,016

j CURRENT FILING DATE: 2000-04-14

j PRIOR PILING DATE: 2000-10-20

j PRIOR PELICATION NUMBER: 60/231,768

j PRIOR FILING DATE: 2000-10-03

j PRIOR PELING DATE: 2000-09-08

j PRIOR PELING DATE: 2000-09-08

j PRIOR PELING DATE: 2000-09-08

j PRIOR PELING DATE: 2000-09-08

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Matches:
Conservative:
Mismatches:
Indels:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herwith
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECHONE: 415-855-0555
TELECHONE: 415-855-0555
TELEPHONE: 415-855-0555
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86.76%
29.65%
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Best Local Similarity:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-949-016-14730
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DB:
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US-09-513-999C-11198
; Sequence 11198, Application US/09513999C
; Patent No. 673961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Dunclert, A.
; APPLICANT: Duclert, A.
; APPLICANT: Duclert, A.
; TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFRENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1909-02-26
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11198
; LEATHER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 LeulleLeuAlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAla 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 GinileAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIle 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 CAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CTGATITITGGCTCTCATITCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 GlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189
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Matches:
Conservative:
Mismatches:
Indels:
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256.00
100.00$
100.00$
27.50$
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CORGANISM: Homo sapiens
US-09-513-999C-11198
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RESULT 27
US-09-248-796A-1905
US-09-248-796A-1905
Sequence 1905, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION WINDER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PELICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
10117 AGCTCTCAGCCCCTCCTGGGTTCCCCCATTCACCTCTGCATGGCTAGGGGGTGGGAGGGC 10176
                                                                                                                                                                                                                                                                                                                                                 10297 GETTTGACTCTTCTCTTCTGGG-TGAGCTGGGAAGGCCGTAAGGGGCAAATGGGGACTT 10355
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                                                                                                                                                                                                                           10177 GACTGTTGGGTAAATTCACAGCATGAGAGGGAATTCCCGGTGGGCTCTGCTGACCCTGAC
                                                                                                                                                                                                                                                                             10057 ACGCAGCTGCGGCACTTCTTCCTGGTAGAAGACCTCGTGGATTCCCTCAAGGTGGCCTGG
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                                                     101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLys
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Matches:
Conservative:
Mismatches:
Indels:
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45.15%
25.24%
15.47%
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US-09-248-796A-1905
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SEQ ID NO 1905
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Query Match:
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                                  APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER; US/09/949,016
CURRENT FILING DATE: 2000-04-14
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77
34
48
209
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                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                   PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEC ID NOS: 207012
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 11161
LENGTH: 15661
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236.50
30.33%
21.04%
25.40%
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Query Match:
                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-13161
                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
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Sequence 119336/c

Sequence 119336, Application US/09949016

Sequence 119336, Application US/09949016

Sequence 119336, Application US/09949016

Sequence 119336, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/0949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-0-08

PRIOR FILING DATE: 2000-0-0-09

PRIOR FILING DATE: 2000-0-0-09

PRIOR FILING DATE: 2000-0-0-09

PRIOR FILING DATE: 2000-0-0-09

PRIOR FILING DATE: 2000-0-0-09
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US-09-949-016-117609/C
Sequence 117609, Application US/09949016
Sequence 117609, Application US/09949016
Sequence 117609, Application US/09949016
GENERAL INFORMATION:
TITLE OF INVERTION:
TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
SPRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                       SeralaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
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                                                                                                            76 TGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAACTGAGGAGGCTCTTCCTTGTCCAG 17
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                               136 AGGCCTACTTGGAGCTTGAGATCACCCTTTCTCAGGAGCAGATTCAGAAGTACACGGAC
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80.00$
62.22$
15.15$
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Best Local Similarity:
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Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-14-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 40170

LENGTH: 601
                                                                              307 GCTTACATTGGTTTATTGATCTCTGCTGCTGAATATTCCGGTAAATTGATTACTGGT 366
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247 CTTGTTTTGGTTTGATTGTCTTGAAAACTGTCAATTTATTCAATATCTTTTTCCATTTA 306
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                                                                                                                         54 rLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLe 74
                                          --- Ala-LeuLeuSerValThrIleSerPheArgileTy 54
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633 CAAGAAAGTTGATGCTGTTGCCGATATTACCAAGACCATTAAAACCAAGTCTGC
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Matches:
Conservative:
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                                          38 AlaTyrileAlaLeu----
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Best Local Similarity:
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ORGANISM: Human
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Best Local Similarity:
Query Match:
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US-08-905-223-178
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 Query Match:
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Patent No. 6476212
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradlay K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REPERENCE: PL.0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                               505 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGTAATTTCCTAA 446
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US-09-313-294A-703
                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 117609
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35.19%
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Best Local Similarity:
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Best Local Similarity:
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ORGANISM: Zea mays
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                                                                                                                            ORGANISM: Human
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US-09-313-294A-703
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SEQ ID NO 703
LENGTH: 266
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                                                                                                               TYPE: DNA
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RESULT 32
US-09-949-016-48087/c

Sequence 48087 Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE PEPERENES: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

FRIOR APPLICATION NUMBER: 60/241,755

FRIOR APPLICATION NUMBER: 60/237,768

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 601
                                                                                                                                                                                                                                                  124 ValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAlaLeuIle 143
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                                                                                                                                                                                             106 LeuPheLeuValAspAspLeuValAspSerLeu----LysPheAlaValLeuMetTrp
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                                                                                    US-09-830-972-29_COPY_990_1178 (1-189) x US-09-313-294A-703 (1-266)
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; Patent No. 6222029
; GENERAL INFORMATION:
    APPLICANT: Edwards, Jean-Baptiste D.
    APPLICANT: Application Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Appl
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Matches:
Conservative:
Mismatches:
Indels:
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102.00
70.00%
52.50%
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FRATURE:

NAME/KEY: other

OTHER INFORMATION: 1397.426

IDENTIFICATION WETHOD: blastn
OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 130.036.48

OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 1314.401

IDENTIFICATION METHOD: blastn
OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 131.4.401

IDENTIFICATION METHOD: blastn
OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 140..212

OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 180..185

OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 269..317

OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 269..317

OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 397.426

IDENTIFICATION METHOD: blastn
OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 269..317

OTHER INFORMATION: est
FRATURE:

NAME/KEY: other
IOCATION: 310..406

OTHER INFORMATION: est
IOCATION: 310..300

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OTHER INFORMATION: est
IOCATION: 310..300

OTHER INFORMATION: est
IOCATION: 400..300

OTHER INFORMATION: est
IOCATION: 400..300

OTHER INFORMATION: est
IOC
     OTHER INFORMATION:
  NUMBERS OF SECUENCES: 5.0.5
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOADE, MARTERS, O1800 & Bear STREET: 501 West Broadway
CITY: San 10:90
TATE: CALIFORNIA
COUNTRY: USE
COMPUTER: LIB PC COMPATIBLE
OF STATE: P3.01.3505
COMPUTER: LIB PC COMPATIBLE
OF STATE: CALIFORNIA
COMPUTER: LIB PC COMPATIBLE
OF STATE: WINDS
CLASSPICATION WINNER: US/08/905,223
FILLING DATE: US/08/905,223
FILLING DATE: US/08/905,223
FILLING DATE: US/08/905,223
FILLING DATE: US/08/905,223
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FILLING DATE: US/08/905,223
FILLING DATE: US/08/905,923
FILLING DATE: US/08/905,923
FILLING DATE: US/08/905,939
FOTHER INFORMATION: GET CEPICO IN CONTING: US/08/905,939
FEATURE: US/08/AND WETHOD: DISATION
FOTHER INFORMATION: GET CEPICO IN CONTING: US/08/905,939
FEATURE: US/08/AND WETHOD: DISATION
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FEATURE: US/08/905,939
FEATURE: US/08/905,939
FOTHER UNCOMMATION: GET CEPICO IN CONTING: US/08/905,939
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FEATURE: US/08/905,939
FOTHER UNCOMMATION: GET CEPICO IN CONTING: US/08/905,939
FEATURE: US/08/905,939
FEATURE: US/08/905,939
FEATURE: US/08/905,939
FEATURE: 
NUMBER OF SEQUENCES: 503
```

```
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::||| :::
836 TTTGTAGGT---ATCCAAGTAGTTATTCAAAATGCACCTCGTTTGTTCAAAGAAGATGAC 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1007 AACTCTGCAGCTGTAAGAGCCGATGCATTAAACAATATGACAGATATTATCGTTTCTTTA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     947 GCTGTTATTATTGGATTGAAAATTTCAATTAAACCTGCCGATCGAAATCATCTAT--- 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1067 TIGAGITIAATIGIATATATATAATCTIATCTATIGITAAGIAIGICACGGITITIGICIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 --------AlaLeuAlaLeuLeuSerValThr------IleSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 ArglleTyrLysGlyValIleGlnAlaileGlnLysSerAspGluGlyHisProPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-830-972-29_COPY_990_1178 (1-189) x US-08-956-171E-407 (1-1722)
                                                                                                                                                                                                                                           COUNTY: 1.0.5

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle---
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                ADDRESSEE: Human Genome Sciences,
STREET: 8410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 407:
US-08-956-171E-407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 407
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.00
48.87%
27.07%
10.20%
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SerValValAspleuLeuTyrTrpArgAsplleLysLysThrGlyValValPheGlyAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-830-972-29_COPY_990_1178 (1-189) x US-08-905-223-178 (1-425)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSer 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rabucks:
NAME/KEY: other
LOCATION: 183..263
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 90
OTHER INFORMATION: est
OTHER INFORMATION: est
OTHER INFORMATION: est
PEATURE:
NAME/KEY: other
LOCATION: 337..401
IDENTIFICATION METHOD: blastn
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OTHER INFORMATION: id AA157365
OTHER INFORMATION: id AA157365
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: 273..326
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 90
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OTHER INFORMATION: identity 90
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OTHER INFORMATION: region 213..266
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OTHER INFORMATION: identity 90
OTHER INFORMATION: identity 90
OTHER INFORMATION: identity 90
                                                                   OTHER INFORMATION: Identity 91
OTHER INFORMATION: dentity 91
OTHER INFORMATION: id HSC16E081
OTHER INFORMATION: est
FEATURE:
NAME/KRX: other
LOCATION: 397.426
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 96
OTHER INFORMATION: identity 96
OTHER INFORMATION: est
FEATURE:
NAME/KRX: other
LOCATION: 85.186
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: est
FEATURE:
NAME/KRX: other
LOCATION: 85.186
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 99
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OTHER INFORMATION: est
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                                                   : blastn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Charles Kunsch
Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.000172
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80.00%
57.14%
10.74%
                            LOCATION: 269.317
IDENTIFICATION METHOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
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836 TITGTAGGT---ATCCAAGTAGTTATTCAAAATGCACCTCGTTTGTTCAAAGAAGATGAC 780
112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
                                                                                                                                                                                      | | | ::: ::|||
-----GCAATAACAATTATCGTCAGCTTA 744
                                                                  92 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
                                                                                                                                                                                                                                                                      743 ATCAGIGGICITGIAAIGITGATIGIAITIGCAGICAAI 705
                                                                                                                                                                                                                                               132 PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSer 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Brown, Martin, Haller & McClain
1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSITICATION: 43.5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    779 GTTGTACCTAAC-------
                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/08487596
; Patent No. 6440681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEPAX. 610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1828 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN CLASSIFICATION: 435
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           both
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                                                                                                                                                                                                                                                                                                                                                            US-08-487-596-7
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112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
                                           -GCAATAACAATTATCGTCAGCTTA 744
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                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE.OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5.255
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           947 GCTGTTATTATTGGATTGAAAATTTCAATTAAACCTGCCGATCGAAATCATCCTTAT--- 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------AlaLeuAlaLeuLeuSerValThr-----IleSerPhe 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 ArgileTyrLysGlyValileGlnAlaileGlnLysSerAspGluGlyHisProPheArg 71
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                                                                                   132 PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSer 144
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
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                                                                                                                                                                        RESULT 35
US-08-781-986A-407/c
; Sequence 407, Application US/08781986A
; Patent No. 6737248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 407:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                         779 GTTGTACCTAAC----
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IYPE: nucleic acid
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48.87$
27.07$
10.20$
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rockville
STATE: Maryland
COUNTRY: USA
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                  1076 AAAGTCATACCTCTAATTGGAGAGTATCTGGTATTTACCATGATTTTTGTGACACTGTCA 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 uleuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLe 103
                                                                                                                                                                                                                                                                                                                                                                                                   51 PheArglleTyrLysGlyValileGlnAlalleGlnLysSerAspGluGlyHisProPhe 70
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Patent No. 6524789
GENERAL INFORMATION:
ENLIGATION: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                -----SerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSer
                                                                                                                                                                                                                          x US-08-487-596-7 (1-1828)
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COTHER INFORMATION: /product= "ALPHA-5 SUBUNIT"
US-08-487-596-7
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                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
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STREET: 1660 Union Street
CITY: San Diego
STATE: CA
                                                                                                    Length:
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38.54%
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COMPUTER READABLE FORM:
                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                     Alignment Scores:
NAME/KEY:
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1136 ATTATGGTAACCGTCTTCGCTÁTCAACATTCATCATCGTTCTTCCTCAACACÁTAATGCC 1195
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nic acetylcholine receptor
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Mismatches:
Indels:
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Matches:
COMPUTER: IDENCE OF COMPUTER: COMPUTER: IDENCE OF COMPUTER: IDENCE OF COMPUTER: IDENCE OF COMPUTER: FEATSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: Unne 7, 1996
CLASSIFICATION DATA:
PRILING DATE: 06/07/95
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
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nicotinic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL STATES TOPOLOGY: Innear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
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38.54%
21.88%
9.56%
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STRANDEDNESS: double
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OTHER INFORMATION: 6
OTHER INFORMATION: 1
LOCATION: 1...154
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Best Local Similarity:
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ORIGINAL SOURCE:
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ANTI-SENSE: NO
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us-09-830-972-29_copy_990_1178.rni

CY 83 ULEUVAIGITHLYSTYTSETABINSETALBUGITHTISVALASNCYSTNTILELYSGIULE 103	Db 1999 TCGGTGGCTTGCTCCTTGGGTGCCTTCAGCTACATTGGGTTGCCCTTGACC 2049
uArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPhe	2050 CTCATTGTGATTGAAGTCATCCTGTTCCTGGTGCTGCTGGTGGAGTGGACAACATCTTC
bb 1375 CATGAAGGAAAATGATGTCCGTGAGGTTGTTGTGAAATTCATAGCCCAGGTTCT 1434	Oy 147 SerValProVallleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
Qy 119AlavalLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLe 137	Db 2110 ATTCTGGTGCAGGCCTACCAGAGAGATGAACGTCTTCAAGGGGAAACCCTGGATCAGCAG 2169
Db 1435 TGATCGGATGTTTCTGTGGACTTTTTCGTTTCA1471	Oy 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174
Qy 137 uLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAl 157	Db 2170 CTGGGCAGGGTCCTAGGAGAGTGGCTCCCAGTATG 2205 RESULT 39
	US-09-949-016-4281 ; Sequence 4281, Application US/09949016 ; Patent No. 68123339 . GENERAL, INFORMATION
RESULT 38 US-09-462-136-1 : Sequence 1. Application US/09462136	; APPLICANT: VENTER, J. Craig et al.; IIILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED ; ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF ; FILE REPERENCE: CLOOI307
Patent No. 6426198 GENERAL INFORMATION: APPLICANT: Carstea, et al.	; CURRENT APPLICATION NUMBER: US/09/949,016 ; CURRENT FILING DATE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/241,755
; TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease ; FILE REFERENCE: 4239-53894 ; CURRENT APPLICATION NUMBER: US/09/462,136	; PRIOR FILING DATE: 2000-10-20 ; PRIOR APPLICATION NUMBER: 60/237,768 ; PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997- NUMBER OF SEQ ID NOS: 13	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 4281 ; LENGTH: 4661
; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 1 ; LENGTH: 4550	; TYPE: DNA ; ORGANISM: Human US-09-949-016-4281
	ent Scores: 0.332 Length:
<pre>j NAME/KEY: CDS j LOCATION: (1)(3837) US-09-462-136-1</pre>	Score: Bercent Similarity: 42.11\$ Conservative: 25 Best Local Similarity: 25.66\$ Mismatches: 51 Anary March. 9 51\$
ent Scores: 0.32 Length:	4.014 THOUSE: 7.
Matches: 39 Conservative: 25	-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-4281 (1-4661)
Best Local Similarity: 25.66% Mismatches: 51 Query Match: 9.51% Indels: 37 DB: 7	<pre>Qy 46 SerValThrIleSerPheArgIleTyrLy8GlyValIleGlnAlaIleGlnLy8SerAsp 65</pre>
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-462-136-1 (1-4550)	Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlalleSerGluGluLeuVal 85
Qy 46 SerValThrileSerPheArglleTyrLysGlyVallleGlnAlalleGlnLysSerAsp 65	Db 1973 GACAGTGATGTCTTCACCGTTGTAATTAGCTATGCCATCATG 2014
1792 AATCTGACCATTTCCTTCACTGCTGAACGAAGTATTGAAGATGAACTAAATCGTGAAAGT	86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArg
66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal	2015 TITCIATATATTCCCTAGCCTTGGGGCACATCAAAAGCTGTCGCAGG
Db 1852 GACAGTGATGTCTTC	dy 106 LeuPheLeuValAspAsp
	7
Oy 106 LeuPheLeuValAspAsp	Db 2120 TCGGTGGCTTGCTCCTTGGGTGCTTCAGCTACATTGGGTTGCCCTTGACC 2170
Db 1942 CTTCTGGTGGATTCGAAGGTCTCACTAGGCATCGCGGCATCTTGATCGTGCTGAGC 1998	Qy 137 LeubeullebeuAlabeulle
Oy 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 136	Db 2171 CTCATTGTGATTGAAGTCATCCCGTTCCTGGTGCTGGTTGGAGTGGACACATCTTC 2230

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OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              785 ATGGCGCCTTTGGTCCGCAAGATATTTCTTCACACGCTTCCCAAACTGCTTTGCATGAGA 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 PheArglleTyrLysGlyVallleGlnAlalleGlnLysSerAspGluGlyHisProPhe 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 uArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPhe------
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.024 TGATCGGATGTTTCTGTGACTTTTCTTTTCGTTTCA-----
      Sequence 5725, Application US/09949016
Fatent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS(
TITLE OF INVENTION: WITH HUMAN DISEASE,
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF I
FILE REPERENCE: CLOOL1307
CURRENT FILING DATE: 2000-04-14
RIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR PILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
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Mismatches:
Indels:
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Matches:
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38.54%
21.88%
9.45%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
JS-09-949-016-5725
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APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIOR PILING DATE: 2000-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2065 CTT----CTGGTGGATTCGAAGGTCTCACTAGGCATCGCGGGCATCTTGATCGTGCTGAGC 2121
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---AlaGlnIleAspHisTyr 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal
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                                                                                       163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174
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Mismatches:
Indels:
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Matches:
147 SerValProValIleTyrGluArgHisGln--
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US-09-814-915A-100
US-09-814-915A-100
Sequence 100, Application US/09814915A
Patent No. 6750015
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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88.50
42.11$
25.66$
9.51$
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Query Match:
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LENGTH: 4673
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146 PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165
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87.50
41.15%
22.92%
9.40%
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SEQ ID NO 2168
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Query Match:
DB:
                                                                              US-09-134-001C-2168
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                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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Sequence 2072, Application US/09134000C

Sequence 2072, Application US/09134000C

Patent No. 6417156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERACCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLIANG DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 2072

LENGTH: 1779
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|TACAGCAAAACTTAACCAATTAATTACCAGTATCGTGACATTTGTGGGTGTACTTTGG 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TICTGGAAAACAGTGAAACGT---------------TTATTTCGATACATG 168
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                                                                                                                                                                                                                                                                                                                                                                                                                              TyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeu
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-134-000C-2072
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Pred. No.:
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANTON: WICCEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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1306 TCTATAGTTGTCGTTGAGAATATATTTAGAAGATTATCTGATCCGAATGAGAAGCTCAAA 1365
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697 TTAATTGTTGTGGTGGTTGTGGCGCCTCGCAAAAACATTTTGCGGCTCAACAAAA 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LeuValAspAsp 111
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Matches:
Conservative:
Mismatches:
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                                                          162 TyrLeuGlyLeuAlaAsnLysAsnValLysAsp 172
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                                                                                                                                                                                                                                           Sequence 2168, Application US/09134001C Patent No. 6380370
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TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
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308 ATTATCAGTGCGACAACTGAAGTATTTAAACCAATAATGTCATCGACACTAGTTACTATT 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-830-972-29_COPY_990_1178 (1-189) x US-08-956-171E-322 (1-1302)
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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42
36
75
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PE248P1
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                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                         ADDRESSEE: Human Genome Scie
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 ATTGGACGT------
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-639
INFORMATION FOR SEQ ID NO: 322:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mark J. Hyman
                                                                                               CITY: Rockville STATE: Maryland
                                                                                                                                      COUNTRY: USA
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Best Local Similarity:
Query Match:
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     --GGCGTT 1590
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APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: PARMICLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR PILE REFERENCE: PL-0017 US CURRENT APPLICATION NUMBER: US/09/313, 294A
CURRENT FILLING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 IleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnVal 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 AAGAAGTATTATGCCATCTTCGATGAGAGTGCCTATCGAAGATTCCAAAGGCCCTCAAG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNTGC-AACTTCCTGACACTGTTCTATATTGTCTTTGTGGCACTGTACACTATACCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700548479H1
NAME/KEY: unsure
                                                                             1591 AAAAATAGGGAACAAAAAGAAGGTCTAGGAACAGTT 1626
                                         166 AlaAsnLysAsnValLysAspAlaMetAlaLysIle 177
   1546 ACCCTAGTGCCTTCTTTAGGTGCAACATTTTTTAAAAAT-
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 322, Application US/08956171E

Patent No. 6593114
GENERAL INFORMATION:

APPLICANT: Charles Kunsch
                                                                                                                                                  Sequence 81, Application US/09313294A Patent No. 6476212 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-830-972-29_COPY_990_1178 (1-189)
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Steven C. Barash
Michael R. Fannon
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9.24%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 109
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                    US-09-313-294A-81
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SEQ ID NO 81
LENGTH: 296
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DB:
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Sequence 149, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Clarles Kunsch
TITLE OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                155 GCTCTGAAATTGAGTGATGTTTCATTGAATATACTAACGTTAGGTGCATTAACAGTAGCG 214
                                                                                                                                                                           ------GTGATAGACGATTCGATTGTAGTT 247
                                                                                                                                                                                                                                           ||| ::: :::::: :!!!|
248 GTTGAAAATTTTATCGACGCTTAACAGATTCAGAAGAAGAACAACTAAAAGGTGAAAATTTA 307
                                                                                                                                                                                                                                                                                              99 ThrileLysGluLeuArgArgLeuPhe-----LeuValAspAspLeuValAspSer 115
                                                                                                                                                                                                                                                                                                                                  308 ATTATCAGTGCGACAACTGAAGTATTTAAACCAATAATGTCATCGACACTAGTTACTATT 367
                                                                                                                                                                                                                                                                                                                                                                           116 LeulysPheAlaValleuMetTrpValPheThrTyrValGlyAlaLeuPheAsn---- 133
                                                                                                                                                                                                                                                                                                                                                                                                  ------GlyLeuThrLeuLeulleLeuAlaLeuIleSerLeuPheSerValPro 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 Valile-----------TyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
                                                                                                                                      ileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaile 80
                                                                                                                                                                                                                  81 SerGluGluLeuValGlnLysTyrSerAsnSer----AlaLeuGlyHisValAsnCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     548 GGATTAGGTGTTGTTAGTACAACTTATAAAAAGTATTA 586
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSDOS version
  NAME: Brookes, A. Anders
REGISTRATION UNDRER: 36,373
REFERENCE/DOCKET UNDRER: PB34
TELECOMMUNICATION INFORMATION:
TELEFONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 12566 base pairs
TYPE: mucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                           215 ATTGGACGT----
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                    ---TyrGluArgHisGlnAlaGlnIleAspHis 161
116 LeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsn---- 133
                                                                         134 -------GlyLeuThrLeuLleLeuAlaLeuIleSerLeuPheSerValPro 149
                                                                                                  428 GCATTGGCTATTGCATTTAGTTTATTAGCATCGTTATTAGTGTAATTACACTCGTTCA 487
                                                                                                                                                                                         488 GCGTTGGCAGCTACACTATTTAAAAAGGCGTTAAACGTCGTAATAAACAACATCAAGAA 547
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TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal---ValPheGlyAla 20
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                                                                                                                                                                                                                                162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174
                                                                                                                                                                                                                                                             548 GGATTAGGTGTTAGTACAACTTATAAAAAAGTATTA 586
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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Indels:
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LALESSEE:
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USD
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REGISTATION NUMBER: 30.446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 322:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/781,986A
                                                                                                                                                                                                                                                                                                                                             Sequence 322, Application US/08781986A Patent No. 6737248 GENERAL INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORWATION:
ATTORNES: BENSON, BOD
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85.00
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Best Local Similarity:
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TOPOLOGY:
US-08-781-986A-322
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CLASSIFICATION:
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Sequence 104, Application US/08961527;
Patent No. 6420135;
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDERSE: 391
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COMMITX: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140
                                                                                                                                                                                                                                                                                                                           496
                                                                                                                                                                                                                                                                                                                                                      SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 AlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457
                                                                                                                                                                                                                                                                                                                                                                                                           101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
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                                                                                                                                                                                        21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
                                                                                                                                                                                                                                             41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486,33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CAPRENT APPLICATION DATA:
PILING DATE:
                                                                                            Conservative:
                                                                                                      Mismatches:
Indels:
                                                                  Length:
Matches:
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84.50
46.39%
24.10%
9.08%
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 double
                linear
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; STRANDEDNESS:
; TOPOLOGY: lin.
US-08-961-527-149
                                                                                            Percent Similarity:
                                                      Alignment Scores:
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3179 GACCTTTGAAAAAAATAATACAGTTGAAAAATTATCAACGCAGGAAGATTATCAAGGTCT 3238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 oValileTyrGlu---ArgHisGlnAlaGlnIleAspHis---TyrLeuGlyLeuAlaAs 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 yValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSe 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 yAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 -----LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3239 AAACCGICTAGTGACTAGCITATCAAATGATGAAATGGTCTATATTTCACGCTAT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 -----SerValThrile-SerPheArgileTyrLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 lAsnCys---ThrileLysGluLeuArgArgLeuPheLeuValAspAsp-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-830-972-29_COPY_990_1178 (1-189) x US-08-961-527-104 (1-6735)
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32
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                           Length:
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                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P834G
TELECPHONE: (301) 309-8504
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 6735 base pairs
TYRE: NUCleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
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46.49%
29.19%
9.02%
  DATA:
PRIOR APPLICATION DAT
APPLICATION NUMBER:
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Best Local Similarity:
Query Match:
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us-09-830-972-29_copy_990_1178.rni

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37973 GCAAGTTCTGTTTCAGCAGCATTAGTAAGCTATTATTTAGAGCAACGTTTCGTCATCAAC 38032
                                                            38153 CAATCTTATGTAAAAACCACGCTTTCTTTAAGCACTGGCGTCATTGATGCGGTCACTCG 38212
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                                                                                                                                                                                                                                                                                                                     38213 ATGATCTCTTACACGATTTTCTTATCCGGATTAGCCGGTCCAATGATAGTGCTTGGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                              135 LeuThrLeuLeulleLeuAlaLeulleSerLeuPheSerValProVallleTyrGluArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hamilton O. Smith
J. Craig Venter
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae
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ADDRESSEB: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
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COMPUTER READABLE FORM:

COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23 Aug-2000
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                  AsnCysThrIleLysGluLeuArgArgLeuPhe---
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NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                 115 SerLeuLysPheAlaValLeuMetTrp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Robert D. Fleischmann
                                                                                                                    89 SerAsnSerAlaLeuGlyHis----
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; Patent No. 6528289
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mark D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MD
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-643-990A-1
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37736 CTTTTGGTGCGTTTTACCCAATGGGBAAACAATTTTGGATGTTTGCAGGCGGTTATCTT 37795
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                                                              Fragments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-830-972-29_COPY_990_1178 (1-189) x US-09-557-884-1 (1-1830121)
                APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1830121
62
28
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97
                                                                               Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
Indels:
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                                                                                                                                                                                                                                         ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
PRILICATION UNDRER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-557-884-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX: 301-309-8439
SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUENCE CHARACTERISTICS:
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84.00
33.71%
23.22%
9.02%
                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               CITY: Rockville
                                                                                                                                                                                                                         COUNTRY: USA
  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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174 tAlaLysileGlnAlaLys 180
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83.50
38.71
20.43
8.97
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                                                                           US-09-543-681A-2003
                                                                                                                                                                                                                                                                                          US-09-543-681A-2003
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                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerAsnSerAlaLeuGlyHis-------
                                                                                                                                                                Length:
Matches:
                                                                                                  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnLysSerAspGluGlyHisProPhe-
                                                              LENGTH: 1830121 base pairs
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                      US-09-830-972-29_COPY_990_1178 (1-189)
           TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                               2.12e+04
84.00
33.71%
23.22%
9.02%
                                                                                                                                                                                                                                                                                                                                 LeuLeuLeuSerLeuThr-
                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                      Alignment Scores:
                                                                                                                             US-09-643-990A-1
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Sequence 2003, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 PheThrTyrValGlyAlaLeu-PheAsnGlyLeuThrLeuLeulleLeuAlaLeuIleSe 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 GGCAGCGAAGTGGTTGTTTTCCTATCAAGCCATATTATGGCTCTCACAGCACAAACCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GIGGIAGGGATCATTIAIGCAIGG-----ATAAAACGCTCTCCTACCCCTAAAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 --------GlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 HisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLyB
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: 05 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
FROM NO 2003
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38441 GCTTTTTATGCAGGCGAAA 38459
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1155 ACGGATGTGTACATTGACATAGATGCATATGAGGAGGGGAA---GAAATTCCTGGAATA 1811
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1151 CACGAGTCCTACAGTGTGGATGTTGGAACTCTTCCTCTGGGGCTACTCCTCCTGCC 1210
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1091 ATTCCTCTAGAGTTCTTTGCTGTGGTGATGGGAACTGGCATTTCCGCGGGGTTTAACTTG 1150
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                                                                                                                                          168 LysAsnValLys-----AspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu 184
                                  1653 GGCTTGGACTACGGACTGATTACCGCGTGATCATTGCTCTGCTCACA------
                                                                              149 ProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGly---LeuAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 2, Application US/09785381
Fatent No. 6602992
GENERAL INVORMATION:
APPLICANT: DALLOS, Peter
APPLICANT: ZHENG, Jing
APPLICANT: AMDISON, Laird
ITILE OF INVENTION: A MAMMALIAN PRESTIN
FILE REFERENCE: 0290-37U1
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/183,461
PRIOR PELING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
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CRGANISM: Meriones unguiculatus
US-09-785-381-2
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83.00
39.08%
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Best Local Similarity:
Query Match:
DB:
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                 134 GlyLeu
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Pred. No.:
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1074 ATTCCTCTAGAGTTCTTTGCTGTGGTGATGGGGACTGGCATTTCTGCAGGATTTAACCTA 1133
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Matches:
Conservative:
Mismatches:
Indels:
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                                                     Sequence 4, Application US/09785381
Patent No. 6602992
GENERAL INFORMATION:
APPLICANT: DALLOS, Peter
APPLICANT: ALBISON, Laird
APPLICANT: MADISON, Laird
TILLE OF INVENTION: A MAMMALIAN PRESTIN
FILE REFERENCE: 0290-37U1
CURRENT FILING DATE: 2001-02-16
PRIOR PILING DATE: 2000-02-16
PRIOR FILING DATE: 2000-02-16
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CTGCTTTTCCTCGCCG 589
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SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 2441
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Mus sp.
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                             RESULT 52
US-09-785-381-4
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US-09-785-381-4
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Sequence 11412, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
                                                      91622 TTAATAAGCTTATTCAAFGACACCATTACTACAAATAAATGGCAFGCATTAAATGGF 91563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677 cgarraarrccg------gcgaccarcgccrrcgcgcgcrrrrccrrcaccarggacgcg 730
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                                 124 ValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIle
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ORGANISM: Pseudomonas aeruginosa
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SEQ ID NO 11432
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Best Local Similarity:
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Sequence 12262, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 117410
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GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCys-----ThrIleLysGluLeu
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 11397
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Patent No. 5925522
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STREET: Washington Way
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FILE REFERENCE:
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                                               Sequence 11439, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-11439/c
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Best Local Similarity:
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Of A
Salmonella Sequence, And Methods Of Detection Of Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               741
                                                                                                                                                                                                                                                                                                                                                                                 478 GGCGCGGTGTTCGGCAAG------CTGATCGAGCTGGCCGGCTTCTCCCGCTCC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 ATCGTCGCGGCGGATCCGCCTGCTCGGCACCCGCCAGGCGATGCTGGCGATCGTACTG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              586 GTCTGCGCGCTGCTCACCTACGGCGCGCGTCTCGCTGTTCGTGGTGTTCGCGGTC--- 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----racccerriceccececearerrececeaeaceaearere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGGCGCG 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGATTGATTCCG-----GCGACCATCGCCCTCGGCGCGTTTTCCTTCACCATGGACGCG
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| TGCCCGGCACCCCGCAGATCCAGAACATCATCCCCTCGACCTTCTTCGGCACCCACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 ServalThralaTyrileAlaLeu------AlaLeuLeuServalThrile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ValileGlnAlaileGln
                                                                                                                                                                                                                                                                                                                GlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleVal
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GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.D.
APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Of A
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         US-09-830-972-29_COPY_990_1178 (1-189) x US-09-252-991A-11397 (1-1665)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835 CTGTTCGTCTTCGCCGTGGGCCTGCTCTACCTGCGACGCGGGCG 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAla 157
Length:
Matches:
Conservative:
Mismatches:
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ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. Box 999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 TGGGTTAATACATCAAATGAACAGTCGTATCTTAACCTGAAGATAAGGAAATTAAATCTT 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              907 GCCTTTTTTATGGTAATCAAGGGTGATGTTACTACTACTGGCGCAATTGTTTCATCTGTCATT 966
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847 ATCTATCAATCTATATTGGGGAGTATGTCATTAACCAAAAAAACTATTATGGTAATA 906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                                                                                                                                                                                                                                                                   the coding nucleotides of SEQ ID
NO:28 correspond to nucleotides 22630 through
24426 of SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 Leu-----LeulleLeuAlaLeulleSerLeuPheSerValProVallle 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-28 (1-1797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                         ZIP: 99352
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PROCESSOR (WordPerfect 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
                                                                                                                                                                                                                                                                                                        double stranded
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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81.50
41.24%
20.34%
8.75%
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                                                                                                                                                         FILING DATE: Unknown CLASSIFICATION: 435
                                                                                                                                                                                                                                                                      LENGTH: 1797 bases
TYPE: nucleotide
STRANDEDNESS: double
TOPOLOGY: linear
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OTHER INFORMATION:
Washington
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Best Local Similarity:
Query Match:
             U.S.A.
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APPLICANT: Wong, K.K.; Saffer, J.D.

TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A

TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7562 ACTAATGAGTTAATGAACAAAAAAAAAAAAGACAGAAGAACAGAATATTTTATCTCA 7621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 ValileGinAlaileGinLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:6 corresponds to nucleotides 15735 through 24701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                  ZIE: 99352
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
FILING DATE: UNKNOWN
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                               ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNUL P.O. Box 999
STREET: Washington Way
CITY: Richland
STATE: Washington
COUNTRY: U.S.A.
US-08-853-659A-6; Sequence 6, Application US/08853659A; Patent No. 5925522; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleotide
STRANDEDNESS: double stranded
TOPOLOGY: linear
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81.50
41.24%
20.34%
8.75%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8967 bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             1286 TGGGTTAATACATCAAATGAACAGTCGTATCTTAACCTGAAGATAAGGAAATTAAATCTT 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                   1166 GCCTTTTTTATGCTAACGGTGATGTTACTACTGGCGCAATTGTTTCATCTGTCATT 1107
                                                                                                                                                                                                                                              94 -----------GlyHisValAsnCysThrIleLysGluLeuArgArg 105
                                                                                                                                                                                                                                                                                                                                                                                              124 ValPheThrTyrVal--------GlyAlaLeuPheAsnGlyLeuThr 136
                     --LeuSerValThrileSerPheArgileTyrLysGly 56
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11466 ATTGTACCTATTACCATGTTTATCTCTCTATTATTATTTCCCTCGTTAACCACCATTAT
                                                                                                                                                                                                                                                                                                                      106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp
                                                                                           57 ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leu-----LeulleLeuAlaLeulleSerLeuPheSerValProValile 151
                                                                                                                                                                 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XT/AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Intellectual Property Services ADDRESSEE: Battelle Memorial Institute ADDRESSEE: PNNL P.O. Box 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/853,659A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/08853659A Patent No. 5925522 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: n/a
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81.50
41.24%
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CITY: Richland
STATE: Washington
COUNTRY: U.S.A.
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: Unknow CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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STRANDEDNESS:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
                                                                                                                                                                       ::::::
'742 ATCIATCAATCTATATTGGGGAGTATGTCATCTATTACCCAAATAACTATTATGGTAATA 7801
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                                                                      106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
                                                                                                                                                --GlyAlaLeuPheAsnGlyLeuThr 136
-----GlyHisValAsnCysThrIleLysGluLeuArgArg 105
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PROCESSOR (WordPerfect 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paul W. Zimmerman
Intellectual Property Services
Battelle Memorial Institute
PNNL P.O. Box 999
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Patent No. 5925522
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PRIOR APPLICATION DATA: APPLICATION NUMBER: none
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8967 bases
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41.24%
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CITY: Richland
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Z
ADDRESSEE: Intellect
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Best Local Similarity:
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US-08-853-659A-9/c
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STATE: Wa
COUNTRY:
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Pred. No.:
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Sequence 2, Application US/08853659A
Sequence 2, Application US/08853659A
Patent No. 592552
GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1166 GCCTTTTTTATGGTAATCAAGGGTGATGTTACTACTGGCGCAATTGTTTCATCTGTCATT 1107
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Mismatches:
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ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. Box 999
                                                                                                                                                                                                                                    Length:
Matches:
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                                                                                              TYPE: nucleotide
STRANDEDNESS: single stranded
TOPOLOGY: linear
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20.34%
8.75%
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: ELENGTH: 8967 bass?
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                                                                                                                                                                  US-08-853-659A-67
                                                                                                                                                                                                                 Alignment Scores:
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TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection

TITLE OF INVENTION: Of A

TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       7382 uggaaugaguuccagaaauuaaacccguuuauuaaacucgaucuuucaacguauagcc 7441
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3742 AUCUAUCAAUCUAUAUUGGGGAGUAUGUCAUCUAUUACCCAAAUAACUAUUAUGGUAAUA 7801
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1622 GAAGUUUUCUUAUUDAAAUGAUCCAUACCUUAAAUAAUCAAGGUUUACUUUUGAU 7681
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                                                                                                                                               TrpArgAspileLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu
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                                                                                                  US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-64 (1-8967)
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette 3.50", 1.44 Mb storage
CMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
           Mismatches:
Indels:
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ADDRESSEE: Intellectual Property Servi
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. BOX 999
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APPLICATION NUMBER: US/08/853,659A
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; Sequence 67, Application US/08853659A
Patent No. 5925522
; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
         20.34%
8.75%
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         Local Similarity:
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           Best Local S.
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23236 ATTGTACCTATTACCATGTTTATCGTCTCTATTATTTTCCCTCGTTAACCACCATTAT 23295
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23476 ATCTATCAATCTATATTGGGGAGTATGTCATCTATTACCCAAATAACTATTATGGTAATA 23535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-2 (1-24701)
                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XT/AT
COMPUTER: IBM PC/XT/AT
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Matches:
Conservative:
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Indels:
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Sequence 3, Application US/08853659A;
Patent No. 5925522
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81.50
41.24%
20.34%
8.75%
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US-08-853-659A-2
U.S.A.
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DB:
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Patent No. 5925522 GENERAL INFORMATION:

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AFFLICANT: Wong, K.K.; Saffer, J.D.

TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Of A
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmermer
ADDRESSEE: Paul W. Zimmermer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1586 İGGAATGAGTITCAGAAAATTAAACCCGİİTTATTAAACİCGATCİİTCAACGTATAGCC 1527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu
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Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
                                                                                                                                                                                                                                                ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. Box 999
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
                                                                                                                                                                                                   Paul W. Zimmerman
Intellectual Property
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41.24%
20.34%
8.75%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24701 bases
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                          CITY: Richland
STATE: Washington
COUNTRY: U.S.A.
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STRANDEDNESS: do.
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Best Local Similarity:
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DB:
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Parent No. 5925522
GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
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23416 UGGGUUAAUACAUCAAAUGAACAGUCGUAUCUUAACUGAACUGAAGAAAAUUAAAUCUU 23475
                                                                                                                                                                                                23536 GCCUUUUUUAUGGUAAUCAAGGGUGAUGUUACUACUGGCGCAAUUGUUUCAUCUGUCAUU 23595
                                                                                           -- GlyHisValAsnCysThrileLysGluLeuArgArg 105
                                                                                                                                                                        106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
                                                                                                                                                                                                                                                   ------GlyAlaLeuPheAsnGlyLeuThr 136
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                                            137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerValProValIle 151
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                  GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu
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Mismatches:
Indels:
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ADDRESSEE: PNNL P.O. Box 999
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US-08-853-659A-61/c
Sequence 61, Application US/08853659A
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COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordP
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,6.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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U.S.A.
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Best Local Similarity:
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                                                                                                                                                                                          Sequence 60, Application US/08853659A
Patent No. 592552
GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
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                        ---GlyAlaLeuPheAsnGlyLeuThr 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- LeuSerValThrIleSerPheArgIleTyrLysGly
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                                                                                                   Leu-----LeulleLeuAlaLeuIleSerLeuPheSerValProValIle 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MS-09-830-972-29 COPY 990 1178 (1-189) x MS-08-853-659A-60 (1-24701)
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Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XT/AT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC/A1/A-COMPUTER: IBM PC/A1/A-COMPUTER: MS-DOS
COMPUTER: Word Processor (WordPerfect 5.1)
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                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. Box 999
STREET: Washington Way
CITY: Richland
STATE: Washington
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
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124 ValPheThrTyrVal-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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81.50
41.24%
20.34%
8.75%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
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U.S.A.
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                                                                                                                                                          RESULT 65
US-08-853-659A-60
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Sequence 1, Application US/09762724
; Sequence 1, Application US/09762724
; Patent No. 6664053
; GENERAL INFORMATION:
; APPLICANT: Kovacs, et al.
; TITLE OF INVENTION: Identification of a region of the major surface
; TITLE OF INVENTION: glycoprotein (MSG) gene of human Pneumocystis carinit
; TITLE OF INVENTION: Qlycoprotein (MSG) gene of human Pneumocystis carinit
; TITLE OF INVENTION: 4239-58054
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US/09/162,724
; CURRENT FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 60/096,805
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NOS: 26
                                                                                                                            1276 GGAAGACAACAGTTTGCATCTCTGGTAGGCGCAGGTGTGATGCTGCTC-----CTGATG 1329
                                                                                                                                                                                                                                                                 1390 AGCAACGTCATTCCTACCTTGAAACCATTTCTAACCTACCCAGCCTGTGGAGGCAGGAC 1449
                                                                                                                                                                                                                                                                                                                                                                                                      1102 AGCTCCTTTCTGCTCATATTTCTGGGCAAGAAGATTGCCAGTCTTCACAATTACAGTGTC 1161
                                                                                                                                                                                                                                                                                                              ------ThrileLysGluLeuArgArgLeuPheLeuValAgp 110
                                                                                                                                                                                                                                                                                                                                                                                  111 AspleuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAla 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 LeuPheAsnGlyLeuThrLeu---LeuIleLeuAlaLeuIleSerLeuPheSerValPro 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 ValileTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsn 169
                                                                                                                                                                                                                                             52 -------ArgileTyrLysGlyValIleGlnAlaileGlnLysSerAsp
                                                                                                                                                                        GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 ValLysAspAlaMetAlaLyslleGln-----AlaLyslleProGlyLeuLys 185
                                   34 ValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPhe--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-830-972-29_COPY_990_1178 (1-189) x US-09-762-724-1 (1-3042)
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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US-09-762-724-1/c
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NAME/KEY: CDS
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APPLICANT: Kieke, James A.
APPLICANT: Kieke, James A.
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: On. 6531309el Human Transporter Proteins and Polynucleotides Ence
                                                                                                                                                                                                   1406 ACTAATGAGTTAATGAACAAACAAAGAAGGACAGAAGAACAGGAATATTTTTATCTCA 1347
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.586 TGGAATGAGTTTCAGAAAATTAAACCCGTTTTATTAAACTCGATCTTTCAACGTATAGCC 1527
                                                                                                                                                                                                                                                                                                                                                                                  106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 ValPheThrTyrVal------GlyAlaLeuPheAsnGlyLeuThr 136
                                                                                                                                                                                                                                             93
                                                                                                  ---SerLeuThrValPheSerIle 33
                                                                  1526 GATATTCCAATATTTATTATATTTCTCATTGTTATATATGTAAATTTAGGTCTGGTTGT
                                                                                                                                                                                                                                                                                                              94 ----------GlyHisValAsnCysThrIleLysGluLeuArgArg
                                                                                                                                                                       57 ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                                                                                                                                                       GluValAlalleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu-----
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                                27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu-
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Matches:
Conservative:
Mismatches:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: LEX-0141-USA
CURRENT APPLICATION NUMBER: US/09/795,927
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/185,956
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
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Patent No. 6531309
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Best Local Similarity:
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Pred. No.:
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US-09-795-927-6
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APPLICANT:
APPLICANT:
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Sequence 740, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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2027 ACTGTT---CGTTCACACAGAGCTAAGATTCTTCTCCTGGGTCAAATCCCTAACACCAAC 2083
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1030 GCATGGTCTCCATTTGCTATTTAACGGTAATGGTCACGATTTGGAGCGTTAAGCCATTT 1089
                     LeuPheAsnGlyLeuThrLeu---LeuIleLeuAlaLeuIleSerLeuPheSerValPro 149
                                                               111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAla 130
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----ThrileLysGluLeuArgArgLeuPheLeuValAsp 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                                                                                                                                                  150 ValileTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsn
                                                                                                                                                                                                                                                                                   2084 ATTATAGAAGCATCAATGATTATCGGGAGATCATCACCATTCCTGGGGTGAAA 2137
                                                                                                                                                                                                                                                                   170 ValLysAspAlaMetAlaLysIleGln-----AlaLysIleProGlyLeuLys 185
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Mismatches:
Indels:
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Matches:
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80.50
43.84%
23.97%
8.65%
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DB:
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                                                                                                                                                                                                                                                                                               | Sequence 8, Application US/09795927
| Patent No. 6531309
| GENERAL INFORMATION:
| APPLICANT: Wilganowski, Nathaniel L.
| APPLICANT: Wilganowski, Nathaniel L.
| APPLICANT: Revelli, James A.
| APPLICANT: Revelli, James A.
| APPLICANT: Revelli, James A.
| APPLICANT: Revelli, James B.
| APPLICANT: Revelli, James B.
| APPLICANT: Revelli, James B.
| APPLICANT: Revelli, James B.
| APPLICANT: Turner, C. Alexander Jr.
| TITLE OF INVENTION: Same 3
| TITLE OF INVENTION: Same 3
| TITLE OF INVENTION: Same 3
| TITLE OF INVENTION NUMBER: US/09/795,927
| CURRENT FILING DATE: 2001-02-28
| PRIOR FILING DATE: 2000-02-29
| NUMBER OF SEQ ID NOS: 11
| SOFTHARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 8
| LENGTH: 3749
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1697 TCTTGTGTGTTTACTGGTGCTATTGCTAGGACTATTATCCAG-----GATAAATCTGGA 1750
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|B05 GTGAAGATGGGACACTTTTTCTACACACTGCCAATGCTGTGTTGTTGTTG 1864
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                                                                                                                                 LeuThrValPheSerIleValSerValThrAlaTyrIleAla-LeuAlaLeuLeuSerVa
                                                                  -ValPheGlyAlaSerLeuPheLeuLeuLeuSer
                                                                                                  2804 GATTTGCATTTCTCTCCGTCTCCTACTGTTTTTTTCTGCTTCT-----TTGACTGTTTCT
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 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal-
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Mismatches:
Indels:
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81.00
42.93%
24.24%
8.70%
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ORGANISM: homo sapiens
US-09-795-927-8
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Query Match:
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Pred. No.:
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US-09-795-927-8
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OCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AME/KEY: misc feature
OCATION: (657203)..(657203)
THER INFORMATION: n equals a,
                                 AGATION: (231980). (231980)
OTHER INFORMATION: n equals a,
NAME/FEX: misc. feature
COCATION: (234187)...(23487)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a,
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ION: (312993)..(312993)
INFORMATION: n equals a,
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FION: (319226)..(319226)
R INFORMATION: n equals a,
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ION: (657081)..(657081)
INFORMATION: n equals a,
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LOCATION: (674435)..(674435)
THER INFORMATION: n equals a,
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ION: (871619)..(871619)
INFORMATION: n equals a,
   INFORMATION: n equals a,
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LOCATION: (234220) .. (234220)
OTHER INFORMATION: n equals a,
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ION: (312837)...(312837)
INFORMATION: n equals a,
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|ION: (559241)..(559241)
| INFORMATION: n equals a,
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ION: (622708)..(622708)
INFORMATION: n equals a,
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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ION: (559167)..(559167)
INFORMATION: n equals a,
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ION: (600992)..(600992)
I INFORMATION: n equals a,
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INFORMATION: n equals a,
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LOCATION: (713552)..(713652)
OTHER INFORMATION: n equals
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OCATION: (741684)..(741684)
THER INFORMATION: n equals
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LOCATION:
                                                                                                                                                                                  Sequence 1, Application US/08916421B

Patent No. 6503729

GENERAL INFORMATION:
APPLICANT: Bull et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: januaschii
FILE REFERENCE: Pazzs
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT PILING DATE: 1996-08-22
PRIOR FILING DATE: 1996-08-22
                         104 ArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t,
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1149 GTATTTACACAAATTGGT 1166
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LOCATION: (28222).*(18222)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (84773)..(184773)
OTHER INFORMATION: n equals a, t,
                                                                           124 ValPheThrTyrValGly 129
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a,
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a,
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LOCATION: (98239) ..(98239)
OTHER INFORMATION: n equals a,
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
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LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1664976
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GOCATION: (191995)..(191995)
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Sequence 1, Application US/09692570
Sequence 1, Application US/09692570
Batent No. 6797466
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanocol
                                                                                                                                                                                                       ----AGGAAATACGGAGGAGT 772358
--GITAAAAGTAATATAAAGGAAGTT 772208
                                                                 --CAAAAATTAAGTTTT 772262
                                                                                                                         139 IleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGln 158
                                                                                                   119 AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu
                                 ------ArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPhe
                                                                                                                                                                                                                                                                           772359 ITGICAGAITCICIAAAAAIAITAGCIAAAACICITGAAGAC 772400
                                                                                                                                                                                                                                           159 IleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAsp 172
                                                       CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR PLICATION NUMBER: US 08/916,421
PRIOR PRIOR DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
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ORGANISM: Methanococcus jannaschii
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LOCATION: (28222)..(28222)
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LOCATION: (84773)..(84773)
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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misc_feature (98266). (98266) RWATION: n equals a, t, c, misc_feature (98343). (98343) RWATION: n equals a, t, c, misc_feature (103998). (103998) RWATION: n equals a, t, c, misc_feature (148948). (163385) RWATION: n equals a, t, c, misc_feature (163385). (163385) RWATION: n equals a, t, c, misc_feature (191998). (191998) RWATION: n equals a, t, c, misc_feature (191998). (191998) RWATION: n equals a, t, c, misc_feature (1314187). (234187) RWATION: n equals a, t, c, misc_feature (234187). (234187) RWATION: n equals a, t, c, misc_feature (234187). (312837) RWATION: n equals a, t, c, misc_feature (3109398). (312837) RWATION: n equals a, t, c, misc_feature (312837). (31293) RWATION: n equals a, t, c, misc_feature (312837). (31293) RWATION: n equals a, t, c, misc_feature (31293). (312926) RWATION: n equals a, t, c, misc_feature (31291). (559167) RWATION: n equals a, t, c, misc_feature (31291). (559167) RWATION: n equals a, t, c, misc_feature (359167). (559241) RWATION: n equals a, t, c, misc_feature (55917). (559241) RWATION: n equals a, t, c, misc_feature (55917). (559241)	Б	מ	מ	מ	ь	57	bi	מ	מ	מ	ס	ס	ס	50	מ	מ	מ	ຫ	
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NAME/KEY: misc feature LOCATION: (779455)..(779455) OTHER INFORMATION: n equals a, t, c, or g c, or g or g Þ c, or g c, or g c, or g c, or g c, or g ör ör c, or ΰ NAME/KEY: misc feature LOCATION: (741684)..(741684) OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEY: misc_feature
LOCATION: (779676).
OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEY: misc_feature
LOCATION: (1130881)
OTHER INFORMATION: n equals a, t, LOCATION: (600992)..(600992) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (622708)..(622708) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (674435)..(674435) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (871619)..(871619) OTHER INFORMATION: n equals a, t, FEATURE: NAME/KEY: misc feature LOCATION: (1119881)..(1119881) OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEY: misc_feature
LOCATION: (1310988).
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (1084830)..(1084830) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (657081)..(657081) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (657203)..(657203) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (682442)..(682442) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (713\overline{652})..(713652) OTHER INFORMATION: n equals a, FEATURE:
NAME/KRY: misc_feature
LOCATION: (855539).(855539)
OTHER INFORMATION: n equals a, FEATURE:
NAME/KEY: misc feature
LOCATION: (1096846)
OTHER INFORMATION: n equals a, FEATURE: NAME/KEY: misc_feature LOCATION: (1349473)..(1349473)

DB: 6	Oy 51 PheArgileTyrLysGlyValileGlnalaileGlnLysSerAsp 65	Oy 66	Oy 79 AlaileSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCys 98 :::	Oy 99 Thrielysglu	Oy 103LeuargargleuPheleuValaspaspleuValaspSerleuLysPhe 118 :::: ::: :::	Oy 119 AlaValLeuWetTrpValPheThrTyr131	Qy 132PheAsnGlyLeuThrLeuLeulleLeuAlaLeulleSerLeuPheSer 147 :::	Oy 148CalProVallleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeu-GlyLe 165	Qy 165 ualaasnLysasnValLysAspalaMetalaLysIleGlnalaLysIleProGly 183	Oy 184 -Leulysarglysalaglu 189 	RESULT 74 5518916-5/C ; Patent No. 5518916 ; Patent No. 5518916 ; Patent No. 5518916 ; Patent No. 5518916 ; TTYLE OF INVENTION: CLONED BABESIA DNA ; NUMBER OF SEQUENCES: 7 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/342,480 ; RILING DATE: 21-NOV-1994 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 989,616 ; FILING DATE: 14-DEC-1992 ; APPLICATION NUMBER: 989,416 ; FILING DATE: 14-DEC-1992 ; FILING DATE: 14-DEC-1992 ; FILING DATE: 14-DEC-1992	APPLICATION NUMBER: 333,155 ; FILING DATE: 04-APR-1989 ; SEQ ID NO:5: ; LENGTH: 1990 5518916-5
Alignment Scores: Pred. No.: Pred. No.: Score: Score: Best Local Similarity: Best Local Similarity: A 1.24 Mismatches: Best Local Similarity: A 6 8 65 Maches: Best Local Similarity: A 74 Mismatches: Best Local Similarity: A 6 6 8 Mismatches: Best Local Similarity: A 74 Mismatches: Best Local Similarity: A 6 6 8 Mismatches: B 6 8 6 8 Mismatches: B 6 8 6 8 Mismatches: A 7 8 6 8 Mismatches: B 7 8 6 8 Mismatches: B 7 8 6 8 Mismatches: B 7 8 6 8 Mismatches: B 7 8 6 8 Mismatches: B 7 8 8 6 8 Mismatches: B 8 6 8 Mismatches: B 8 6 8 Mismatches: B 8 6 8 Mismatches: B 7 8 Mismatches: B 7 8 Mismatches: B 7 8 Mismatches: B 8 6 8 Mismatches: B 8 6 8 Mismatches: B 8 6 8 Mismatches: B 8 6 8 Mismatches: B 9 Mismatches: B 9 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 8 Mismatches: B 1 9 Mismatches: B 1 8 Mismatches: B 1	Qy 6 LeuTyrTrpArgAspile	Qy 19 GlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThr 37 Db 771933 GACGAAAAAAAGTTTATATTATTATAATTATAGCTGCGATACCTCCCTAATATACA 771992	Qy 38 AlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyVal 57 Db 771993 TATTATTTACACTTAACCCTAAAAGTATGATTATATTTGTAGTTATATACGTGGGAGCT 772052	Qy 58 Ile	Oy ' 69 ProPheArgAlaTyr	Qy 84 LeuValGInLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeu 103 	OY 104ArgargLeuPheLeuValaspaspLeuValaspSerLeuLygPhe 118	Oy 119 AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 138	Oy 139 IleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGln 158 :::	Qy 159 IleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAsp 172	RESULT 73 5171685-5/c ; Patent No. 5171685 ; Patent No. 5171685 ; Patent No. 5171685 ; TRAVIS C.; PALMER, GUY H.; JASMER, DOUGLAS P.; REDUKER, DAVID W.; GOFF, WILL L.; PERRYMAN, LANCE E.; DAVIS, WILLIAM C.; TITLE OF INVENTION: CLONING OF THE BABESIA BOVIS 60 KD ANTIGEN ; TOWNER OF SEQUENCES: 7 ; CURRENT APPLICATION DATA: ; RELIGATION NUMBER: US/07/504,461 ; FILING DATE: 04-APR-1990 ; SEQ ID NO:5: ; LENGTH: 1990	Alignment Scores: 1.32 Length: 1990 Score: 80.00 Matches: 50 Percent Similarity: 37.89% Conservative: 36 Best Local Similarity: 22.03% Mismatches: 64 Query Match: 8.59% Indels: 77

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80.00
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8.59%
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Best Local Similarity:
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;PATENT N. S171685
;RAPLICANT: MCELMAIN, TERRY F.;HINES, STEPHEN A.;MCGUIRE,
;RRAVIS C.;PALMER, GUY H.; JAGNER, DOUGIAS P.;REDUKER, DAVID W.
;GOFF, WILL L.;PERRYMAN, LANCE E.;DAVIS, WILLIAM C.
; TITLE OF INVENTION: CLONING OF THE BABESIA BOVIS 60 KD ANTIGEN
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/504,461
; FILING DATE: 04-APR-1990
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Matches:
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; Patent No. 5518916
; Patent No. 5518916
; Pouglas P.; Patent No. 5518916
; DOUGLAS P.; REDUKER, DAVID W.; GOPF, WILL L.; STILLNER, DAVID
; TITLE OF INVENTION: CLONED BABESIA DNA
; TUMBER OP SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/342,480
; FILING DATE: 21-NOV-1994
; APPLICATION NUMBER: 989,616
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: 594,461
; FILING DATE: 14-DEC-1990
; FILING DATE: 04-APR-1990
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Mismatches:
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CURRENT APPLICATION NUMBER: US/08/916,421B CURRENT FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: US 60/024,428 PRIOR FILING DATE: 1996-08-22 NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin version 3.1 SEQ ID NO 1
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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LOCATION: (982<sup>3</sup>9)..(98239)
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
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LOCATION: (234187)
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LOCATION: (163385)..(163385)
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   FILE REFERENCE: PB275
                                                                                                                                   LENGTH: 1664976
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; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INVENTION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
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564 TTCCTCGTGCACAACATTGTTGTTCAA-----CAGACCAGTGACGAAGTAGTGGTAATC 611
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                                                                                                                                                                                                                                                                                                769 GTTGAAGAACTTGGCGTT-----CATACTGTTTACTGTCAAATAAGTCTTGTAGTT 719
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Matches:
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APPLICATION NUMBER: 333,155
FILING DATE: 04-APR-1989
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Sequence 1, Application US/09692570;
Patent No. 6797466
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6797466
TITLE OF INVENTION: jannaschii
FILE REFERENCE: P8275C1
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CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: US 08/916,421
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I INFORWATION: n equals a,
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LOCATION: (981<u>2</u>0)..(98120)
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PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
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LOCATION: (779455)..(779455)
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Sequence 2219, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Number: US/09/583,110

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-12

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322
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-----TTCGCATTGGATGTTAAGTTTACTTATTTTAGGATATCTTTTAGTGATT 657
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
1609511 TAAAAATAGGAAGGATGAGCTA 1609490
                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2219
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38.24%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 IleLysGluLeuArgArgLeuPheLeu---------ValAspAspLeu 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThr 99
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Mismatches:
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NAME/KEY: misc_feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                          PEATURE:
NAME/KEY: misc feature
LOCATION: (1084830)
OTHER INFORMATION: n equals a,
                                                                                                                                                NAME/KEY: misc feature
LOCATION: (871519)..(871619)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (1130881)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (1096846)
OTHER INFORMATION: n equals a,
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LOCATION: (855539) ..(855539)
OTHER INFORMATION: n equals a,
INFORMATION: n equals a,
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8.59%
                         NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals
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Query Match:
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133 -----AsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProVal 150
292 TITITGACTIATACCGIAITAAIAAGIGIITITIAITCCIAGAGIIAGCAAICITICAITIA 351
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-125CP
CURRENT PELLORION NUMBER: US/09/602,787A
CURRENT FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR PILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
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PRIOR PILING DATE: 1999-07-09
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                                                                  20 AlaSerLeuPheLeuLeuLeuSerLeuThrValPhe-----
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FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932125.6
FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 301, Application US/09602787A Patent No. 6696561 GENERAL INFORMATION: APPLICANT: Pompejus, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kr<sup>n</sup>ger, Burkhard
Sch<sup>n</sup>der, Hartwig
Zelder, Oskar
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US-09-602-787A-301
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APPLICANT:
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                               SerValValAspLeu---LeuTyrTrpArgAspIleLysLysThrGlyValValPheGly 19
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US-09-107-433-2215
US-09-107-433-2215
Sequence 2215, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
THERAPEUTICS
THERAPEUTICS
    -----AsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProVal
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...774
SEQUENCE DESCRIPTION: SEQ ID NO: 2215:
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COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2215:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECTLE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
STATE: Massachusetts
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24.51%
8.54%
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    133
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FACELICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 15236
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                                                                                                                                                                           221 ATTCAAAAA -----GTAGTG 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 cercharitégreserecrecéricirecresaanacecericiritésecereacrere 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 ACCCGAGCCAGCAATGATCTCACCGCGGTGCCAATTGGGTGGCTTTGGGCATTGTTCCG 394
                                                                                                                                                     21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
                                                                                                                                                                                                                                  41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
                                                                                                                                                                                                                                                                                                           61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
                                                                          TrpArgAspIleLysLys-----ThrGlyval-----valPheGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPhe---
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                                    US-09-830-972-29_COPY_990_1178 (1-189) x US-09-602-787A-301 (1-1500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 AIGGICACCGGGCTGCCTTGATTGCGATTGTGCTGGTGGCGTTGTTT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPhe 146
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Matches:
Conservative:
Mismatches:
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236 GCAGAAGATCTAGGCCAGCATTAT----
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ORGANISM: Human
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Matches:
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R FILING DATE: 1999-08-27

R APPLICATION NUMBER: DE 19941378.9

R FILING DATE: 1999-08-31

R FILING DATE: 1999-08-31

R PILING DATE: 1999-08-31

R APPLICATION NUMBER: DE 19941395.9
                                                                                       FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932190.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1999-07-14
PPLICATION NUMBER: DE 19940764.9
FILING DATE: 1999-08-27
APPLICATION NUMBER: DE 19940765.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DE 19942077.7
FILING DATE: 1999-09-03
APPLICATION NUMBER: DE 19942078.5
FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: DE 19942079.3 PRIOR FILING DATE: 1999-09-03 PRIOR APPLICATION NUMBER: DE 19942088.2 PRIOR FILING DATE: 1999-09-03 NUMBER OF SEQ ID NOS: 678 SEQ ID NO 301 LENGTH: 1500
DE 19932128.0
                                    DE 19932180.9
                                                                          APPLICATION NUMBER: DE 19932182.5
                                                                                                                               FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932191.4
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                                                                                                                                                                                                            FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932212.0
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LING DATE: 1999-07-09
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FILING DATE: 1999-07-09
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FILING DATE: 1999-07-09
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APPLICATION NUMBER: DE 19940766.5
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FILING DATE: 1999-08-27
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FILING DATE: 1999-08-27
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US-09-602-787A-301
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Query Match:
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Pred. No.:
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US-09-134-001C-118/C
Sequence 118, Application US/09134001C
Sequence 118, Application US/09134001C
Sequence 118, Application US/09134001C
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: S674
SEQ ID NO 118
SEQ ID NO 118
                                                                                                                                                                                                                                                                                                                                                                       148
                                                                                                                    96 ValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSer 115
                                                                                                                                                                                                                                                                                                      ---agartreccrarcre---regrirriccaacraarreaacragegerirararagea 136
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707 TTATACTCATTTGAATTAGTGAAATCTTCACTTTTTTTAATAATAATAAATTATCTATT 648
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                                                                                                                                                        ::: ||| ::: ||| ::: ||| :::||||::: :::||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: || ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: |
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------GluGluLeuValGlnLysTyr----SerAsnSerAlaLeuGlyHis
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Matches:
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISNS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

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WHING APPLICATION NUMBER: 60/231,498

WHING APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

WUMBER OF SEQ ID NOS: 207012
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Patent No. 6812339
GENERAL INFORMATION:
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Best Local Similarity:
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US-09-949-016-73264
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LENGTH: 601
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GTAGAAAGATATGGTGGAFTTGATACTTTAGAGTTATCCGAAGCAATATTTTGTGCCGAT 3015
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                 129 GlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAlaLeuIleSerLeuPheSer---147
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Batent No. 6448034

GENERAL INFORMATION:
APPLICANT: Good, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 2074/70

CURRENT APPLICATION NUMBER: US/08/836,687B

CURRENT FILING DATE: 1995-11-20

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 29

LENGTH: 7454
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                            APPLICATT: VENTER, J. Craig et al.
APPLICATT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307;
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3567
LENGTH: 3811
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383 TTTGTGATA-----ATTAATATCATAAAGTTTATCAATCTTTTAATAGCACTTACA 333
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Patent No. 6812339
476 AGACACTTATACAAATGTTTT
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ORGANISM: Human
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Sequence 1387, Application US/09949016

Sequence 1387, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOFFWARE: PEASESEC FOR Windows Version 4.0
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 15309
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                                                          Sequence 15309, Application US/09949016 Patent No. 6812339
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Best Local Similarity:
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US-09-949-016-15309
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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105633 TGGCATGAAATTTTTAAAATTGAAAATTGCATGGAATGCTACATTCACCATGTAATGG 105574
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43
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Matches:
Conservative:
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Indels:
                                     PRIOR APPLICATION NUMBER: 08/09/949,016

PRIOR PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-3

PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 14543

LENGTH: 387902
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                FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(387902)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14543
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38.46%
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NAME/KEY: misc_feature
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US-09-949-016-12557/c
                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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DB:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-0-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASISE Of FOR Windows Version 4.0
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105633 TGGCATGAAATTTTTAAAATTGAAAAATTGCATGGAATGCTACATTCACCATGTAATGGG 105574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 SerAspGluGlyHis-------ProPheArgAlaTyrLeuGluSerGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 AlaileSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHis-----
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-543-681A-2407
; Sequence 2407, Application US/09543681A
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79.00
38.46%
25.44%
8.49%
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) LOCATION: (1)...(421883)
) OTHER INFORMATION: n = A
US-09-949-016-12557
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                  LENGTH: 421883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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RESULT 93
US-09-949-016-12900
i Sequence 12900, Application US/09949016
j Patent No. 6812339
i GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
PILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-30
PRIOR FLING DATE: 2000-10-03
PRIOR FLING DATE: 2000-10-03
PRIOR FLING DATE: 2000-09-08
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 GIGTCATTACTGTCCCTGGTGCCGCTGATTGCCGTCGTGTTCGCGCTGTTTGCGGCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-830-972-29_COPY_990_1178 (1-189) x US-09-489-039A-5041 (1-879)
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255
655
655
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuTyrTrpArgAspIleLysLys------
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   TITLE OF INVENTION: NUCLEIC ACID AND AMING TITLE OF INVENTION: PREDMONIAE FOR DIAGNOS FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                         ORGANISM: Klebsiella pneumoniae US-09-489-039A-5041
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 14342
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                           GENERAL INFORMATION:

APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2709 .1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2407
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         Patent No.
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, ORGANISM: Human
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                              ValileGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12990
LENGTH: 462589
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                                                       TYPE: DNA
ORGANISM: Human
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Sequence 1, Application US/09198452A;
Patent No. 6559294
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments;
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever ITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT APPLICATION NUMBER: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124336 CCCTTGTGTTATCCCCCAGTTCTTGCACAGAACTTGTGGCACGCAGATTAATCATAGAAA 124395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124276 AACTCTTAATAAAGCTTGGCTATTAGTCTTGCTAAACGGTAAAGACTGTTTCTGTCTTAT 124335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124396 TTATTGAATAAATTAATGGTCCCATTTTTTTCCTAGCTCCACTGTGGTGAAGTCTCAGAT 124455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SerValThrlleSerPheArglleTyrLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 Asn------CysThrIleLysGluLeuArgArgLeuPheLeuValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TyrValGlyAlaLeuPheAsnGlyLeu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrieuLeulleLeuAlaLeulleSerLeuPheSerValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-12412 (1-476044)
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 12412
LENGTH: 476044
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78.00
38.17%
24.19%
8.38%
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Best Local Similarity:
Query Match:
DB:
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NAME/KEY: misc feature
LOCATION: (120001). (135000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (135001)..(150000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (150001)..(155000)
OTHER INFORMATION: n=a or c or g or t
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or t
LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (300001)..(315000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
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LOCATION: (165001)..(180000)
OTHER INFORMATION: n=a or c or g or t
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OCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (285001)..(300000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c or g or
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CCCATION: (225001)..(240000)
THER INFORMATION: n=a or c or g or
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THER INFORMATION: n=a or c or g or
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LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or
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                                                                                                                                                     LOCATION: (1)...(15000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc. feature
CATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or
                                                TYPE: DNA
ORGANISM: Chlamydia pneumoniae
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OTHER INFORMATION: n=a or c or
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LOCATION: (270001)..(285000)
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LOCATION: (330001)..(345000)
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                                                                                                                             NAME/KEY: misc_feature
SEQ ID NO 1
LENGTH: 1230025
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (43501)..(45000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (45001)..(46500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (46501)..(48000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (480001)..(49500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (49501)..(51000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (49501)..(51000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (495001)..(52500)
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LOCATION: (390001)..(405000)
OTHER INFORMATION: n=a or c or g or
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OCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (645001)..(660000)
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                                                                                                                                            NAME/KEY: misc feature
LOCATION: (360001)..(375000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (405001)..(420000)
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LOCATION: (525001)..(540000)
THER INFORMATION: n=a or c or g or
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OCATION: (540001)..(555000)
OTHER INFORMATION: n-a or c or g or
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OCATION: (615001)..(630000)
THER INFORMATION: n=a or c or g or
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LOCATION: (375001)..(390000)
OTHER INFORMATION: n=a or c or g or
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COCATION: (585001)..(600000)
THER INFORMATION: n=a or c or g
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OCCATION: (555001)..(570000)
YTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
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LOCATION: (660001)..(675000)
OTHER INPORMATION: n=a or or
NAME/KEY: misc_feature
AME/KEY: misc feature
LOCATION: (34501)..(36000)
THER INFORMATION: n=a or c
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1043296 CATCACCATTATGAATATCAGGGCCTCCCAGAGACTAAAATCGTCATGCGCTTTTGGATC 1043355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1033117 CTACAAGTACTTAGTTGTTGATTAAGGAAA---AAACGCCTTTTCTTATGCTCTCCATTG 1033173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1032877 GTAGCTCTAAGAAGTTCTACAATTCCTATAGCTCAAGATGTGGCTTATGTTTTAGCTGCT 1032936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1032997 GGAGATACCGGGTCACTACTTCTAGGGGGCCTGCTAGGGAGCTGCGGCTGTTATGCTGCGC 1033056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1033057 GCAGAATGCATCCTAGTCGTGATCGGAGGAGTTTTTGTTGCTGAAGCGGGATCTGTCATT 1033116
            112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112
                              1032937 CTTGTAGGGGCTTGTATGGATTCTTATGGTATAATGGTTTCCCGGCCCAGCTCTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu
                                                                                   6 LeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 LeuSerLeu-----ThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 LeuleuSerValThrileSerPheArgileTyrLysGlyValileGlnAlaileGlnLys
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34
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65
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APPLICANT: Kalman, Sue
APPLICANT: Roalin
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: PastSEQ for Windows Version 3.0
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                                                                                                                                                                                       1043356 TTTAGTTTTGTATGCGCA 1043373
                                                                                                                                                                                                                                                                               Sequence 1, Application US/09438185A
Patent No. 6822071
GENERAL INFORMATION:
                                                                                                                                                                 PheThrTyrValGlyAla 130
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78.00
40.41%
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8.38%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                              RESULT 96
US-09-438-185A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1043119 GGAGATACCGGGTCACTACTTCTAGGGGGCCTGCTAGGGAGCTGCGCTGTTATGCTGCGC 1043178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLys 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ProPheArgAlaTyrLeuGlu 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerGlu------ValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92
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Mismatches:
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OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or
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LOCATION: (82501)..(84000)
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OTHER INFORMATION: n=a or c or g
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OTHER INFORMATION: n=a or c or g
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ON: (73501)..(750000)
INFORMATION: n=a or c or
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LOCATION: (855001)..(870000)
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                              NAME/KEY: misc feature
LOCATION: (720001).(735000)
OTHER INFORMATION: n=a or c.
COCATION: (70501)..(720000)
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LOCATION: (765001)..(780000)
OTHER INFORMATION: n=a or c
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Best Local Similarity:
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Sequence 215. Application US/09543681A
Patent No. 6605709
GENERAL INPORTATION:
GENERAL INPORTATION:
TITLE OF INVENTION:
UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIJ
TITLE OF INVENTION:
UNCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION:
UNREWT APPLICATION NUMBER: US/09/543,681A
CURRENT PILING DATE:
PRIOR FILING DATE:
1999-04-09
NUMBER: OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 TTGATATCCAGAAGGATAGCCGCCATTTCTAACGATGCTGTACAAGAAGGTGTTAACAGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIle 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 TCACCACAGAGGTTGCCACTTTCCATCGCCTGTTTCATATTCTGTGCCAACA 63
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Mismatches:
Indels:
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; Sequence 751, Application US/09620312D
; Patent No. 6569662
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                                                                                                                                                                                                                                                                             ORGANISM: Proteus mirabilis
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77.50
43.85%
23.08%
8.32%
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Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
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Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
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Best Local Similarity:
Query Match:
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JS-09-543-681A-215/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 730
                       1033174 CATCACCATTATGAATATCAGGGCCTCCCAGAGACTAAAATCGTCATGGGCTTTTGGATC 1033233
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250 GTCAATTCCTTGAAATTAACCGTTTATCAAGCATTAATCAATTTCCCACTTGATGATGTT
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Matches:
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                                                                                                                                                                        Sequence 730, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:
                                                                                          1033234 TTTAGTTTTGTATGCGCA 1033251
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CURRENT APPLICATION NUMBER: US/09/949,016
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Job time : 2629.5 secs
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Batent No. 6812319
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REFERENCE: CLO01307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 LeuValAspAspLeuValAspSerLeuLysPheAla---ValLeuMetTrpValPheThr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 TyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPhe 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluSerGluValAlaIleSer-----GluGluLeuValGlnLysTyrSerAsnSerAla 92
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GTAGGACAGGATTCTGTGCCCTATATGATTTGTCTGATTCACATACTCGAAGAATGGTTT
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34
18
44
25
6
                                                        APPLICANT: Obn Tillinghast
APPLICANT: Dranac, Radoje T.
TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_f_genes Version 1.0
SEQ ID NO 751
LENGTH: 2020
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Matches:
Conservative:
Mismatches:
Indels:
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77.50
42.98%
28.10%
8.32%
           Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
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US-09-620-312D-751
                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ArglleTyrLysGlyValileGlnAlaIleGlnLysSerAspGluGlyHisProPheArg
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASLESEQ for Windows Version 4.0
SEQ ID NO 12735
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Best Local Similarity:
                                                                                                                                                                                                                                                           , ORGANISM: Human
US-09-949-016-12735
                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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-Q=/Cgn2_1/USPTO spool p/USOS330972/runat_16062005_153944_18950/app_query.fasta_1.654
-DE-Published Applications NA -OFMT-fastap -SUPFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=bluman40.cdi -LIST=48 -DOCALIGN=200 -THR SCORE-pct -THR MAX=100
-THR MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT-pto -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000
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-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 - YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7
                                                                                                     (without alignments)
2633.504 Million cell updates/sec
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1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189
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1: /cgn2_6/ptodata/1/Pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/Pubpna/PCT_NEW PUBL.seq:*
3: /cgn2_6/ptodata/1/Pubpna/PCT_NEW PUBL.seq:*
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11: /cgn2_6/ptodata/1/Pubpna/US09_PUBCOMB.seq:*
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                                                                   ; Search time 445.5 Seconds
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- nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6054689 seqs, 3103772919 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                June 19, 2005, 03:56:06
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Btribution.		Description	Sequence 9764, Ap	equence 9	9	e 4	'n	equence 22	~	æ	æ ·	Ω,	'n	'n	m .	4		N.	'n	ä	Sequence 4		'n	ö	H	4	m	4 1	4,6	Sequence 22, Appl	10	sednence 387	- :	1	191	77.	10,	Sequence 976	349,	976	976	Sequence 976	8477	ce 333	e 213	210.	Sequence 3	
of the total score di	SUMMARIES	QI.	6-157-976	6-157-976	6-157-	6-157-452	-386-1	-348-2	7-502-	7-2	6-258-8	0-653-	-140-5	-599A-5	7-597-310	6-157-45	0-036-5	0-946-	-386-5	5-523	6-157-45	-205-5	7-669-5	9-388-62	6-157-1	6-157-453	6-258-3	6-157-4	0-036-5	US-10-220-891-22	8-35UA-	1-643-38	-346-1/	71-559-019-	-194-1	-267-502-21	-466-258-10	-956-157-97	323-245A-349	10-956-157-97	-10-956-157-976	-10-956-157-976	52-84	8-10-084-817-33	-10-267-502-21	-09-954-456-210	8-10-172-118	
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and is de		Score	931	931	931	931	931	931	931	931	931	931	931	931	931	931	931	927	927	927	927	927	927	927	927	927	. 927	927	927	921	816	414	808	806	905	904.5	886	872	867	805	802	718	695	682	682	682	682	
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US-10-956-157-9764

/pubpna/US11_NEW_PUB.seq:*/pubpna/US60_NEW_PUB.seq:*

/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

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Sequence 9764, Application US/10956157
PUBLICACION NO. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 9764
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Substance 4529, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: HUMAN OSTBOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PATENTIN Version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             968 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuMetTrpValPheThrTyrValG1yAlaLeuPheAsnG1yLeuThrLeuLeuIleLeu
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189
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                                                           Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
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; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9764
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ORGANISM: Homo sapiens
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Best Local Similarity:
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       Mismatches:
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Fatent No. US20020010324A1
GENERAL INFORMATION:
APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REPRENCE: GP-30165-C1;
CURRENT APPLICATION NUMBER: US/09/789,386
CURRENT FILING DATE: 2001-02-21
FRIOR APPLICATION NUMBER: U.K. 9916898.1
FRIOR APPLICATION NUMBER: U.K. 9916024.5
FRIOR APPLICATION NUMBER: U.K. 9916024.5
FRIOR FILING DATE: 1998-07-19
FRIOR FILING DATE: 1998-07-2
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRSESEQ FOR WINDOWS VERSION 3.0
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ORGANISM: HOMO
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 4528
LENGTH: 3478
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Matches:
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Mismatches:
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                                                                                       Gaps:
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3.08e-106
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931.00
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ORGANISM: Homo sapiens
                                    Percent Similarity:
Best Local Similarity:
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US-10-956-157-4528
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Pred. No.:
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Mismatches:
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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 212
SEQ ID NO 212
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931.00
100.00%
100.00%
LENGTH: 3579
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                          ; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22
                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                     NAME/KEY: CDS
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Pred. No.:
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APPLICANT: CHENKAN, PIERRE
APPLICANT: CHENKAN, PIERRE
APPLICANT: MOSUREGO, ALON
APPLICANT: MOSUREGO, ALON
APPLICANT: MOSUREGO, ALON
APPLICANT: MOSUREGO, ALON
APPLICANT: MOSUREGO, ALON
APPLICANT: MOSUREGO, ALON
APPLICANT: MOSUREGO, ALON
APPLICANT: MOSUREGO, BOLIA
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
CURRENT APPLICATION NUMBER: US 09/314,161
PRIOR PILING DATE: 1998-12-22
PRIOR PILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: PCT/US98/14715
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-31
SETOR APPLICATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-07-31
SOFTWARE: PALCATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
SOFTWARE: PALCATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
SOFTWARE: PALCATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
SOFTWARE: PALCATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
SOFTWARE: PALCATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
SEQ ID NO 22
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                                                                                                                            US-09-830-972-29_COPY_990_1178 (1-189)
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Patent No. US20020072493A1
GENERAL INFORMATION:
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               Percent Similarity:
Best Local Similarity:
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(3579)
US-10-466-258-8
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Best Local Similarity:
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ORGANISM: Homo e
FEATURE:
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Pred. No.:
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LENGTH: 3579
        US-10-327-213-8
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Sequence 8, Application US/10327213

Sequence 8, Application US/10327213

Publication No. US20040121341A1

GENERAL INFORMATION:

APPLICANT: FILBIN, MARIE T.

APPLICANT: DOMINICANI, MARCO

APPLICANT: CAO, ZIXUAN

TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)

TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION FILE REFERENCE: CUNY/003

CURRENT APPLICATION NUMBER: US/10/327,213

CURRENT APPLICATION NUMBER: US/10/327,213

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: DNA

TYPE: DNA
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               TYPE: DNA ORGANISM: Homo sapiens
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Query Match:
DB:
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                                   ; ORGANISM: Hom
US-10-267-502-212
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LENGTH: 3579
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Publication No. US20040132096A1
GENERAL INPORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENITON: ASSAY
FILE REFERENCE: P80966 GCW
CURRENT APPLICATION NUMBER: US/10/466,258
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
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US-09-758-140-5

Sequence 5, Application US/09758140

Sequence 5, Application US/09758140

Sequence 5, Application US20020012965A1

GENERAL INFORMATION:

APPLICANT: Strittmatter, Stephen M.

APPLICANT: Strittmatter, Stephen M.

TITLE OF INVENTION: NO. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth FILE REFERENCE: 44574-5073-US

CURRENT APPLICATION NUMBER: US/09/758,140
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PRIOR APPLICATION NUMBER: IL 124
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
LENGTH: 3579
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                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                       NAME/KEY: CDS
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Pred. No.:
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Publication No. US20040253218A1
GENERAL INFORMATION:
GENERAL INFORMATION:
FUBLICANT: COHEN, Irun R.
FAPLICANT: CHEN, Irun R.
FAPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
TILLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
FILE REPRENCE: EIS-SCHWARTZ=2A
CURRENT APPLICATION NUMBER: US/09/893,348
FRIOR APPLICATION NUMBER: US/09/893,348
FRIOR APPLICATION NUMBER: US/09/893,348
FRIOR PELLING DATE: 2001-06-28
FRIOR PELLING DATE: 1999-05-19
FRIOR FILING DATE: 1999-05-19
FRIOR FILING DATE: 1999-05-19
FRIOR APPLICATION NUMBER: US 09/218,277
FRIOR PELLING DATE: 1999-05-19
FRIOR FILING DATE: 1999-05-19
FRIOR FILING DATE: 1999-05-19
FRIOR FILING DATE: 1999-12-22
FRIOR FILING DATE: 1999-12-22
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OTHER INFORMATION: Human DNA encoding for No. US20020077295Alo protein (KIAA0886, Ge OTHER INFORMATION: Accession No. US20020077295Al AB020693)
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                GENERAL INFORMATION:

APPLICANT: STRITMATTER, STEPHEN M.

TITLE OF INVENTION: NGCORGEREPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REPERENCE: CO77 CIP US
CURRENT PELLIGE OFFE: 2001-10-06
CURRENT FILING DATE: 2001-10-06
FRIOR PELLORION NUMBER: 09/758,140
FRIOR PELLORION NUMBER: 09/758,140
FRIOR PILING DATE: 2001-01-12
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NAME/KEY: CDS
LOCATION: (135)..(3710)
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PRIOR APPLICATION NUMBER: US 60/175,707
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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US-09-972-599A-5
; Sequence 5, Application US/09972599A
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ORGANISM: Homo sapiens
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                                                                                                                                      Sequence 310, Application US/10717597

Publication No. US20040110221A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Twine, Natalie C.

APPLICANT: Twine, Natalie C.

APPLICANT: Trepicchio, William L.

APPLICANT: Store, Jennim, Donna K.

APPLICANT: Store, Jennim, Donna K.

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APPLICANT: Store, Jennim, Donna K.

APPLICANT: Store, Jennim, Donna K.

FILE REFERENCE: AM101080L

CURRENT APPLICATION NUMBER: US 60/459, 782

PRIOR FILING DATE: 2003-11-21

NUMBER OF SEQ ID NOS: 4904

SOFTWARE: PatentIn version 3.2

LENGTH: 4053

LENGTH: 4053
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Mismatches:
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Matches:
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Gaps:
                                                                       3684 ATCCCTGGATTGAAGCGCAAAGCTGAA 3710
                                                 IleProGlyLeuLysArgLysAlaGlu 189
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100.00%
100.00%
100.00%
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; ORGANISM: Homo sapiens
US-10-717-597-310
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                  -10-717-597-310
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Pred. No.:
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Sequence 4532, Application US/10956157
Publication No. US20050118625A1
GENERAL INRORMATION:
GENERAL INRORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPRENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-110-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 4532
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                               3624 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTAATGGCTAAAATCCAAGCAAAA 3683
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                                                                                                                   HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp 160
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Matches:
Conservative:
Mismatches:
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3631 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 3690
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                                                                                                                                                                                                                                                                                                                                                                                                           Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
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COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/660,946
FILING DATE: 12-Sep-2003
APPLICATION NUMBER: US/09/228,213A
FILING DATE: CUNKNOWN:
APPLICATION NUMBER: 08/700,607
FILING DATE: CUNKNOWN:
ATTORNEY/AGRY INFORMATION:
NAMME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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Indels:
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                                                                                                                                   181 IleProGlyLeuLysArgLysAlaGlu 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                   Sequence 2, Application US/10660946 Publication No. US20040063131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-855-0555
TELEFAX: 415-945-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
Au-Young, Janice
Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 799 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity:
Query Match:
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                                                               3631 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 3690
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                                                                                                                                                                                                                                      Sequence 53, Application US/10060036
| Sequence 53, Application US/10060036
| Publication No. US20030073144A1
| GENERAL INFORMATION:
| APPLICANT: Benson, Darin R. |
| APPLICANT: Lodes, Michael D. |
| APPLICANT: Lodes, Michael J. |
| APPLICANT: Persing, David H. |
| APPLICANT: Jiang, Yuqiu T. |
| APPLICANT: Jiang, Yuqiu T. |
| APPLICANT: Jiang, Yuqiu A. |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| FILE REFERENCE: 210121.566 |
| CURRENT APPLICATION NUMBER: US/10/060,036 |
| CURRENT APPLICATION NUMBER: US/201-30 |
| NUMBER OF SEQ ID NOS: 4560 |
| NUMBER OF SEQ ID NOS: 4560 |
| SOFTWARE FEASTSEQ for Windows Version 4.0 |
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: BLOCAME, COLLEGE
APPLICANT: BLOCAME, David
APPLICANT: Hook, Derek
APPLICANT: Klincak, Leszek
APPLICANT: Rajan, Michael
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
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APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANTON: WUMBER: US/10/175,523
CURRENT FILING DATE: 2002-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR PLICATION NUMBER: US 60/399,151
PRIOR PLICATION NUMBER: US 60/317,828
PRIOR PLING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-25
PRIOR PLING DATE: 2001-09-25
PRIOR PLING DATE: 2001-11-14
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
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PRIOR PLING DATE: 2002-01-18
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                          676 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
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ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                          22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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US-10-175-523-156
; Sequence 156, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
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| FEACHL NO. USCULLUISTANI
| APPLICANT: MICHALOVICH, DAVID
| APPLICANT: MICHALOVICH, DAVID
| APPLICANT: PRINJTA, RABINDER KUMAR
| TITLE OF INVENTION: NOVEL COMPOUNDS
| FILE REPERENCE: GP-30165-C1
| CURRENT APPLICATION NUMBER: US/09/789,386
| CURRENT FILING DATE: 1999-07-19
| PRIOR APPLICATION NUMBER: U.K. 9916898.1
| PRIOR PILING DATE: 1999-07-12
| PRIOR FILING DATE: 1998-07-22
| PRIOR FILING DATE: 1999-07-22
| PRIOR FILING DATE: 1999-07-22
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 5
| LENGTH: 1122
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Patent No. US20020010324A1
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| Patent No. US200203034800A1
| GENERAL INFORMATION:
| APPLICANT: Cao, Li
| TITLE OF INVENTION:
| FILE REFERENCE: 1459.004/200130.449
| CURRENT APPLICATION NUMBER: US/09/765,205
| CURRENT FILING DATE: 2001-01-17
| PRIOR APPLICATION NUMBER: US/09/212,440
| PRIOR FILING DATE: 1998-12-16
| NUMBER OF SEQ ID NOS: 46
| SOFTWARE: PastSEQ for Windows Version 3.0
| LENGTH: 1610
| TYPE: DNA
| US-09-765-205-5
                                                                                                                                                                                                        22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wouth

TITLE OF INVENTION: HUANA OSTBOARTHRITTS AND HUMAN PROTEASES

TITLE OF INVENTION: HUANA OSTBOARTHRITTS AND HUMAN PROTEASES

TITLE OF INVENTION: UNMER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 4527
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Conservative:
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COGANISM: Homo sapiens
US-10-956-157-4527
; ORGANISM: Homo sapiens
US-10-175-523-156
                                                                      Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-956-157-4527
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                                                                     2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                         Sequence 62, Application US/10439388;
Publication No. US20030228617A1;
GENERAL INFORMATION:
APPLICANT: Aune, Thomas M
TILE OF INVENTION: Method for Predicting Autoimmune Disease;
FILE REFERENCE: 1242/68
CURRENT FILING DATE: 2003-05-16;
PRIOR APPLICATION NUMBER: US/10/439,388
CURRENT FILING DATE: 2003-05-16;
PRIOR PAPLICATION NUMBER: US 60/381,055;
PRIOR PILING DATE: 2002-05-16;
NUMBER OF SEQ ID NOS: 70;
SOFTWARE: Patentin version 3.2;
SEQ ID NO 62
                                           US-09-830-972-29_COPY_990_1178 (1-189) x US-10-347-669-5 (1-1610)
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Best Local Similarity:
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US-10-439-388-62
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Publication No. US20050084850A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 1458.004/200130.449
CURRENT FILING DATE: 2003-01-16
PRIOR PEPLICATION NUMBER: US/09/212,440
PRIOR PILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SETWARE: 1610
TYPE: DNA
                                                                                                        2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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US-10-347-669-5
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Pred. No.:
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US-10-347-669-5
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: MOUNE, William
APPLICANT: MOUNE, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITE AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE PATELICATION NUMBER: PATELICATION NUMBER OF SEQ ID NOS: 319805
SECTIMARE PATELICATION NUMBER: PATELICATION NUMBER OF SEQ ID NOS: 319805
LENGTH: 2050
                                                                                                                                   TIGECCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAGCTATC 426
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US-10-956-157-4530
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APPLICANT: Wounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-0431000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 1705
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                               ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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US-09-830-972-29 COPY 990 1178 (1-189) x US-10-439-388-62 (1-1785)
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US-10-956-157-1705
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Sequence 4531, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
ITILE OF INVENTION: UCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT PAPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 4531
LENGTH: 2226
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Best Local Similarity:
Query Match:
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US-10-956-157-4531
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Publication No. US20040132096A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: ASSAY
FILE REPERENCE: P00966 GCW;
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SOFTWARE: 2052
LENGTH: 2052
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US-10-466-258-3
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ORGANISM: Homo sapiens
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                                                 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
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Sequence 54, Application US/10060036

Publication No. US203073144A1

GENERAL INFORMATION:

APPLICANT: Benson, Darin R.

APPLICANT: Lodes, Michael D.

APPLICANT: Persing, Michael D.

APPLICANT: Persing, David H.

APPLICANT: Persing, David H.

APPLICANT: Persing, David H.

APPLICANT: Persing, David H.

APPLICANT: Persing, David H.

APPLICANT: Persing, David H.

APPLICANT: PERSING: William T.

APPLICANT: William T.

APPLICANT: Jiang, Yuquiu

TITLE OF INVENTION: AND DIAGNOSIS OF PANCERATIC CANCER

FILE REFERENCE: 210121.566

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 54

LENGTH: 2235

TANDER OF SEQ ID NOS: 4560
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Sequence 22, Application US/10220891

Sequence 22, Application US/10220891

Sequence 22, Application US/10220891

GENERAL INFORMATION:

APPLICANT: NAKAGAWARA, AKIRA

TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS

TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS

TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH TAVORABLE PROGNOSIS

TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS

FILE REFERENCE: 7388-73435

CURRENT FILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: UP 2000/140387

PRIOR APPLICATION NUMBER: UP 2000/140387

PRIOR PILING DATE: 2000-05-10

PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 108

SEQ ID NO 22

SEQ ID NO 22

SEQ ID NO 22
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Matches:
                                   FEATURE:
NAME/KEY: CDS
LOCATION: 35..631
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 35..160
OTHER INFORMATION: GCORE 8.6
OTHER INFORMATION: GCORE 8.6
OTHER INFORMATION: Seq ASLFLLLSLTVFS/IV
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US-10-641-643-382
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; Publication No. US20040077003A1
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NAME/KEY: polyA_site

; LOCATION: 979..994

US-09-978-360A-110
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Clusel, Catherine
APPLICANT: Clusel, Catherine
APPLICANT: Clusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-04-13
PRIOR PLILOR DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-12-17
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Publication No. US20040110939A1
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
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US-09-978-360A-110
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GENERAL INFUGRATION:

GENERAL INFUGRATION:

APPLICANT: BISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.

APPLICANT: BESERANN, Pierre
APPLICANT: BESERANN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
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APPLICANT: MOSONEGO, Alon
APPLICANT: MOSENBER: US/09/893,348
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT PILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-12-2
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
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SOFTWARE: PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT
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; Patent No. US20020072493A1
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CTHER INFORMATION
US-09-893-348-17
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                                                                                                                             TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL.
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: UNKnown>
PRIOR APPLICATION NUMBER: vUnknown>
ATTORNEY AGBNT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: 37,071
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 845-4166
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Matches:
Conservative:
Mismatches:
Indels:
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STREET: 3174 PORTER DRIVE
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                           APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Seilhamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 382:
SEQUENCE CHARACTERISTICS:
LENGTH: 2610 base pairs
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STRANDEDNESS: single
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                                                                                                                                                                                          NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION
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Pred. No.:
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Sequence 165, Application US/10205194

Publication No. US20030134301A1

GENERAL INFORMATION:

APPLICANT: Warner-Lambert Company

APPLICANT: Dixon, Alistair

APPLICANT: Brookebank, Robert

APPLICANT: Brookebank, Robert

TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

TITLE OF INVENTION: US-2010-07-24

CURRENT APPLICATION NUMBER: US/10/205,194

CURRENT FILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 177

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 165

LENGTH: 2782
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                                                                                   US-09-830-972-29_COPY_990_1178 (1-189)
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Best Local Similarity:
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APPLICANT: BESERMAN, Fierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USF
FILE REFERENCE: EIS-SCHWARTZ=2A
CURRENT APPLICATION NUMBER: US/09/893,348
PRIOR FILING DATE: 2001-06-28
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATCHIN VETSION 3.1
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                                              3295 GCCTTGCCCTCCTCTCGGTGACTATCAGCTTTAGGATATATAAAGGCGTGATCCAGGCT
                                                                                                     141 AlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp
                      41 AlaLeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValileGlnAla
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Publication No. US20040253218A1
GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, ITUN R.
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LOCATION: (253)..(3744)
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2920 TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTATTTTGGT 2979
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                                                                                                                                 20 AlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39
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                                                                        1 SerValValAspLeuLeuTyrTrpArgAsplleLysLysThrGlyValVal---PheGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla
                                         US-09-830-972-29_COPY_990_1178 (1-189) x US-10-267-502-214 (1-3492)
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Sequence 10, Application US/10466258
Publication No. US20040132096A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TILE REFERENCE: P80966 GCW
CURRENT APPLICATION NUMBER: US/10/466,258
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 1798
 Indels:
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ORGANISM: Homo sapiens
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; LOCATION: (215)..(814)
US-10-466-258-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
                                                                                                                                                                                             SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
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                                                                                                                                 1 ServalvalAspLeuLeuTyrTrpArgAspIleLysLysThrGlyvalValPheGlyAla
                                                                                                                                                                                                                                                      AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla
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   Length:
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US-10-267-502-214
IS-10-267-502-214
Sequence 214, Application US/10267502
Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 214
SEQ ID NO 214
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96.83%
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CORGANISM: MUS musculus
US-10-267-502-214
                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                              AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
                                                                                                                                                                                                                                                                                                                          LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
                                                                                                                                                                                                                                                                                                                                                                                                     TTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrGluargHisGlnalaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLys 171
SerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPhe
                                                                                                 AGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTT
                                                                                                                                               ArgileTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg
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APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics InstituteOffice.
FITLE OF INVENTION: POLYNUCLEOTIDES
FILE REFERENCE: GIN 6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGCTATGCTAAAATCCAAGCAAAATCCCTGGATTGAAGCGCAAAGCTGAA
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Matches:
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US-00-823-245A-349
; Squence 149, Application US/09823245A
; Publication No. US20020039760A1
; GRNERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
appLICANT: Clark, Hilary
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US-09-823-245A-349
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TYPE: DNA
ORGANISM: HOM
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Publication No. US20050118625A1
Publication No. US20050118625A1
Publication No. US20050118625A1
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin Version 3.2
SEQ ID NOS: 9765
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                                                                                248 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 307
                                                                                                                                                487
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                                                                                                                               41
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                      US-09-830-972-29_COPY_990_1178 (1-189) x US-10-466-258-10 (1-1798)
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ORGANISM: Homo sapiens
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US-10-956-157-9765
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	Db 63 TCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAGGTATCCAGAAATCAGAT 122
£ 6	GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85
Oy 33 IleValSerValThralaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArg 52 Db 63 ATTGTGAGCGTAACAGCCTACATTGCCTTGTGTTCTGTGTTTTAGG 122	98
Oy 53 IleTyrLysGlyValileGinalaileGlnLysSerAspGluGlyHisProPheArgAla 72 Db 123 ATATACAAGGGTGTGATCCAAACTATCCAGAAATCAATAAAGCCCACCCA	Db 183 CAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGC 242 Oy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125
Oy 73 TyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysFtyrSerAsnSerAla 92 Db 183 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 242	243
Oy 93 LeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112 	303
Oy 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132	363 TTCAGTGTTCCTGTTATTTATGAACGCCATCAGGCACAGATAGAT
Qy 133 AsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyr 152 Db 363 AATGGTCTGACACACACACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT	423 186
Oy 153 GluargHisGlnalaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAsp 172	Db 483 CGCAAAGCTGAA 494 RESULT 39 US-10-956-157-9767
Qy 173 AlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189 Db 483 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAA 533	; Sequence 9767, Application US/10956157 ; Publication No. US20050118625A1 ; GENERAL INFORMATION: ; APPLICANT: Wyeth
RESULT 38 US-10-956-157-9762 ; Sequence 9762, Application US/10956157 ; Publication No. US20050118625A1 ; GENERAL INPORMATION: ; APPLICANT: Wyeth ; APPLICANT: Wyeth ; TITLE OF INVENTION: UNCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH ; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES ; FILE REPERRINGE: 031886-043000 (AM 101081) ; CURRENT APPLICATION NUMBER: US/10/956,157 ; CURRENT FILING DATE: 2004-110-04	### FYPLICANI; MOUNTE, MOULEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITT TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITT TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES; FILE REPERRINGE 301896-043000 (AM 101081); CURRENT APPLICATION NUMBER: US/10/956,157; CURRENT FILING DATE: 2004-110-04; NUMBER OF SEQ ID NOS: 319805; SOFTWARES PATENTIN VERSION 3.2; SEQ ID NO 9767; LENGTH: 1400; TYPE: DNA; ORGANISM: HOME Sapiens US-10-956-157-9767
o i	.88e-91 05.00 00.00% 00.00%
Alignment Scores: 7.88e-91 Length: 1400 Score: 805.00 Matches: 164 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 86.47% Indels: 0	09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157 26 LeuSerLeuThrValPheSerIleValSerValThrAlaT
-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157	Oy 46 SerValThrileSerPheArgileTyrLysGlyValileGlnAlaileGlnLysSerAsp 65
Oy 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeu 45 	66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaileSerGluGluLeuVal
Oy 46 SerValThrileSerPheArglleTyrLysGlyValileGlnAlaileGlnLysSerAsp 65	DD 123 GAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGATGGTT 182 Qy 86 GlnLysTyrSerAsnSerAlâLeuGlyHisValAsnCysThrIleLysGluLeuArgArg 105

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MOLECULES ASSOCIATED WITH LACTATION AND
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                                                                           62 GTGATCCAGGCTATCCAGAAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCT
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                            303 TricaGriditicricitarirarGaacGCCArcaGGCCACAGATAGATCATTATCTAGGACTT
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PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 ThrAlaTyrileAlaLeuAlaLeuSerValThrileSerPheArgileTyrLysGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CGANIEM: Bos taurus
OTHER INFORMATION: Clone ID: 36-LIB34-048-Q1-E1-A8
US-09-960-352-8477
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Matches:
Conservative:
Mismatches:
Indels:
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| Sequence 8477, Application US/09960352
| Patent No. US20020137139A1
| GENERAL INFORMATION:
| APPLICANT: Warren, Wesley C.
| APPLICANT: Tao, Nengbing
| APPLICANT: Byatt, John C.
| APPLICANT: Mathialagan, Nagappan
| TITLE OF INVENTION: NUCLEIC ACID AND CTHER MOLECUT
| TITLE OF INVENTION: NUCLEIC ACID AND FAT DEPOSITION
| FILE REFERENCE: 16511.006/37-21(10298)C
| CURRENT APPLICATION NUMBER: US/09/960,352
| CURRENT PILING DATE: 2001-09-24
| NUMBER OF SEQ ID NOS: 15112
| SEQ ID NOS: 15112
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Best Local Similarity:
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US-09-960-352-8477
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US-10-956-157-9766

US-10-956-157-9766

Sequence 9766, Application US/10956157

Sequence 9766, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: UNDER: US/10/956,157

CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PatentIn version 3.2

SEQ ID NO 9766

LENGTH: 1400
                                                                                                      302
                                                                                                                                                               PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165
                                                                                                                                                                                     AlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
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                                                            243 CTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGGTATTT
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               CAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGC
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US-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157-9766 (1-1400)
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; ORGANISM: Homo sapiens
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68.45%
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Best Local Similarity:
Query Match:
                      RESULT 43
US-10-267-502-213
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US-09-954-456-210
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                                                                                             ACTIVATION
                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
      Sequence 333, Application US/10084817
Publication No. US20030119009A1
GENERAL INFORMATION:
APPLICANT: Susan Stuart
APPLICANT: Susan Stuart
APPLICANT: Sharon B. Plon
APPLICANT: Sharon B. Plon
APPLICANT: Sharon B. Plon
APPLICANT: Sharon B. Plon
CURRENT PRILION SERES REGULATED BY MYCN ACT:
FILE REFERENCE: PA-0046 US
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE PERL PROGram
SEQ ID NOS: 365
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                                                                                                                                                                                                                                                               Incyte ID No.
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682.00
85.03$
68.45$
73.25$
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incy
US-10-084-817-333
                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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1828 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGGTGAGCGTCGTGGCCTACCTGGCCCTG 1887
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Matches:
Conservative:
Mismatches:
Indels:
Sequence 213, Application US/10267502

Publication No. US20040071700A1

GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: PatentIn version 3.2
SEQ ID NO 213
LENGTH: 2331
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2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAAGATTCAGGCTAAAATCCCA 2429
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                                                                                                       2310 GTTTCAATGTTTACTCTACCTGTAGTGTTAAGCACCAGGCACAGATTGACCAATAT
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                                                       IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr
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APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
TITLE REPREBUCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 386
LENGTH: 3202
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Mismatches:
Indels:
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Matches:
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Publication No. US20030224374A1
GENERAL INFORMATION:
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PUBLICATION INPORMATION:
DATABASE ACCESSION NUMBER: 110333
DATABASE ENTRY DATE: 2001-06-18
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Roberts, Chris
Van 't Veer, Laura
Van de Vijver, Marc
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85.03$
68.45$
73.25$
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APPLICANT: He, Yudong:
APPLICANT: Linsley, Peter
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Best Local Similarity:
Query Match:
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APPLICANT:
APPLICANT:
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                                       GENERAL INFORMATION:

APPLICANT: Young, Paul
TITLE OF INVENITION: Seces
FILE REPRENEUR: 692300-76
GURRENT PILL OF INVENITION: Seces
FILE REPRENEUR: 692300-76
GURRENT APPLICATION NUMBER: US/60/234,456
CURRENT APPLICATION NUMBER: US/60/234,652
FRIOR FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-25
FRIOR FILING DATE: 2000-09-25
FRIOR FILING DATE: 2000-09-25
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Application US/09954456
20020115057A1
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; ORGANISM: Homo sapiens
US-09-954-456-210
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Sequence 1480, Application US/10723860
; Sequence 1480, Application US/2004025506A1
; Sequence 1480, Application No. US2004025506A1
; GENERAL INFORMATION:
; APPLICANT: AZIZ, Natasha
; APPLICANT: Zlornik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR PILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SEQ ID NOS: 8393
; SEQ ID NOS: 8393
; SEQ ID NO 1480
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2130 GAGCAGATTCAGAAGTACACGGACTGCCTGCAGTTCTACGTGAACAGCACCTTAAAGGAA
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CORGANISM: Homo sapiens
US-10-723-860-1480
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APPLICANT: He, Yudong
APPLICANT: He, Yudong
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Wan 't Veer, Laura Johanna
APPLICANT: Van 'd Veer, Laura Johanna
APPLICANT: Van 'd Veer, Laura Johanna
APPLICANT: Van 'd Veer, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: 08/10/342,887
CURRENT APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2001-06-18
PRIOR PLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 386
IEBNGTH: 3202
                                                                                        2250 TGGCTCCTGACCTACGTTGGCGCTCTTCAATGGCCTGACCCTGCTGCTGCTGTGGCTGTG
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103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet
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; Publication No. US20040058340Al
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
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ORGANISM: Homo sapiens
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US-10-342-887-386
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US-10-342-887-386
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Pred. No.:
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APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT PILING DATE: 2003-11-26
PRIOR PILING DATE: 2002-11-26
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                                                                                       3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu
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                                           US-09-830-972-29_COPY_990_1178 (1-189) x US-10-843-641A-3237 (1-3202)
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SOFTWARE: Patentin version 3.2
SEQ ID NO 5926
LENGTH: 3305
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 6390-189
CURRENT APPLICATION NUMBER: US/10/843,641A
CURRENT FILING DATE: 2004-05-12
                                                                                         2190 CTGAGGAGGCTCTTGTCCAGGACCTGGTGGATTCCTTAAAATTTGCAGTCCTGATG 2249
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                                                               GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLysGlu 102
                                                                                                                                                    LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
2070 AAAACCGACGAACGACCCTTTCAAGGCCTACTTGGAGCTTGAGATCACCTTTTCTCAG
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NUMBER OF SEQ ID NOS: 8447
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PRIOR PELLON UNIMER: US/09/873,367
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PRIOR PELLON UNIMER: US/09/954,531
PRIOR PELLON UNIMER: US/09/954,456
PRIOR PELLON UNIMER: US/09/954,456
PRIOR PELLON UNIMER: US/09/962,436
PRIOR PELLON UNIMER: US/09/962,436
PRIOR PELLON UNIMER: US/09/962,436
PRIOR PELLON UNIMER: US/09/962,832
PRIOR APPLICATION NUMBER: US/09/964,824
PRIOR PELLON UNIMER: US/09/967,768
PRIOR PELLON UNIMER: US/09/967,768
PRIOR PELLON UNIMER: US/09/967,768
PRIOR PELLON UNIMER: US/09/967,768
PRIOR PELLON UNIMER: US/09/969,007
PRIOR PELLON UNIMER: US/09/969,007
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR PELLON UNIMER: US/09/969,347
PRIOR PELLON UNIMER: US/09/969,347
PRIOR PELLON UNIMER: US/09/969,708
PRIOR PELLON UNIMER: US/09/969,708
PRIOR PELLON UNIMER: US/09/969,708
PRIOR PELLON UNIMER: US/09/969,708
PRIOR PELLON UNIMER: US/09/969,708
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LENGTH: 3202
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US-10-843-641A-3237
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                                                                                                                                                119 ATTGACCTTCTGTACTGGCGGGACATCAAGCAGACGGGGATTGTGTTCGGGAGCTTCCTG
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                                                                                         US-09-830-972-29_COPY_990_1178 (1-189) x US-10-205-219-94 (1-1502)
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APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REPERRNCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 215
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, Publication No. US20040071700A1
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Percent Similarity:
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APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILER REFERENCE: WL-A-018200
CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR PILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 94
LENGTH: 1502
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                                                                       3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu
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Pred. No.:
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US-10-205-219-94
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206 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTTGTAGAGGTCGTCGCCTACCTGGCCCTG 265
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                                                                                          4 AACTIGITICCTGCTCTCGCTGACAGIAITTCAGCATIGIGAGIGIAACGGCCTACATT
ys-09-830-972-29_COPY_990_1178 (1-189) x US-09-960-352-11567 (1-422)
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APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Brooksbank, Robert
TITLE OF INVENTION: Identification and Use or
FILE REFERRNCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 5200-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR APPLICATION NUMBER: GB 0118354.0
NUMBER OF SEQ ID NOS: 177
SEQ ID NO 128
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ORGANISM: Rattus norvegicus
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US-10-205-194-128
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Sequence 11567, Application US/09960352;
Sequence 11567, Application US/09960352;
Parent No. US20020137139A1;
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagapan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACT;
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352;
CURRENT FILING DATE: 2001-09-24,
NUMBER OF SEQ ID NOS: 15112
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                                US-09-830-972-29_COPY_990_1178 (1-189) x US-10-267-502-215 (1-2343)
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 50-BOVMS1-005-Q1-E1-E6
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US-10-106-698-1945

Sequence 1945, Application US/10106698

Sequence 1945, Application US/10106698

Sequence 1945, Application US/10106698

Sequence 1945, Application US/10106698

Third Date: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

TITLE OF INVENTION UNMBER: US/10/106,698

CURRENT APPLICATION NUMBER: PCT/US00/26524

PRIOR PELING DATE: 1999-09-28

PRIOR PELING DATE: 1999-09-28

PRIOR PELING DATE: 1999-11-03

PRIOR FILING DATE: 1999-11-03

NUMBER: OF SEQ ID NOS: 8564

SEQ ID NO 1945

LENGTH: 1330
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                            ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT
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US-10-106-698-1945
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Publication No. US20040063161A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Van, Ridiang
APPLICANT: Lu, Yifeng
TITLE REPRENCE: OGD205
CURRENT APPLICATION NUMBER: US/10/408,967
CURRENT FILING DATE: 2003-04-08
CURRENT FILING DATE: 2003-04-08
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 1
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ORGANISM: Homo sapiens
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645 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCCATTGTTGAAAAGATCCAAGCAAAA 704
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Publication No. US20050003491A1
GENERAL INFORMATION:
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Steininger II, Robert
Spaulding, Vikki
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APPLICANT: McCoy, John M.
BAPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
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SOFTWARE: Patentin Ver. 2.0
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Treacy, Maurice
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Clark, Hilary
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CORGANISM: Homo sapiens
US-10-913-553-19
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SEQ ID NO 19
LENGTH: 1656
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US-10-913-553-19
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61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
                                                                         141 AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp
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APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                        717 GCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCCAGATTGAT
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Matches:
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US-09-729-674-19
; Sequence 19, Application US/09729674
; Patent No. US20010039335A1
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Steininger II, Robert J
Spaulding, Vikki
Wong, Gordon G.
Clark, Hilary
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APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins Racie, Lisa A.
APPLICANT: Bvans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Staininger II, Robert
APPLICANT: Spanlding, Vikki
APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
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US-09-729-674-19
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Query Match:
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Sequence 25, Application US/10347669

Sequence 25, Application US/10347669

Publication No. US20050084850A1

GENERAL INFORMATION:

APPLICANT: Cao, Li

TILE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

TILE REFERENCE: 1458.004/200130.449

CURRENT APPLICATION NUMBER: US/10/347,669

CURRENT PILING DATE: 1003-01-16

PRIOR FILING DATE: 1998-12-16

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 25

LENGTH: 1668
                                                                                                                                               61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle
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ORGANISM: human
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TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REPERENCE: 1458.004/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001-01-17
PRIOR PRILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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CRGANISM: human
US-09-765-205-25
                            Alignment Scores:
Pred. No.:
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US-09-765-205-25
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
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CTCCCTGGAATGGCCAAAAAAAAGGCAGAA 856
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CURRENT PELLING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US/809,391
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 1998-09-08
PRIOR PILING DATE: 1998-09-08
PRIOR PILING DATE: 1998-09-08
PRIOR PILING DATE: 1998-09-08
PRIOR PILING DATE: 1998-03-06
PRIOR PILING DATE: 1998-03-06
PRIOR FILING DATE: 1997-03-07
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PRIOR APPLICATION NUMBER: 60/040,626
PRIOR PELING DATE: 1997-03-07
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PRIOR PELING DATE: 1997-03-07
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Publication No. US20030175858A1
GENERAL INFORMATION:
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US-09-882-171-254
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Publication No. US20030049618A1

GENERAL INFORMATION:

APPLICANT: Ruben

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: PZ002P2

CURRENT PFLING DATE: 2001-03-16

Prior application data removed - consult PALM or file wrapper

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

LENGTH: 1766
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NUMBER: 60/047,6 1997-05-23 NUMBER: 60/047,5 1997-05-23 NUMBER: 60/047,6 1997-05-23 NUMBER: 60/047,6 1997-05-23 NUMBER: 60/047,5 1997-05-23 NUMBER: 60/047,6 1997-05-23	1997-05-23 1997-05-23 1997-05-23 1997-05-23 NUMBER: 60/047, 58 1997-05-23 NUMBER: 60/047, 58 1997-05-23 NUMBER: 60/047, 59 1997-05-23 NUMBER: 60/047, 59 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 61 1997-05-23 NUMBER: 60/047, 62 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-05-23 NUMBER: 60/047, 63 1997-06-23	1997-04-11 NUMBER: 60/043,5 1997-04-11 NUMBER: 60/043,6 1997-04-11 NUMBER: 60/043,6 1997-04-11 NUMBER: 60/043,6 1997-04-11 NUMBER: 60/043,6 1997-04-11 NUMBER: 60/043,3 1997-04-11 NUMBER: 60/043,3 1997-04-11 NUMBER: 60/043,3 1997-04-11 NUMBER: 60/043,3 1997-04-11 NUMBER: 60/043,3 1997-04-11 NUMBER: 60/043,3 1997-04-11 NUMBER: 60/048,9 NUMBER: 60/056,8 NUMBER: 60/056,8 NUMBER: 60/056,8
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PRIOR FILING DATE: 1997-08-28

PRIOR APPLICATION UNDERS: 60/056,630

PRIOR APPLICATION NUMBER: 60/056,630

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PRIOR APPLICATION NUMBER: 60/056,662

PRIOR PELING DATE: 1997-08-22

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US-10-164-861-254
iSequence 254, Application US/10164861
sequence 254, Application US/10164861
publication No. US20030225248A1
GENERAL INFORMATION:
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT FILING DATE: 2002-66-10
PRIOR APPLICATION NUMBER: US/10/164,861
PRIOR PRIOR PILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: PatentIn Ver. 2.0
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Mismatches:
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Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: 60/056,664
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,876
PRIOR APPLICATION NUMBER: 60/056,881
PRIOR FILING DATE: 1997-08-22
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                                        Publication No. US20040053245Al

SUBJICANT: TANG, APPLICANT:
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; ORGANISM: Homo sapiens
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Query Match:
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                                                               APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 255
LENGTH: 2664
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             Sequence 255, Application US/09809391
Publication No. US20030049618A1
GENERAL INFORMATION:
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OTHER INFORMATION:
NAME/KEY: SITE
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Query Match:
DB:
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OTHER INFORMATION:
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OTHER INFORMATION:
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,674
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APPLICATION NUMBER: 60/043,313
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FILING DATE: 1997-08-22
                                            PPLICATION NUMBER: 60/047,596
                                                                            60/047,612
                                                                                        FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
                                                                                                                      FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,601
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APPLICATION NUMBER: 60/043,568
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,669
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APPLICATION NUMBER: 60/043,312
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FILING DATE: 1997-04-11
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682 GCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 741
                                                          742 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 801
                            161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys
                                                                                                                                                                           Sequence 255, Application US/09882171
Publication No. US20030175858A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
                                                                                       181 IleproGlyLeu---LysArgLysAlaGlu 189
                                                                                                           CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/889,391
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DAFE: 1998-609-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
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PRIOR APPLICATION NUMBER: 60/040,626
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
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FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,583
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APPLICATION NUMBER: 60/047,618
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APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/040,334
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APPLICATION NUMBER: 60/040,163
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APPLICATION NUMBER: 60/047,597
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APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,617
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APPLICATION NUMBER: 60/047,587
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R FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,586
FILING DATE: 1997-05-23
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,876
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,887
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,908
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,761
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,875
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APPLICATION NUMBER: 60/056,862
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FILING DATE: 1997-09-05
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,614
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APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
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FILING DATE: 1997-08-22
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PILING DATE: 1997-06-06
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                                                60/056,864
                                                                                              APPLICATION NUMBER: 60/056,631
FILING DATE: 1997-08-22
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                            FILING DATE: 1997-08-22
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Alignment Scores:

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SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
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US-09-830-972-29_COPY_990_1178 (1-189) x US-09-882-171-255 (1-2664)
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
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LOCATION: (2640)
OTHER INFORMATION: n equals a,t,g,
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US-10-108-260A-449
Sequence 449, Application US/10108260A
Publication No. US20040005560A1
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFRENCE: H1-A01.06
CURRENT APPLICATION NUMBER: US/10/108,260A
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PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6867
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LOCATION: (2743)..(2747)
OTHER INFORMATION: n is a,
                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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Query Match:
DB:
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APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ziotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION VUMBER: 108/10/723,860
PRIOR APPLICATION NUMBER: 60/429,739
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Publication No. US20040253606A1
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
           LOCATION: (2652)
OTHER INFORMATION:
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LOCATION: (2662)
OTHER INFORMATION:
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PRIOR FILING DATE: 2002-04-25
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Publication No. US20040009154A1
GENERAL INFORMATION:
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: BELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
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CURRENT APPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
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        SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 449
LENGTH: 3637
                                                                                                                             Percent Similarity:
Best Local Similarity:
NUMBER OF SEQ ID
                                           TYPE: DNA
CRGANISM: HOMO
US-10-108-260A-449
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US-10-159-563-443
                                                                                           Alignment Scores:
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1499 ATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 1558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agostino, Michael J.
Howes, Steven H.
Resnick, Richard J.
Gulukota, Kamalakar
Graham, James R.
Genetics Institute, Inc.
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NUMBER OF SEQ ID NOS: 444
SOFTWARE: Patentin version 3.1
SEQ ID NO 443
LENGTH: 3637
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619.50
80.53%
60.53%
66.54%
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Best Local Similarity:
Query Match:
DB:
                                                                                                         ; ORGANISM: Homo
US-10-159-563-443
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US-09-823-245A-510
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-960-352-9092
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Pred. No.:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS FILE REPERBENCE: GTM 6401
CURRENT APPLICATION NUMBER: US/09/823,245A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/194,941
PRIOR PILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver: 2.0
LENGTH: 1636
                                                                                                                                                                                                                                                                                                   US-09-830-972-29_COPY_990_1178 (1-189) x US-09-823-245A-510 (1-1636)
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Matches:
Conservative:
Mismatches:
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US-09-960-352-5154
; Sequence 5154, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Weeley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
                                                                                                                                                                                                    1.57e-64
597.50
80.53%
60.00%
                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-510
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Best Local Similarity:
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Sequence 9092, Application US/09960352

Patent No. US20020137139A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Mathalagan, Wagappan
APPLICANT: Mathalagan, Wagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUSCLE AND FAT DEPOSITION
FILE REFREENCE: 16511.006/37.21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 423
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILER REFERENCE: 16511.006/37-21(10298)C CURRENT APPLICATION NUMBER: U5/09/960,352 CURRENT PILLING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 15112 SEQ ID NOS: 15112 LENGTH: 389
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; OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
US-09-960-352-9092
                                                                                                                                                                       TYPE: DNA CRANISM: BOS taurus OSGANISM: BOS taurus OTHER INFORMATION: Clone ID: 22-LIB34-043-Q1-E1-F5 US-09-960-352-5154
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Conservative:
Mismatches:
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100.00%
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61.55%
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2966 CTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTGTTTCTTACCTCATC 3025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAla 173
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                        LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
                                                                                                                                                                            GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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Goli, Surya K.
Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRESERO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/660,946
FILING DATE: 12-Sep-2003
PRIOR APPLICATION DATA:
FILING DATE: CUNKNOWN:
APPLICATION NUMBER: US/09/228,213A
APPLICATION NUMBER: 08/700,607
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US-10-660-946-4
; Sequence 4, Application US/10660946
; Publication No. US20040063131A1
; GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ATTORNEY/AGENT INFORMATION:
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Publication No. US2004005325041

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Dramanc, Radong J.

TITLE OF INVENTION: No. US20040053250Alel Arginine-rich Protein-like Nucleic Acids and TITLE OF INVENTION: No. US20040053250Alel Arginine-rich Protein-like Nucleic Acids and TITLE OF INVENTION: No. US20040053250Alel Arginine-rich Protein-like Nucleic Acids and TITLE OF INVENTION: NO. US20040053250Alel Arginine-rich Protein-like Nucleic Acids and TITLE OF INVENTION: NUMBER: US 10/205,172

CURRENT APPLICATION NUMBER: US 10/225,251

PRIOR FILING DATE: 2002-08-20

PRIOR FILING DATE: 2002-08-20

PRIOR FILING DATE: 2001-03-05

PRIOR FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 950

SEQ ID NO 111

LENGTH: 3517

LENGTH: 3517
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                                                                                                                                                                                                                63 GGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT 122
                                                                                                                                                                                                                                                                        AspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsn 133
                                                                                                                                                                                                                                                                                                      123 GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT 182
                                                                                                                                                                                                                                                                                                                                                  GlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGlu 153
                                                                                                                                                                                                                                                                                                                                                                      ArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAspAla 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT 302
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                                                                                                                                        3 TIGGAATCTGAAGTIGCTATATCTGATGAGTIGGTICAGAAGTACAGCAATICTGCTCTT
                                                                                                                                                                                          94 GlyHisValAsnCysThrIleLysGluLeuArgArgLeuDheLeuValAspAspLeuVal
                                                                                                                  LeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu
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                                                                              US-09-830-972-29_COPY_990_1178 (1-189) x US-09-960-352-9092
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Matches:
Conservative:
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Gaps:
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; NAME/KEY: CDS
; LOCATION: (196)..(654)
US-10-302-172-111
Local Similarity:
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Best Local Similarity:
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Pred. No.:
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                    Query Match:
DB:
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104
35
30
22
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Matches:
Conservative:
Mismatches:
Indels:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIleProGlyLeu---LysArgLysAlaGlu 189
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                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                               7.63e-56
526.50
72.77%
54.45%
56.55%
                                                                                                                                                                                       LIBRARY: THP1NOB01
CLONE: 31870
                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                         IMMEDIATE SOURCE:
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US-10-267-502-211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                                                                                                                                                                                                                                                                                                                               Mismatches:
Indels:
APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Patentin version 3.2
SOFTWARE: 1000-021
SEQ ID NO 211
LENGTH: 669
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                                                                                                                                                                                                             ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                  2.31e-55
520.00
73.40%
51.06%
55.85%
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Query Match:
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1998-09-08
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CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 102
LENGTH: 794
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102
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Matches:
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Mismatches:
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Publication No. US20030175858A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PZ002P2
CURRENT FILING DATE: 2001-06-18
FRIOR APPLICATION NUMBER: US/09/882,171
FRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
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508.50
76.37%
56.04%
54.62%
                                                                                                                   TYPE: DNA
COGANISM: Homo sapiens
US-09-809-391-102
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Query Match:
DB:
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US-09-882-171-102
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APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: PCT/US98/0449
PRIOR APLICATION NUMBER: 60/040,162
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PRIOR PELLING DATE: 1997-03-07
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PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,569
PRIOR FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,671
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PRIOR APPLICATION NUMBER: 60/043,674

RIOR PILING DATE: 1997-04-11

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R APPLICATION NUMBER: 60/047,599

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R APPLICATION NUMBER: 60/047,588
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APPLICATION NUMBER: 60/047,586
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80 leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThr1 100

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Scoult David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 57998
                                                                                                                                                                                                            sphisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaL 180
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                                      lelysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaV
                                                                                                 TCTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTC
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Publication No. US20040031072A1
GENERAL INFORMATION:
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ORGANISM: Glycine max
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                                                                                            alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL
                                                                                                             TGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCC
                                                     euAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleA
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FILLE REPERENCE: PZO02P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILLING DATE: 2002-06-10
PRIOR FILLING DATE: 1998-09-08
PRIOR PELICATION NUMBER: PCT/US98/04493
PRIOR FILLING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 102, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
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US-10-164-861-102
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Pred. No.:
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; OTHER INFORMATION: n = A,T,C \
US-09-918-995-15830
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                                GluteuArgArgteuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                             MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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Fublication No. US20040009491A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR PREDICATION NUMBER: PCT/US01/16450
PRIOR PRELIGNORMER: US 60/205,515
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR APPLICATION NUMBER: US 60/205,515
SPRIOR FILING DATE: 2001-05-19
NUMBER OF SEC ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (586)..(586)
OTHER INFORMATION: n equals
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LOCATION: (590)..(590)
OTHER INFORMATION: n equals
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LOCATION: (198)..(198)
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US-10-264-237-163
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Pred. No.:
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LENGTH: 668
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APPLICANT: Chondrocene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US 60/305,340
PRIOR PELIGN APPLICATION NUMBER: US 60/305,340
PRIOR PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
SEQ ID NO 17576
                                 PheServalProvalIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165
                                                                                                   166 AlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
 120 ACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTC 179
                                                                                                                                   240 GCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAATCCCTGGATTGAAG 299
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                                                         1 CAGAAGCACAGTAATTCTGCTCTTGG-CATGTGAACTGCACGATAAAGGAACTCAGGCGC
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Matches:
Conservative:
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US-10-085-783A-17576
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Publication No. US20040013663A1

GENERAL INPORMATION:

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4211/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SEQ ID NO 17576

LENGTH: 566
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114 ATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCTCATCCTGGCT 173
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                                 LeuLeuSerValThrileSerPheArgileTyrLysGlyValileGlnAlaileGlnLys
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US-10-242-535A-17576
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US-10-242-535A-17576
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ORGANISM: Human
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Pred. No.:
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THILE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH FILE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH FILE OF THE TELL OF A 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTROL OF 123 CONTRO
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NUMBER OF SEQ ID NOS: 114
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-830-972-29_COPY_990_1178 (1-189) x US-10-491-213-80 (1-2017)
CANT: BECHA, Shanya D.;

CANT: BAUGHN, Mariah R.; BECHA, Shanya D.;

CANT: BAUGHN, Mariah R.; BECHA, Shanya D.;

CANT: BLLIOTT, Vicki S.; EMERLING, Brooke M.;

CANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.;

ANT: GANDHI, Ameena R; GIETZEN, Kimberly J.;

ANT: GANDHI, April J.A.; ISON, Craig H.;

NT: HAFALIA, April J.A.; ISON, Craig H.;

NT: KABLE, Amy E.; KALAFUS, Daniel P.;

NT: KABLE, Amy E.; KALAFUS, Daniel B.;

NT: RAMKUMAR, Joseph P.; NGUYEN, Danniel B.;

VT: RAREHT, Stephanie K.; SWARNAKAR, Anita;

T: TANG, Y. Tom; TRAN, Uyen K.;

T. WARREN, Bridget A.; XU, Yuming;

YUB, Henry

INVENTION: C.
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Mismatches:
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; OTHER INFORMATION: Incyte ID No: 7503970CB1
US-10-491-213-80
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ORGANISM: Homo sapiens
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                              US-10-424-599-51318

Sequence 51318, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AROAIT David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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Matches:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 51318
LENGTH: 613
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Sequence 7073, Application US/10723860

| Sequence 7073, Application US/20641
| Publication No. US2004025360641
| GENERAL INCORMATION:
| APPLICANT: Aziz, Natasha
| APPLICANT: Aziz, Natasha
| APPLICANT: Albert
| TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
| TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
| TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
| TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
| TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
| TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
| FILE REFERENCE: 10582.0193.NPUS01
| FILE REFERENCE: 2003-11-26
| PRIOR APPLICATION NUMBER: 60/429,739
| WUMBER OF SEQ ID NOS: 8393
| SOFTWARE: Patentin Version 3.2
| SEQ ID NO 7073
                                                                                                                            .222 ATGGTCTCCTCCTCTGCCTCCTGCACTTTAGCATCGTGTCCGTGGCCGCGCACTTGGCT 1281
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1642 TATGTGGGGTTGGTGACCAATCAGTTGAGCCACATCAAAGCTAAGATCCGAGCTAAAATC 1701
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                                                         CIGITECTECTCTCTCCCCATCTCTCTCAGGGTTTACCGCAAAGTGCTGCAGGCCGTG
                                                                                                        62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                     LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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US-10-723-860-7073
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US-10-723-860-7073
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US-10-723-860-3043
Sequence 3043, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: A212, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Disgnosis of Soft Tissue Sarcoma, Compositions of TITLE OF INVENTION: Methods for Soft Tissue Sarcoma Modulators FILE REPRENCE: 05882.0193.NPUG01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT APPLICATION NUMBER: 0003-11-26
PRIOR FILING DATE: 2003-11-26
1074 CTGTTGCTGCTCTCTCGCGCACCATCTCTCTCAGGGTTTACCGCAAAGTGCTGCAGGCCGTG 1133
                                                                                                                            122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIeLleuAla 141
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                                                           1134 CACCGGGGGGATGGAGCCTACCGTTCCAGGCCTACCTGGATGTGGACCTCACCCTGACT
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SOFTWARE: Patentin version 3.2
SEQ ID NO 3043
LENGTH: 2190
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ORGANISM: Homo
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ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

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                                                                                                                                                                221 TIGITICCIGCIGCICCICGCIGACAGIAITICAGCAITGIGAGIGIAACGGCCIACAITGCC
                                                                                                                                                                                                                    281 TIGGCCCTGCTCTCTGTGACTATCAGCTNTAGGATATAAAGGGTGTGATCCAGGCTATC
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                                                                                                       161 GTTGTTGACCTCCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
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                                                                             ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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                                              US-09-830-972-29_COPY_990_1178 (1-189) x US-09-960-352-2205 (1-431)
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Publication No. US20030064379A1

GENERAL INFORMATION:
APPLICANT: BAREY.Kevin P.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE REFERENCE: P2751R1C1
CURRENT APPLICATION NUMBER: US/10/052,283
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: PCT/US00/20006
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 564
SEQ ID NO 137
SEQ ID NO 137
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Query Match:
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Machialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
SEO ID NOS: 15112
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                                                                                                            122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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                                                     332 ATGGTCTCCTCCTCTTCTGCTGCACTTTAGCATCGTGTCCTGCTGCCGCGCACTTGGCT
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                                LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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Clone ID: 10-LIB3058-011-Q1-K1-C5
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Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local Similarity:
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NAME/KEY: unsure
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Acoustic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 152719
LENGTH: 745
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Matches:
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                                                            ; Sequence 152719, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
                               RESULT 91
US-10-425-115-152719/c
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ORGANISM: Zea mays
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                                                                                                                                                    Sequence 1065, Application US/10764420
GENERAL INFORMATION:
APPLICANT: Lum, Per Yee
APPLICANT: Tan, Yejun
APPLICANT: Dai, Hongyue
ITILE OF INVENTION: Methods For Determining Whether An Agent
TITLE OF INVENTION: Possesses A Defined Biological Activity
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/10/764,420
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,797
PRIOR PILING DATE: 2003-01-24
PRIOR PLILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-05-30
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1065
LENGTH: 682
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| LOCATION: 267, 544, 623

| OTHER INFORMATION: n = A,T,C

US-10-764-420-1065
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Best Local Similarity:
Query Match:
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US-10-764-420-1065
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LOCATION:
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Matches:
Conservative:
Mismatches:
Indels:
                                                             APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILLE REFERENCE: PZO39P1
CURRENT FILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: 09/684,524
FRIOR APPLICATION NUMBER: 09/684,524
FRIOR APPLICATION NUMBER: 09/684,524
FRIOR APPLICATION NUMBER: 07/US00/08979
FRIOR FILING DATE: 2000-04-06
FRIOR FILING DATE: 1999-04-06
FRIOR FILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-09
FRIOR APPLICATION NUMBER: 60/128,693
FRIOR FILING DATE: 1999-04-06
FRIOR SEQ ID NOS: 344
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Sequence 93, Application US/10798512
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REPERBURE: PZ03991
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT FILING DATE: 2004-03-12
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; OTHER INFORMATION: n equals a,t,g, or
US-10-050-704-93
              Sequence 93, Application US/10050704 Publication No. US20030050442A1 GENERAL INFORMATION:
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SEQ ID NO 93
LENGTH: 2454
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US-10-798-512-93
US-10-050-704-93
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111 AspleuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAla 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 GTCTATGAGAAGTACAAGACCCAGATTGATCACTATGTTGGCATCGCCCCAGATCAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 LysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---LysArgLysAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 SeralaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAsp
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Patent No. US20020142981A1

Fatent No. US20020142981A1

FAPLICANT: HORMANION:

APPLICANT: Horner, Darci T.

APPLICANT: GeneLogic, Inc.

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer; TILE OF INVENTION: Gene Expression Profiles in Liver Cancer; TURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

FRIOR PAPLICATION NUMBER: US 60/211,379

FRIOR APPLICATION NUMBER: US 60/211,379

FRIOR APPLICATION NUMBER: US 60/237,054

FRIOR PILING DATE: 2000-06-14

FRIOR PILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-830-972-29_COPY_990_1178 (1-189) x US-10-798-512-93 (1-2454)
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: US/09/684,524
PRIOR PILING DATE: 2000-10-10
PRIOR PELING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 1900-04-09
PRIOR PILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-26
PRIOR PILING DATE: 1999-04-26
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PRIOR PRIOR PILING DATE: 1999-04-26
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361.50
77.50%
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38.83%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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US-10-798-512-93
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US-09-880-107-3484
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us-09-830-972-29_copy_990_1178.rnpb

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US-09-758-140-19
; Sequence 19, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
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341.00
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Pred. No.:
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; Publication No. US20040191240A1
; GENERAL INFORMATION:
APPLICANT: Yamashitat, Tobhyama, Masaya
APPLICANT: Yamashitat, Toshihide
: TITLE COP INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
FILE REFERENCE: 59150-8033.0500
CURRENT APPLICATION NUMBER: US/10/633,423
CURRENT APPLICATION NUMBER: US/10/427,741
; PRIOR APPLICATION NUMBER: US 10/427,741
; PRIOR PILING DATE: 2003-01-328
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
: LENGTH: 60615
                                                        FEATURE:
CTHER INFORMATION: Genbank Accession No. US20020142981A1 W27023
NAME/RET: unsure
LOCATION: (1)..(639)
CTHER INFORMATION: n = a or c or g or t
US-09-880-107-3484
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                            TYPE: DNA
ORGANISM: Homo sapiens
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Query Match:
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Best Local Similarity:
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Pred. No.:
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SEQ ID NO 3484
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US-10-633-423-9
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46076 TIGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 46135
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                                                                                                                     ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tohyama, Masaya
APPLICANT: Yamaahita, Toshihide
TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
FILE REPERENCE: 5915.0-8023
CURRENT APPLICATION NUMBER: US/10/427,741
CURRENT FILING DATE: 2003-04-30
PRIOR PILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-08-2923
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                      US-09-830-972-29_COPY_990_1178 (1-189) x US-10-633-423-9 (1-60615)
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Matches:
Conservative:
Mismatches:
Indels:
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Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                           62 GlnLysSerAspGluGlyHisProPheArg
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DOCATION: (1)..(198)
CTHER INFORMATION: Full receptor binding region of No. US20020077295Alo gene US-09-972-599A-19
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT.
TITLE OF INVENTION: RROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-756
CURRENT FILING DATE: 2001-07-30
PRIOR PPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-09-918-995-5532
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331.00
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100.00%
35.55%
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330.50
81.55%
59.22%
35.50%
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ORGANISM: Homo sapiens
                           sapiens
                                                                                                                                                                                                                                 Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
                                                                                                                                                                                                               Percent Similarity:
     TYPE: DNA
ORGANISM: Homo
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US-09-918-995-5532
                                         FEATURE:
NAME/KEY: CDS
                                                                                                                                                          Alignment Scores:
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LENGTH: 497
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APPLICANT: Strittmatter, Stephen M.
TITLE OF INVENTION: NO. US20020012965Alo Receptor-Mediated Blockade of Axonal Growth
FILE REPERENCE: 44574-5073-US
CURRENT APPLICATION NUMBER: US 60/175,140
CURRENT FILING DATE: 2001-01-12
PRIOR PAPLICATION NUMBER: US 60/175,707
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: US 60/207,366
PRIOR PLING DATE: US 60/236,378
PRIOR PLING DATE: US 60/236,378
                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020012965Alo gene
US-09-758-140-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
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Sequence 19, Application US/09972599A

Patent No. US20020077295A1

GENERAL INPORMATION:

APPLICANT: STRITMATTER, STEPHEN M.

TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

FILE REFERENCE: C077 CIP US

CURRENT APPLICATION NUMBER: US/09/972,599A

CURRENT APPLICATION NUMBER: D01-10-06

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 57

LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC
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Conservative:
Mismatches:
Indels:
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100.00%
35.55%
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SEQ ID NO 19
LENGTH: 198
                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                      128 ValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSer 147
                                                                                                                                                                                                           148 ValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsn 167
                                                                                                                                                                                                                                                                                                                    168 LysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---LysArg 186
                                                                                                                                                                                                                                                                                                                                                      297 GATCAGACCAAGTCAATTGTTGAAAAGATCCAAGGCAAAACTCCCTGGAATCGCCAAAAAA 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09972599A

Betent No. US2002007295A1

GENERAL INFORMATION:

APPLICANT STRITTMATTER, STEPHEN M.

ITILE REFERENCE: C077 CIP US

CURRENT PAPLICATION NUMBER: US/09/972,599A

CURRENT FILING DATE: 2001-00-6

PRIOR FILING DATE: 2001-01-12

PRIOR PLICATION NUMBER: 09/758,140

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2000-09-29

PRIOR PLICATION NUMBER: 60/236,378

PRIOR PLILING DATE: 2000-09-29

PRIOR PLILING DATE: 2000-09-29

PRIOR PLILING DATE: 2000-09-29

PRIOR PLILING DATE: 2000-09-29

PRIOR PLILING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 21

LENGTH: 198
                                                                                                                                  LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Nucleotide sequence encoding amino acids 1055-1120 OTHER INFORMATION: of human No. US20020077295AloA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-830-972-29_COPY_990_1178 (1-189) x US-09-972-599A-21 (1-198)
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
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US-09-972-599A-21
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Search completed: June 19, 2005, 07:09:22 Job time : 509.5 secs
                                     181 rradridaricicidade 198
112 LeuValAspSer
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Sequence:

Run on:

Searched:

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598 bp mRNA linear EST 23-JUL-2003
f8543.z1 fs 103-105d fetal sheep skin library Ovis aries CDNA, mRNA
Sequence.
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(aparinae; Ovis.)

Adelson, D.L., Cam, G.R., DeSilva, U. and Franklin, I.R.

Gene expression in sheep skin and wool (hair)

Contact: Adelson, David L.

CSIRO Livestock Industries
306 Carmody Road, St Lucia QLD 4067, Australia

Tel: +61 7 3214 2700

Fax: +61 7 3214 2900
                                                                                                                                                           602675631
AGENCOURT
ILLUMIGEN
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602848410
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|lab_host="BM25.8"
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CN061127
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(sex="male"
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Location/Qualifiers
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EST.
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                      Ovis aries
RESULT 1
CF118424
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
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  Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-G=/CG2005 153945_19031/app_query.fasta_1.654
-G=/CG2002_1/USPTO_spool_p/US09830972/runat_16062005_153945_19031/app_query.fasta_1.654
-DECALLGED_200_TEN_SCORE=pct -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -GTRE CORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL
-UNITS=pct -NORM=ext -HEAFSIZE=560 -MINLEN=0 -MAXLEN=200000000
-USER=US09830972_@CGN 1 1 6628_@runat_16062005_153945_19031 -NCPU=6 -ICPU=3
-NO_MARP -LARREQUERY -NGG SCORES=0 -MAXT -DSPBALCCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AY404970 Homo sapi
CB215381 NISC_mp05
CM42972 170006000
CK977984 4109431 B
CB162885 K-EST0223
CK971318 4087182 B
CCD102817 AGENCOURT
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2812.411 Million cell updates/sec
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1 SVVDLLYWRDIKKTGVVFGA.....VKDAWAKIQAKIPGLKRKAE 189
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                                                                              June 19, 2005, 06:25:42; Search time 2558 Seconds
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            GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Database

Result No.

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102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                             1 (bases 1 to 600)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Clark, A.G., Glanowski, S., Nielson, R., Tu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, M.D. and Cargill, M.D. and Cargill, M.D. and Cargill, M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M
                                                                                                                                                                                                                                       Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submitseion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 CTATTCCTGCTGCTGCTTCATTGACAGTATTCAGCATTGTGGAGCGTAACAGCCTACATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 AIGIGGGATTTTACCTATGTGGGCCTTGTTTAATGGTCTGACACTACTGATTTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GITGITGACCICCIGIACIGGAGAGACATTAAGAAGACIGGAGIGGIGTITGGIGCCAGC
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       Eutheria; Primates; Catarrhini; Hominidae; Homo
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM2068"
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האסבר-2003 (GSS 16-DEC-2003 Homeo sapiens RTN4 gene, VIRTUAL TRANSCRIPT, partial sequence, מאל מאסבר survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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153 61 213 81

41

93 21

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/organism="Homo sapiens" .

/mol_trep="mxNa" .

/db xref="mxNa" | 606"

/tissue_type="mmbryonic stem cell, retinoic acid and

mitogen_treated hbS cell line H71"

/clone lib="GNN PRENEU"

/note="oligo dT primed, full-length enriched cDNA library

from hBS cell line H7 (p29) maintenined in feeder-free

conditions. Embryoid bodies were generated in the presence

of all-trans retinoic and mitogens."
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 TIGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 198
                                                                                                                                                                       318
                                                                                                                                                                                                                                319 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 378
                                                                                                                                                                                                                                                                                                                                                          CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 258
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                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                    MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLyslleGlnAlaLysIle 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Mat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 667)

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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
                                                                                                                                                       GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                    GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667 bp mRNA linear EST 16-MAY CN429712 CN429712.1 GI:47417306
                                                            GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 667 Std Brror: 0.00.
Location/Qualifiers
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Homo sapiens
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Plate: LLAM13163 row: G column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Listue type="normal endometrium, late proliferative phase, Cycle day 13"

That host="DH10B (T1-resistant)"
/clone_lib="NICHD_HS_UTED"
/clone_lib="Organ: uterus; Vector: pCMV-SPORT6.1.ccdb (ResGen, Invitrogen Corporation); Site_1: Not1; Site_2: EcoRV; Cloned unidirectionally from microquantity amounts of mRNA from normal endometrial tissue (late proliferative phase, cycle day 13). Average insert size 1.9 kb. Library constructed by ResGen (Invitrogen Corporation)."
                                                                                                                                                                     CB215381 650 bp mRNA linear EST 06-FEB-2003
NISC np05d12.y1 NICHD_HS_Ut1 Homo sapiens cDNA clone IMAGE:5937070
65', mRNA sequence.
CB215381
                       573
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                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 650)
NCI-(CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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Matches:
Conservative:
Mismatches:
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Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Gaps:
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                          ProGlyLeuLysArgLysAlaGlu 189
                                                                               574 CCTGGATTGAAGCGCAAAGCTGAA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, P
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
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Email: tads@anri.barc.usda.gov Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt "-trim_fasta. Vector identified by cross match using options -minmatch 12 -minscore 18 Plate: 37 row: I column: 06 Seq primer: CCCAGACCATGTAAAACG High quality sequence stop: 672. Location/Qualifiers Location/Qualifiers 1. 672 Organism="Bos taurus" mol type="mana" fall type="mana" fall type="mana" clone="grows" clone="grows" clone="grows" clone="grows" clone="prope="mones amounts of mana amounts of mana amounts of mana amounts of mana amounts of mana amounts of mana fundic and pyloric abomasums of 18 and 21 weeks Exposure to Ostertagia ostertagi was initiated at 15 weeks	ORIGIN Alignment Scores: 3.24e-104	Oy 2 ValValAspLeufeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21	Oy 42 LeualaLeuLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAlaile 61		Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141 Db 465 AIGTGGGTATTTACCTATGTTGGTCCTTGTTCAATGGTCTGACTACTATTTGGCT 524 Qy 142 LeuIleSerLeuPheSerValProValIleTyrGlAurGHisGlnAlaGInIleApHis 161 Db 525 CTGATTTCACTCTTCAGTTATTTATGAACGGCATCAGGCGAATAGATCAT 584 Qy 162 TyrLeuGlyLeuAlaAsnValLy8AspAlaMetAlaLy81leGlnAlaLy81le 181 Db 585 TATCTGGGACTTGCAATAAGAATGCTAATGGCTAAAAACGCCAAAAAAACGCCAAAAAAACGCAAAAAAACGCAAAAAA
Score Similarity 100.00	Qy 82 GludluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101 Db 323 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAG 382 Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121 Db 383 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTTGAAGTTTGCAGTGTTG 442 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141 Db 443 ATGTGGGGTATTTACCTATGTTGATGCTTTAATGGTCTGACACTACTGATTTTGGCT 502	Qy 142 LeuIleSerLeuBheSerValProVallleFyrGluArgHisGlnAlaGlnIleAspHis 161 Db 503 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGCATCAGGCACAGATAGAT	Oy 182 ProGlyLeuLysArgLysAlaGlu 189	CK977884 CK9779	REFERENCE 1 (Dases 1 to 672) AUTHORS Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C. TITLE activated bovine gut JOURNAL Unpublished (2004) Contact: Tad S. Sonstegard Body Contact: Tad S. Sonstegard Animal and Natural Resources Institute Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA Tel: 3015048414

us-09-830-972-29_copy_990_1178.rst

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/lab host="DH10B Tl phage resistant"
/lab host="DH10B Tl phage resistant"
/clome_lib="BARC 9BOV"
/note="Organ: Abomasum; Vector: pAgen-1; Site_l: EcoRV;
Site_2: Not1; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CK971318 112 bp mRNA linear EST 16-MAR-2004
4087182 BARC 9BOV Bos taurus cDNA clone 9BOV3_J07 5', mRNA
                    355 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 414
                                                                      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                                                                        415 GAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 474
                                                                                                                                        122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAla 141
                                                                                                                                                                                                              LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                                        TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                                                                                                                                                                                                                                      595 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC 654
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                              'organism="Bos taurus"
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                                                              682 bp mRNA linear EST 30-JAN-2003
K-EST0223580 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-41-F04
5', mRNA sequence.
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/lab_host="Top10F'"
/clone lib="Li8POOLIN1"
/note="Organ: Liver; Vector: pT773-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
colture."
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1. (Dases 1 to 682)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R. Oh, K.J., Cheong, J.B., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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                                                                                                                                                                                                                                                                                                                                                                                      Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 41 row: F column: 04
High quality sequence stop: 682.
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Contact: Kim YS
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="mRNA"
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/ggccattatggcc); Site_2: Sfil (ggccgcccggcc); Library is
oligo-dT primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from Skin,
meninges, duramatter, pia matter and choroid plexus.
and 3' adaptors were used in cloning as follows: 5'
adaptors sequence: 5'-ATCTGAGCCTATATGGCC.3' and 3' adaptor
sequence: 5'-ATCTGAGCCTATATGGCC.3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCCGAGGGGGGCGAACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 147 kb (range 0.50-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
taborary."
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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDCA166 row: m column: 24
High quality sequence stop: 617.
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Email: cgpDbs-r@mail.nih.gov
Tissue Procurement: Dr. Michel Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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IMAGE:30373271 5', mRNA sequence.
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Homo sapiens
Homo sapiens
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 743)
INH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/cone_lib="Homo sapiens ADULT BRAIN"

/cone_lib="Organ: brain; Vector: pCWVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
                                                                            431
                                                                                                                                                                                                                                               141
                            GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLys 101
                                                                                                                                 121
                                                                                                                                                                         492 AIGIGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTTGGCT 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                  LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis
                                                                                                                                    GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                         372 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                                                                                                                            MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence belongs to sequence cluster 1423.r. For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODN004DE04QPl&c=1423.r.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN004YJ08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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AL533461.3 GI:45708351
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927.00
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Pred. No.:
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                                                                                                                                                                                                                                            BG697436 17-MAY-2001 758 bp mRNA linear EST 07-MAY-2001 005660623F1 NCI_CGAP_SKn3 Homo sapiens cDNA clone IMAGE:4804012 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:4804012"
/clone="IMAGE:4804012"
/clone lib="NGI CGAP $813"
/note="Organ: 8kin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/Link at:
http://image.llni.gov
Plate: LiLAM10700 row: m column: 05
High quality sequence stop: 756.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 758)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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2 ValValAspLeuLeuTyrTrpArgAsplleLysLysThrGlyValValPheGlyAlaSer
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Mismatches:
Indels:
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Matches:
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                            182 ProGlyLeuLysArgLysAlaGlu 189
                                                                                                                   691 CCTGGATTGAAGCGCAAAGCTGAA 714
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BG697436
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Pred. No.:
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                                                                                                                                                                                                                                                                      DEFINITION
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VERSION
KEYWORDS
SOURCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 AIGIGGGATTTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 421
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                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
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Indels:
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               Location/Qualifiers
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   High quality
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Best Local Similarity:
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602590632F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717662 5',
mRNA sequence.
BG570231. GI:13577884
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 843)
                                                                                                                         GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
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                                                                                                                                                                                                                              LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                276 TIGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llhl.gov
Plate: LLCM1567 row: o column: 07
                                                                           US-09-830-972-29_COPY_990_1178 (1-189) x AL533461 (1-788)
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Mismatches:
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Homo sapiens (human)
Homo sapiens
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Percent Similarity:
Best Local Similarity:
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (basea 1 to 875)

1. (basea 1 to 875)

1. (basea 1 to 875)

1. (basea 1 to 875)

1. (bull-length cDNA libraries and normalization

1. Unpublished (2001)

1. On Feb 16, 2001 this sequence version replaced gi:31294840.

1. Contact: Genoscope

2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Cloned into the Not I and Cone was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                              509
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone=Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                    450 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTTG
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                                                                                                                                122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeulleLeuAla
                                                                                                                                                              142 LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis
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/db xref="taxon:9606"
/clone="CS0DI051YB11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-holedberg.de; sequenced by Medigenomix
(Martinsried/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp669C2134) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469C2134
Further information about the clone and the sequencing project is
available at http://mips.gf.de/projects/cdna/.
      EST 23-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo. I (bases) 1 to 849) Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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                                 pkid1) Pongo pygmaeus cDNA clone
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Deutschenbaur,S., et al.)
Unpublished (2004)
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Matches:
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/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469C2134"
849 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                 DKFZp469C2134_rl 469 (synonym: p
DKFZp469C2134_5', mRNA sequence.
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/lab_host="DH10B"
/clone_lib="469 (sy
                                                                                                                                                                                         Pongo pygmaeus (orangutan)
Pongo pygmaeus
                                                                                                                             CR765672.1 GI:52605968
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AFUT/1050
1785 bp mRNA linear HTC 21-NOV-2002
Homo sapiens neuroendocrine-specific protein C homolog mRNA,
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluGluLeuValGlnLysTyrSerAanSerAlaLeuGlyHisValAanCysThr11eLys 101
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1 (bases 1 to 1785)
Song, H., Peng, Y., Zhou, J., Huang, Q., Dai, M., Mao, Y., Yu, Y., Xu, X., Luo, B., Hu, R. and Chen, J.
Human neuroendocrine-specific protein C (NSP) homolog gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 GTTGTTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
                                                                                                                                                                                                                                                                                                                                                                216 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAATGAT
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                                                                                                                                                                                                                                                                                                                                                22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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188
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                                                                                                                                                                Conservative:
Mismatches:
Indels:
Gaps:
/mol_type="mRNA"
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/clone="CSODNO04YJO8"
/tissue_type="Adult brain"
/plasmid="pcMvSPORT_6"
                                                                                                                                   Length:
Matches:
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Homo sapiens
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR611869 1540 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DN004YJ08 of Adult brain of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                               GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
                                   816
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Catarrhini; Hominidae; Homo.
                 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                    TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
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                                                                                     CTATTCCTGCTGCTTTCATTRACAGTATTCAGCATTGTGGGGGTAACAGCCTACATTGCC
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   ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia: Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 1540)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unll-length cDNA libraries and normalization
Unpublished
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HTC; CNSLT_cDNA.
Homo sapiens (human)
Homo sapiens
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AU297347 female adult cerebrum, full-length enriched chimpanzee CDNA library Pan troglodytes verus cDNA clone PorA0834 5' similar to human RefSeg mRNA NM_007008, mRNA seguence.
                                                                                                                                         Pan troglodytes verus
Pan troglodytes verus
Pan troglodytes verus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 730)
Sakate, R., Osada, N., Hida, M., Sugano, S., Hayasaka, I., Shimohira, N. Yanagi, S., Suto, Y., Hashimoto, R. and Hirai, M.
Analysis of 5'-end sequences of chimpanzee cDNAs
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                                                                                                                                                                                                                                                                                                                                   of Frontier Sciences
                                                                                                                                                                                                                                                                                                                  Department of Integrated Biosciences
The University of Tokyo, Graduate School of Fronti
5-1-5 Kashiwancha, Kashiwa, Chiba 277-8562, Japan
TT-1: 81-4-7136-368
Fax: 81-4-7136-3687
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pan troglodytes verus"
/mol_type="mRNA"
/sub_species="verus"
/db_xref="taxon:37012"
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Matches:
Conservative:
Mismatches:
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/clone_lib="female adult
chimpanzee_cDNA_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type="cerebrum"
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                                                                                                                                                                                                                                                                                                                                                                                          Email: mhirai@k.u-tokyo.ac.jp.
Location/Qualifiers
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Contact: Momoki Hirai
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             Song. H.
Song. H.
Birect Submission
Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai Institute of Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai 200025, P.R. China
Shanghai 200025, P.R. China
Location/Qualifiers
                                                                                                                         /organism="Homo sapiens"
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61

41

Alignment Scores: 1.65e-103 Length: 634 Pred. No.: 921.00 Matches: 187 Procent Similarity: 99.47\$ Conservative: 0 Reat Local Similarity: 99.47\$ Mismatches: 1	98.93% Indels: 6 Gaps:	2	22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	42 LeualaieuLeuSerValThrileSerPheArgileTyrLysGlyValileGlnAlaile	Oy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101	Qy 102 GluLeuargArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121	Oy 122 MetrovalPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141	Qy 142 LeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161	Oy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181	Oy 182 ProGlyLeuLysAlaGlu 189 	RESULT 18 CV030029 CV030029 LOCUS CV030029 DEFINITION 9024 Full Length cDNA from the Mammalian Gene Collection Homo sanions chna 5, similar to RC014366, mRNA semione.	ACCESSION CV030029 VERSION CV030029.1 GI:51488245 KEYWORDS EST. SOUNCE Homo sapiens (human) ORGANISM Homo sapiens	ENKARYOCE, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE I (bases 1 to 670) AUTHORS Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Ditoot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clindingemith T. R. Hartley J. L. Ranostito D., Cheo, D., Moore, T.,	Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. TITLE Human ORPeome Version 1.1: a Platform for Reverse Proteomics JOURNAL Genome Res. (2004) In press
	Qy 142 LeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161 	Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181 	Qy 182 ProGlyLeuLysAlaGlu 189 	N ON	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	<pre>REFERENCE 1 (bases 1 to 634) AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,</pre>	Schmitt, A., Thealing, B., Kitter, E., Konko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. TITLE Endocrine Pancreas Consortium	Cont	Harvard University, Howard Hugnes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-485-1812		(hinoue@im.wustl.edu) Seq primer: -40UP from Gibco High quality sequence stop: 460. FEATURES Location/Qualifiers		/lab host="DH10B" /clone_lib="HR85 islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_l: Not1; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~lkb. 5'	Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

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960 Dp mRNA linear EST 13-WAY-2004 ILLUMICEN MCQ 26335 Katze MMBR Macaca mulatta cDNA clone IBIUW:8548 5, similar to Bases 129 to 958 highly similar to human RTN4 (Hs.435349), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
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/clome_lib="Ratze_MMBR"
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State_2: Xho I; Created from Strategene ZAP-cDNA Synthesis kit [catalog #200400) and ZAP-CDNA Gigapack III Gold cloning Kit (Catalog #200450)"
                                                                                 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Catarrhini, Cercopithecidae, Cercopithecinae; Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Macaca.

1 (bases 1 to 960)

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)

Contact: C. Magness

Illumigen Biosciences Inc.

2203 Aliport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 205376040
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                        142 LeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis
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Matches:
Conservative:
Mismatches:
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Email: cmagness@illumigen.com
Sequenced on 2004.03.09. 743 020 bases.
PCR PRIMEYE
FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 960 Std Brror: 0.00
Plate: CL000173 row: H column: 11
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA-NO.
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/organism="Macaca mulatta"
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/clone="IBIUW:8548"
                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (rhesus monkey)
Macaca mulatta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
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LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5739

Email: Marc_Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThr11eLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAACTGCACGATAAAG 333
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Collection"
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Plate: 11045 row: 02 column: B
seg primer: ACTGGCGTCGTTTTACAAGGTCGTGAAAAC
High quality sequence start: 101
High quality sequence stop: 669
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Matches:
Conservative:
Mismatches:
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1031 bp mRNA linear EST 13-MAY-2004 ILLUMISEN MCQ 28658 Katze MMBR Macaca mulatta cDNA clone IBJUW:7529 5. similar to Bases 129 to 1018 highly similar to human RTN4 (Hs.436349), mRNA sequence.
CN647521.1 GI:47160964
                                                                        /dev stage="adult"
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/clone lib="Katze MMBR"
/clone="Organ: brain, Vector: Uni-ZAP XR; Site_1: EcoR I;
/note="Organ: brain, Vector tratagene ZAP-CDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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186
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Mismatches:
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Matches:
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Gaps:
 /mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:11396"
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                                                                                                                                                                                                                                  3.09e-103
921.00
100.00%
98.94%
98.93%
                                                            /sex="female"
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Best Local Similarity:
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983 bp mRNA linear EST 26-MAY-2004
ILLIMIGEN MCQ 32945 Katze_MMBR Macaca milatta cDNA clone
ILLIMIGEN MCQ 32945 Katze_MMBR Macaca milatta cDNA clone
ILLIMIGEN MCQ 32945 Katze_MMBR Macaca milatta cDNA clone
RTN4 (88.436349), mRNA sequence.
CN803408
GCN803408.1 GI:47699384
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Cercopithecinae; Macaca.

1 (bases 1 to 983)

Katze, M. G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)

Contact: C. Magness

Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
                                                            248
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                                                                                           LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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BACKWARD: CACTATAGGGCGAATTGGGTA
INSET Length: 983 Std Brror: 0.00
Plate: CL000275 row: C column: 03
Seg primer: CCCTCACTAAAGGGAACAAAA
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/organism="Macaca mulatta"
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Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.04.03. 731 (
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SILEO4C10012f1 squirrel embryo library l Spermophilus lateralis cDNA clone 10012 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 72B
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4510
Email: cossinsoliv.ac.uk
Vector has been trimmed from this EST.
Plate: 10 row: o column: 12
Seq primer: pflc 7(5'-AATACGACTCACTATAGGG-3')
High quality sequence stop: 805.
Location/Qualifiers
                             141
                                                                                                        142 LeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                           608
                                                                                                                                                                                   TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 805)
Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
Knogers, J. and Cossins, A.R.
Microarray analysis of transcriptional changes during hibernation
in the golden mantled ground squirrel, Spermophilus lateralis
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
Spermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male and female"
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/note="Wector: pFLC; Site 1: SalI GTCAAG; Site 2: BamH1
                                                                                                                                 549 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGAAAGATCAT
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                                                    489 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACGCTACTGATTTGGCT
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/mol_type="mRNA"
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/lab_host="E. coli SOLR"
/clone lib="Katze MMBR"
/clone lib="Katze MMBR"
/note="Yogan: brain, Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit [catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
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Macaca mulatta (rhesus monkey)
Macaca mulatta
Macaca mulatta
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chormates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 1031)
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 CTATTCCTGCTTTCATTGACAGTATTCAGCATTGTGAGTGTAACAGCCTACATTGCC
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                                                                                                                                                                                                  Illumigen Biosciences Inc.
223 Airport Way S, Suite 450, Seattle, WA 98134, USA
219 Airport Way S, Suite 450, Seattle, WA 98134, USA
Fax: 2063780400
Email: cmagness@illumigen.com
Email: cmagness@illumigen.com
PCR PRimers
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                              BACKWARD: CACTATAGGGGAATTGGGTA
Insert Length: 1031 Std Error: 0.00
Plate: CL000187 row: G column: 05
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Macaca mulatta"
'mol_type="mRNA"
'strain="Indian"
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clone="IBIUW:7529"
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921.00
100.00%
98.94%
98.93%
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Best Local Similarity:
Query Match:
DB:
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JOURNAL
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BG715173 177 bp mRNA linear EST 08-MAY-2001 602675631F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4798279 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
/clone="IMAGE:5558493"
/tissue type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NH1M MGC 88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site 1: Not1; Site 2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                               186 TIGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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Indels:
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Matches:
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AGENCOURT 6458941 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5558493
5', mRNA sequence.
BM801698
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 958)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
       21
                                                                                            240 TTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGTGTAACAGCCTACATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGATTTCACTCTTCAGTGTTCCTGTTATTACGAACGGCATCAGGCACAAAATAGATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660 TATCTAGGACTTGCATATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATT
                                                                                                                                             LeuAlaLeuLeuSerValThrileSerPheArgileTyrLysGlyValIleGlnAlaile
                                                                                                                                                                                                                  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                      LeuPheLeuLeuLeuSerLeuThrValPheSer1leValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                     360 CAGAAATCAGATGAAGGCCACCCATTCAGGGCTTATTTGGAATCTGATGTTGCTATATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGREGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTGGCT
   ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                      .80 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTAGTGTTTGGTGCCAGC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information cloud through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM12281 row: i column: 22
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/mol_type="mRNA"
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High quality sequence stop: 579.
Location/Qualifiers
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/tissue_type="teratocarcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH-MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
Xho1; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/Xho1 sites using the following 5; adaptor:
GGCACCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superseript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BU845601 924 bp mRNA linear EST 16-OCT-2002 AGENCOURT 10414454 NIH MGC_109 Homo sapiens cDNA clone IMAGE:6579264 5', mRNA sequence.
ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 598
                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: ArCc
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2782 row: e column: 24
High quality sequence stop: 696.
                                                                                                                                                                                            TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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1. (Dases 1 to 924)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Nammalian Gene Collection (MGC)

Optubulished (1999)
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                                                                                                                            Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10685 row: n column: 08

High quality sequence stop: 757.

Location/Qualifiers
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                          1 (bases 1 to 757)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Indels:
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Homo sapiens cDNA clone hw24h12 5', mRNA sequence.
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CM482802.1 GI:46564306
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kit [catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Xit (catalog #200450)"
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Matches:
Conservative:
Mismatches:
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Gaps:
           /strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:12670"
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                                                            /sex="female"
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98.40%
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Best Local Similarity:
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CN805577.1 GI:47701553
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1 (bases 1 to 1042)

Katze, M.G. Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Large-scale Rhesus Macaque CDNA Sequencing
Unpublished (2003)
                           GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
                                                                                    LeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                     CAGAAATCAGAATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT
                                                                                                                                                                                                                GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                                                                                                                                GAGGAGTIGGTICAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                                                                                                                                                                             544 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTTG
                                                                                                                                                                                                                                                                                                                                      MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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                                                                                                                                                                                                                                                                                                                                                        ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134,
Tel: 2063780400
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Macaca mulatta
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/clone lib="NIH MGC 148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
directionally cloned using primer
5'-TTTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC
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141 AlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAsp 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 871)
                                                                                                                                                                                               395 TIGATGIGGGIATTIACCIAIGITGGIGCCTIGITTAAIGGICTGACACIACIGATTITG
                                                                                                                                                                                                                                                                                                                     NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT 13994940 NIH MGC 148 Homo sapiens CDNA clone IMAGE:30331865 5', mRNA sequence.
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/lab_host="DH10B_TonA"
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/db_xref="taxon:9606"
/clone="IMAGE:30331865"
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                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 592) 1 (bases 1 to 592) 1 (bases 2 to 592) 1 (bases 2 to 592) 1 (bases 3 to 592) 1 (bases 4 to 592) 1 (bases 4 to 592) 1 (bases 5 to 592) 1 (bases 5 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 (bases 6 to 592) 1 
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Section on Molecular Structure and Function
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Matches:
Conservative:
Mismatches:
Indels:
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Plate: 24 row: h column: 12
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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6/331, NIH, Bethesda, MD 20892-2740, USA
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Fax: 301 496 0078
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/clone lib="NCI CGAP Mam3"
/note="Organ: māmmary; Vector: pCMV-SPORT6; Site 1: Sal1;
Site 2: Not1; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                BI157842 108-JUL-2001
602923001F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5062944 5',
                                                                        TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                               517 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAAGCAAAAATC 576
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                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.I.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMII170 row: b column: 01
High quality sequence stop: 708.
        LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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NIH *MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Matches:
Conservative:
Mismatches:
Indels:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; E. 1 (bases 1 to 679)

In Chases 1 to 679;
Mational Institutes of Health, Mammalian Gene Collection (MGC)

Longulished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Silbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC Clone distribution information can be http://image.llnl.gov
Plate: LLAM11062 row: Column: 04
High quality sequence stop: 679.
Location/Qualifiers
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
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/strain="CZECH II"
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/tissue type="Brain - Pooled from several tissues from one or more_individuals"
/lab_host="Blu10B TonA"
/lab_host="Blu10B TonA"
/clone lib="NIH MGC 255"
/note="Organ: brain/CNS; Vector: pExpress-1; Site_1:
BCONY, Site_2: Not1; RNA obtained from brain tissue of 8
wk old animal. Tissues were snap-frozen and kept at -80C
before RNA extraction and purification (Tri-reagent
method). cDNA was primed using oligo-dr primer:
5'-pGACTACTTCTAGATGCGGAGGCGCCCC(7)25-3' and cloned into
the BCORV/Not1 sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This primary
library is a normalized (primary library is NIH MGC_254)
and was constructed by Express Genomics (FrederIck, MD).
Note: this is a NIH_MGC library"
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ILLUMIGEN MCQ 38898 Katze MMBR Macaca mulatta cDNA clone
IBIUW:16203 5' similar to Bases 112 to 991 highly similar to human
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MAGE:7317070 5', mRNA sequence.
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Rattus.

Rattus.

I (bases 1 to 779)

IS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contract: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical

College of Wisconsin

CONNA Library Preparation: Express Genomics

CONNA Library Preparation: Express Genomics

CONNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DN Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI533 row: o column: 20

High quality sequence start: 23

High quality sequence start: 23

Location/Qualifiers
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGGATTGAAGCGCAAAGCAGAA 622
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CO401465.1 GI:49583381
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531

591

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CN801888 1018 bp mRNA linear EST 26-MAY-2004 ILLUMIGEN MCQ 37222 Katze MMBR Macaca mulatta cDNA clone IBIUW-16016 5 similar to Bases 146 to 1018 highly similar to human RTN4 (Hs.436349), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gex="female"
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/clone lib="Kaze MMBR"
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Site 2: Xho 1; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
412 GAACTCAGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 471
                                                                                                                                                                    122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                                                                           142 LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                             162 TyrLeuGlyLeuAlaAsnLysAsn-ValLysAspAlaMetAlaLysIleGlnAlaLysIl 181
                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Macaca.

1 (bases 1 to 1018)

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)

Contact: C. Magness

Illumigen Biosciences Inc.
2203 Altrport Way S, Suite 450, Seattle, WA 98134, USA

Fal: 2063780400

Pax: 2063780408
                                                                                    102 GlubeuArgArgLeuPhebeuValAspAspbeuValAspSerbeuLysPheAlaValLeu
                                                                                                                                                                                                 472 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACGCTACTGATTTTGGCT
                                                                                                                                                                                                                                                                               Email: cmagness@illumigen.com
Sequenced on 2004.05.14. 594 Q20 bases.
PCR PRimers
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/mol_type="mRNA"
/strain="Indian"
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BACKWARD: CACTATAGGGGAATTGGGTA
Insert Length: 1018 Std Brror: C
Plate: CL000272 row: B column: J
Seg primer: CCCTCACTAAAGGGAACAAA
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1. .1018
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/clone lib="Katze MMBR"
/note="Organ: braIn; Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit [catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Xit (catalog #200450)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGTGTAACAGCCTACATTGCC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTATC 291
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                                                                                                                                                                                                                                                                                                                                                                                   Email: cmagness@illumigen.com
Sequenced on 2004.05.13. 609 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

1 (Dases 1 to 1013)

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Large-scale Rhesus Macaque CDNA Sequencing Unpublished (2003)

Contact: C. Magness

Illumigen Biosciences Inc.
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                                                                                                                                                                                                                                                                                                                     2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400
Fax: 2063780408
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Matches:
Conservative:
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BACKWARD: CACTATAGGGGAATTGGGTA
Insert Length: 1013 Std Brror: 0.00
Plate: CL000160 row: G column: 08
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POLYA-Yes.
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/strain="Indian"
/db xref="taxon:9544"
/clone="IBIUW:16203"
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    (Hs.436349), mRNA sequence.
                                                                                  Macaca mulatta (rhesus monkey)
Macaca mulatta
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                      CO048918
CO048918.1 GI:48688540
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PCR PRimers
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/close="Organ: brain; Vector: pME185-FL3; 1st strand cDNA was primed with an oligo(dT) primer war primed with an oligo(dT) primer ATGTGCCTTTTTTTTTTTTTTT double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME185-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing: 5' end primer [CTTCTGCTCTAAAAGCTGG3], 3' end primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
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1184
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Mismatches:
URL: http://www.nih.go.jp/yoken/genbank/
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 ProGlyLeuLysArgLysAlaGlu 189
                                                                                                                     /dev_stage="adult"
/lab_host="TOP10"
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97.87%
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

E 1 (bases 1 to 794)

E 1 (bases 1 to 794)

Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method

Unpublished (1999)

Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
National Institute of Infectious Diseases
Sali, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

Email: khashi@nih.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUG80127 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-5261
5', mRNA sequence.
                                                                                                                                                                205
                                                                                                                                                                                                                                                                                                                                                                                                               MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  565
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//lab_host="DH10B TonA"
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AGENCOURT 31475102 NIH MGC_251 Rattus norvegicus cDNA clone
IMAGE:7388978 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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National Cancer Institute / NIH

Bldg. 31 Rml0A07 Betheada, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical

College of Wisconsin Drs. Josef Lazar & Consortium (LLML)

College of Wisconsin Drs. Josef Lazar & Consortium (LLML)

DNA Library Preparation: Open Biosystems

CDNA Library Preparation: Open Biosystems

CDNA Library Arrayed by: The 1.M.A.G.E. Consortium/LLNL at:

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://imagg.llnl.gov

Plate: LLAML5561 row: c column: 24

High quality Sequence stop: 696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetTrpValPheThrTyrValG]yAlaLeuPheAsnG]yLeuThrLeuLeuIleLeuAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582 TATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCACGCCAAAAATCCAAGCAAAAAATC 641
                                                                                                                                                                                             82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLys 101
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                       282 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA
                                                                                                                                                                                                                                             342 GAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA
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                                               GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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//dev stage="adult"
//lab_host="TOP10"
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//note="Organ: brain; Vector: pWE18S-FL3; 1st strand cDNA
was primed with an oligo(dT) primer retranded cDNA was
ATGTGGCCTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and
cloned into distinct DraIII sites of the pWE18S-FL3. XhoI
sites just outside the DraIII sites can be used to isolate
the cDNA insert. Size selection was performed to exclude
fragments <1.5 kb. Library was constructed by Sugano et
al. (University of Tokyo, Institute of Medical Science).
Custom primer used for sequencing: 5' end primer
[CTTCTGCTCTAAAAGCTGGG], 3' end primer
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Context: Robbert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
contact: Robbert Strayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Incyte Genomics, Inc.
clond Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Incyte Genomics, Inc.
clond distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
thtp://image.llhi.gov
Plate: LiAMMo633 row: f column: 20
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the ScartAgTrcTAGATCGGGGGGGCGC(T(1) 25-3' and cloned into the EcoRTAGATCGTAGATGGGGGGGCGC(T) 25-2' and cloned into the EcoRY/Note isites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.6 kb. This primary library is normalized (non-normalized primary library is NIH MGC 250) and was constructed by Open Biosystems. Note: this is a NIH_MGC library.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 758)

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CN641703 12-MAY-2004 ILLUMIGEN MCQ 5216 Katze MMBR Macaca mulatta cDNA clone IBIUW:6014 5, similar to Bases 156 to 1013 highly similar to human RTN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MMBR"
/note="Organ: brain, Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
                                                                                                                                          407 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 466
                                      121
                                                                                                                   141
                                                                                                                                                                                                   LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                                                                                  TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                                                                                                                                                                                                                            647 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 706
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1 (bases 1 to 1081)

Ratze, M.G., Thomas, M., Korth, M., Iadonato, S.P., and Magness, C.L.

Large-scale Rheaus Macaque cDNA Sequencing
Unpublished (2003)

Contact: C. Magness

Illumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
                                                                                                                                                                                                                           467 GAACTGAGGCGGCTTTTCTTAGTTGATTTTAGTTGATTCCCTGAAGTTTGCAGTGTTG
                                                                                                            MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cmagness@illumigen.com
Sequenced on 2003.12.04. 735 Q20 bases.
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BACKWARD: CACTATAGGGCGAATTGGGTA
INSert Length: 1081 Std Error: 0.00
Plate: CL000043 row: H column: 10
Seg primer: CCCTCACTAAAGGGAACAAAA
POLYA=Yes.
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/mol_type="mRNA"
/strain="Indian"
                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9544"
/clone="IBIUW:6014"
                                                                                                                                                                                                                                                                                                                                                                     ProGlyLeuLysArgLysAlaGlu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (rhesus monkey)
Macaca mulatta
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/mol_type="mRNA"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="Retinal Ganglion Cells"
/tab_host="hat retinal ganglion cell"
/lab_host="hat retinal ganglion cell"
/cloe="Organ: Eye, Vector: pDNR-LIB; Site_1: Sfil; Site_2: Sfil; The library was constructed from purified rat retinal ganglion cells. The Creator SMART CDNA Library method (Clontech) was used. EST analysis was performed on the unamplified, non-normalized, non-subtracted library."
                                                                                         791 bp mRNA linear EST 24-JUN-2004 F26A06 048.abl.R Rat retinal ganglion cell Rattus norvegicus CDNA, CP977898
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                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 791)
Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
Gene Expression Profiling of Highly Purified Rat Retinal Ganglion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
Rattus norvegicus (Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
Johns Hopkins Street, Baltimore, MD 21287, USA
Tel: 410 502 5330
Fax: 410 502 5382
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Matches:
Conservative:
Mismatches:
Indels:
eProGlyLeuLysArgLysAlaGlu 189
                     670 CCCTGGATTGAAGCGCAAAGCTGAA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rfarkas@jhmi.edu.
Location/Qualifiers
                                                                                                                                                                                                   CF977898.1 GI:49173356
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I (bases 1 to 747)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                         336 CCAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCGATATC
                                                                                                                                                                                                                                                                                                                                                                       396 TGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                 SGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aLeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi
                                                                                                                                  TTGGCCCTGCTCTCTGTGACCATCANGCTTTAGGATATACAGGGGTGTGATCCAAGCTAT
                                                                                                                                                                                                                                                                                               eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACGCTACTGATTTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                GGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTT
                                                                                                                                                                                                                                                                                                                                                       rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLy
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                                                                                                                                                                                                                                     LeuAlaLeuLeuSerValThrile-SerPheArgIleTyrLysGlyValIleGlnAlaIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
185
1
1
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                                                                                     US-09-830-972-29_COPY_990_1178 (1-189) x CN641703 (1-1081)
             Conservative:
Mismatches:
Indels:
 Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cccrecarreaacccaaaccreaa 720
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Homo sapiens
904.00
98.94%
97.88%
97.10%
         Percent Similarity:
Best Local Similarity:
Query Match:
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141

552 161 181 672

141 451 511

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/note="Organ: pooled pancreas and spleen, Vector:
pcMv-SpORT6; Site 1: Not1; Site 2: ECGRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dr primed and directionally cloned
(ECGRV site is destroyed upon cloning). Average insert
size 1:5 kb, insert size range 1-2; kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B1838242 742 bp mRNA linear EST 04-OCT-2001
                                                                                           212 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 271
                                                                                                                                         82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
                                                                                                                                                                   272 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 331
                                                                                                                                                                                                                                                                             332 GAACTCAGACGCCTCTTCTTAGTTGATGTTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 391
                                                                                                                                                                                                                                                                                                                                                                                                                      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 571
  152 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGTGATCCAGGCTATC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 742)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                                                                                                             MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                                                                                                                                                                                                                                     392 ATGIGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                452 CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLML at:
http://image.llnl.gov
Plate: LLAM11559 row: k column: 15
High quality sequence stop: 734.
Location/Qualifiers
                                             62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5222534"
/lab host="DH108"
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ProGlyLeuLys 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 CCTGGATTGAAG 583
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BI838242
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                                             ; 585 bp mRNA linear EST 23-JUN-2004
BARC 8BOV Bos taurus cDNA clone 8BOV_51K20 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt '' -trim_fasta. Vector identified by cross match using options -minmatch 12 -minscore 12 Plate: 5I row: K column: 20 Reg primer: CTRATTAGGTGACACTATAGGAAC High quality sequence stop: 585.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev stage="Lactating, Neonatal"
/lab_host="DHIOB TonA"
/clone lib="BARC BBOW"
/note="Organ: Intestine; Vector: pCMVSport6.1; Site_1:
Not! Site_2: EcoR!, Normalized cow cDNA intestinal
library in pCMVsport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
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                                                                                                                                                                                                                                                                                                1 (bases 1 to 585)
Baumann, K.C., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.
Matukumalli, L.K.
Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Conpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
                                                                                                                                                                                                                   buκaryoca; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyVallleGlnAlaIle 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="Epithelial, Muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:9913"
/clone="8BOV_51K20"
/sex="Female"
                                                                                                              CO259245
CO259245.1 GI:49144047
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Best Local Similarity:
Query Match:
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4130644 B
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                                                                                                            ACCESSION
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayadahida, K., Hayatun, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamara, M., Nishi, K., Nomura, K., Numaza, K., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takku-Akahira, S., Takeda, Y., Tanaka, T., Togawa, A., Tokanashi, R., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Direct Submission
                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, X., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramstsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9212, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
6 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA library was prepared and sequenced in Mouse Genome Bncyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryonic body between diaphragm region and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The FANTOM Consortium and the RIKEN Genome Exploration Research
                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="9430059L06"
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/mol_type="mRNA"
/strain="C57BL/6J"
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AK034902.1 GI:26084268
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Note: this is a NIH_MGC Library
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AUTHORS
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/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site_2: NotI; Cloned undirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LinAM1052 row: k column: 01
High quality sequence stop: 773.
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/dev stage="5 months"
/lab_host="DH10B"
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:5008248"
                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="FVB/N-3"
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (Dases 1 to 731)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                   LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1040 GAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTTGCAGTGTTG
/dev stage="12 days embryo"

1. 3533

/note="RETICULON 4 (NEURITE OUTGROWTH INHIBITOR)
PROFIEIN) (FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN)
[Rattus norvegicus] (SWISSPROT|Q9JK11, evidence: 95.8%ID, 100%length, match=1068)"
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184
2
2
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Mismatches:
Indels:
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Matches:
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BI691132 990 bp mRNA linear EST 18-SEP-2001
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/dev stage="infiltrating ductal carcinoma"
/dav stage="infiltrating"
/lab_nost="DH10B"
/clone lib="NCI CGAP Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
                                348
                                                                                                    408
                                                                                                                                                                                                                                                                                                                588
                                                                                                                                       82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 990)
                  289 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                                                                                                                                                           109 GAGGAGNIGGTICAGAAGIAACAGIAATICIGCICTIGGICATGAGAACIGCACGATAAAG
                                                                                         349 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGCTATATCT
                                                                                                                                                                                                            102 GluLeuArgArgLeuPheLeu-ValAspAspLeuValAspSerLeuLysPheAlaValLe
                                                                                                                                                                                                                              529 GATGTGGGTATTTACCTATGTNGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGC
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LeuAlaLeuLeuSerValThrileSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                     62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: defrey Green M.D.
Tissue Procurement: defrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can bettp://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 758.
High quality sequence stop: 758.
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/clone="IMAGE:5354477"
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Mus musculus
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BI691132.1 GI:15653761
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BI691132
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693 TATCTAGGACTTGCAAACAAGAGGGTTAAGGATGCCATGCGCAAAATCCAAGCAAAAATC 752
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 774)

                                                                                                                  774 bp mRNA linear EST 07-MAY-20
602678946F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4811674 5',
BG699274
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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186
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Matches:
Conservative:
Mismatches:
Indels:
                               182 ProGlyLeuLysArgLysAlaGlu 189
                                                    BG699274.1 GI:13967408
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Matches:
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/organism="Homo sapiens"
/mol_type="mann"
/db xref="taxon:9606"
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Homo sapiens (human)

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 784)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                      71
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Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                    CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATC
                                                                                                                                                                                                                                                                                                                                                                           LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLys-GlyValIleGlnAlaIl
                                                                                                                                                                                                                                                        TIGECCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAACGGCTGTGATCCAAGCTAT
                                                                                                                                                                                                                                                                                     eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi
                                                       990
1184
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10
                                                                                                                                US-09-830-972-29_COPY_990_1178 (1-189) x BI691132 (1-990)
                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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BG699748.1 GI:13968365
                                                    9.27e-100
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98.41
97.35
95.92
                                                                                   Best Local Similarity:
Query Match:
DB:
                                                                          Percent Similarity:
                                           Alignment Scores:
Pred. No.:
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CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10709 row: m column: 07
High quality sequence stop: 747.
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Mismatches:
Indels:
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569 bp mRNA linear EST 21-OCT-2002
HR85 islet Homo sapiens cDNA clone IMAGE:6126776 5'
TR:Q9Y2Y7 Q9Y2Y7 FOOCEN-M. [2] TR:O94962 ;, mRNA
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Menton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Hillier, L., Marra, M., Pape, D., While, T., Marra, M., Pape, D., While, T., Marra, M., Pape, D., While, T., Marrin, J., Blistain, S., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCan, R., Ronko, I., Bennett, J., Williams, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Unpublished (2000)
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                           215 TTATTCCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC
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                                                                           2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                   22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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                                       US-09-830-972-29_COPY_990_1178 (1-189) x AA986233 (1-718)
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Tel: 617-495-1812
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 718)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                       AA986233 718 bp mRNA linear EST 28-MAY-1998 7073912.1,1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1431334 5' similar to TR:016801 016801 NEUROENDOCRINE-SPECIFIC PROTEIN C. ;, mRNA sequence.
                       708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:915402
649 TTATCTAGGACTTGCAAATAAGAATGTTCAAGATGCTATGGCTAAAATCCAAGCAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong strand Seq primer: primer name ambiguous High quality sequence stop: 489... Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Washu-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
Washington Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
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Matches:
Conservative:
Mismatches:
Indels:
                                                         Mus musculus (house mouse)
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Best Local Similarity:
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DEFINITION
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AUTHORS
                                                                                                                                     RESULT 49
                                                                                                                                                         AA986233
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DOZ339712F1 NIH_MGC_94 Mus musculus CDNA clone IMAGE:4505499 5', mRNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 749)
                                                                                                                                                                                                                                                                                                                                                                                               B I (Dases I Lo /4*)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.lnl.gov

Plate: LLAM10379 row: g column: 04

High quality sequence stop: 745.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 riescecrecrerererateacrareacrirassarararassererererererere 304
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/lab_host="NHIOB (phage-resistant)"
/clone_lib="NHI MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_l: Notl;
Site_2: Sall; Cloned unidirectionally; oligo-dr primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."
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/organism="Mus musculus"
/mol type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
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// Clone="INAGE: 612676"
// Clone="INAGE: 6126776"
// Lissue type="Purified pancreatic islet"
// Lissue type="Purified pancreatic islet"
// Lissue type="Purified pancreatic islet"
// Lissue type="Purified pancreatic islet"
// Lissue type="Purified pancreatic islet"
// Lissue type="Purified pancreatic islet"
// Lissue type="Purified pancreatic islet"
// Lissue type="Purified pancreatic islet"
// NotI: Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -lkb. 5'
XhoI site was destroyed after directional cloning.
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311
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                  Email: dmelromebiohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 488.
Location/Qualifiers
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617-495-8557
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Best Local Similarity:
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DKFZp469H1132_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKFZp469H1132_5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 CTATTCCTGCTGCTTTCATTGACAGTATTCCAGCATTGTGAGCGTAACAGCCTACATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                 368 TIGGCCCTGCTCTGTGTGACCATCAGCTTTAGGATATACAAGGGTGAGTCCAAGCTATC
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
YLERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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1 (bases 1 to 1798)
2 (Salang, T.O. 1798)
2 (Shang, C.H., Ye, M., Y.Y., Ren, S.X., Zhao, M., Zhao, C.J., Fu, G., Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W., Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z. Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic Generals
General Res. 10 (10), 1546-1560 (2000)
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Dai, M., Huang, Q., Chen, S. and Chen, Z.
Dai, M., Huang, Q., Chen, S. and Chen, Z.
Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China
Location/Qualifiers
                                                                                                                                                                                                                              [bases 1 to 1798]

Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H.,
Dai,M., Huang,Q., Chen,S. and Chen,Z.
Human neuroendocrine specific protein c homolog mRNA, complete cds
Unpublished
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                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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215. -814
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                                                                                    GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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Homo sapiens
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/tissue_type="kidney"
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/clone_libe_NIH_MGC_95"
/clone_libe_NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_l: BamHI; Site_2: Sall-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2: kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/MHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BIS44917 731 bp mRNA linear EST 05-SEP-2001
603242368F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5284672 5',
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                                                                                                                                                                                                                                                                                    Homo sapiens
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Conservative:
Mismatches:
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/tissue_type="hippocampus"
/lab_host="bH108"
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/db_xref="taxon:9606"
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COS04431 647 bp mRNA linear EST 13-JUL-2004 GGEZCB1023A09.g chicken breast muscle - CB1 Gallus gallus cDNA clone GGEZCB1023A09, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                  82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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1 (Bases 1 to 647)
Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B., Patricio, M., Ledur, M.C. and Coutinho, L.L.
Discovery of new genes expressed in the chicken breast muscle Unpublished (2004)
Contact: Helena J. Alves
                                                                                                                                                   216 TTATTCCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC
                                                                                                                                                                                                                                       276 TIGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC
                                                                                   156 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
                                                                                                                                                                                                               42 LeuAlaLeuLeuSerValThrIleSerPheArgileTyrLysGlyValIleGlnAlaile
                                                                                                                                                                                                                                                                                                  62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                             LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 ATGTGGGTATTTACTTACGTTGGTGCCTTGTTCAATGGTTTGACACTACTGATTTTAGCT
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ESALQ - University of Sao Paulo
Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4434
Eax: 55 19 3429 4285
Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br
US-09-830-972-29_COPY_990_1178 (1-189) x BU503291 (1-921)
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/organism="Gallus gallus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 Pro-GlyLeuLysArgLysAla 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        696 CCTTGGATTGAAGCGCCAAAGC 717
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Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGENCOURT 8933519 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6490526
5', mRNA sequence.
BU503291.1 GI:22809480
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organisme="Mus musculus"

/mol_type="mRNA"

/mol_type="mRNA"

/do _refe[reaxon:10090"

/clone="INAGE:6496526"

/tissue_type="retina"

/lab_host="bD108 (phage-resistant)"

/clone=lb="NNIH MGC 94"

/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;

Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.

Average insert size 3:3 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."
                                                                                   490
                                                                                                                                                                                                                                                         610
                                                                                                                                                                                                                                                                                                                                        670
                                                                                                                                                                                                                                                                                                                                                                                                                              730
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                                                                                                                                                                                                            MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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                                                                                                                                                                                                                                                                                                LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 921)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Enail: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM14040 row; h column: 15
High quality sequence stop: 627.
371 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT
                                                                          431 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                                   491 GAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                     671 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGCTAAAAAATCCAAGCAAAAATC
                                     82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                           102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                       551 ATGTGGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mismatches:
Indels:
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Mus musculus
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Best Local Similarity:
Query Match:
DB:
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DEFINITION
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VERSION
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SOURCE
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AUTHORS
TITLE
JOURNAL
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BU503291
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- 'pak-TracharCaccaccaccacc(T)25-3' and cloned into
the BCORV/Norl sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 2 kb. This primary
library is not normalized (normalized primary library is
NIH MGC 214) and was constructed by Express Genomics
(Frederick, MD). Note: this is a NIH_MGC library."
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conteact: Daniela S. Gerhard, Ph.D.
Conteact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A77 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM19964 row: g column: 16
High quality sequence stop: 685.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AGENCOURT 17155981 NIH_MGC_233 Rattus norvegicus cDNA clone CX357937
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Matches:
Conservative:
Mismatches:

    751
    organism="Rattus norvegicus"

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/db_xref="taxon:10116"
/clone="IMAGE:7105386"
                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                          CK357937.1 GI:40323869
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Query Match:
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                                                                                                                                                                                                                                                                                              ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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Matches:
Conservative:
Mismatches:
                             clone="GGEZCEN023A09"
fissue type="breast muscle"
dev stage="l and 21 days old"
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The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior
Unpublished (2004)
Contact: David F. Clayton
University of Illinois
Bl07 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 3668
Fax: 217 244 1648
Email: dclayton@uiuc.edu
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Taeniopygia guttata
Taeniopygia guttata
Taeniopygia guttata
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
1 (bases 1 to 736)
Clayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M., Mello, C.V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.
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                                                                                                                                                                                                                                                                               297 TTGGCCCTGCTTTCTGTGACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCAATC
                                                                                                                                                                                                                                                                                                                                               357 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTAGCTGTGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        657 TATTTGGGACTAGTGAACAAGAACGTCAAAGATGCGATGGCAAAGATCCAAGCAAAGATC
                                                                                                                                                                                                                                                           LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                            GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                     rTrpArgAspileLysLysThrGlyValValPheGlyAlaSer
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SB02029A2B02 fl normalized Keck-Tagu Library SB02 Taenlopygia
guttata cDNA clone SB02029A2B02.fl 5, mRNA sequence.
CK305449.1 GI:44815023
                                                                                   x CN219472 (1-821)
 0 4 0 0
Conservative:
Mismatches:
Indels:
                                                                                     (1-189)
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97.85%
94.62%
94.52%
                                                                                     US-09-830-972-29_COPY_990_1178
                                                                                                                       {\tt ValValAspLeuLeuTy}
Percent Similarity:
Best Local Similarity:
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DB:
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CK305449
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Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and Lundeberg, J.

EST analysis of brain and testis cDNA libraries from White leghorn and Red Jungle Fowl
Lundeblished (2004)
Contact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology
Royal Institute of Technology
SE-106 91 Stockholm SWEDEN
Tel: +46 (0)8 5537 8481
Fax: +46 (0)8 5537 8435
Email: Peter. Savolainen@biotech.kth.se
Seq primer: M13 reverse primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #EAD MEANA linear EST 08-APR-2004 WIA006H01.abl Wibrain Gallus gallus cDNA 5', mRNA sequence. CN219472 CN219472.1 GI:46298814
                                                                                                                                      458
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                                   81
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Gallus gallus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae;
Phasianinae, Gallus.
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the
 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                     519 ATGTGGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT
                                                                                                                                                                       GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                                                                                                                 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                           MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="ElectroMAX DH10B (Invitrogen)"
/clone lib="Wibrain"
/note="Organ: brain: Vector: pSPORT-1; Site_1: Hind :
Site_2: EcoR1; The CDNA libraries were created with !
Superscript Plasmid System (Invitrogen)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              821
176
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
/organism="Gallus"
/ortain="White Leghorn"
db xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProGlyLeuLysArgLys 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGGATTGAAGCGCAAG 716
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880.00
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Pred. No.:
Score:
 279
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                                   62
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ACCESSION
VERSION
KEYWORDS
SOURCE
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CN219472
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AUTHORS
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COMMENT
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us-09-830-972-29_copy_990_1178.rst

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The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior

The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior

Unpublished (2004)

Contact: David F. Clayton
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B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA

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Fax: 217 244 3668

Fax: 217 244 1648

Email: dclayton@winc.edu

Base Calling/Quality Scores: PHRED from Washington University
Genome Center.

Vector Trimming: Cross_match from Washington University Genome
Center PHRAP suite. Low quality bases (Phred score < 20) were

trimmed from both ends of the sequence by an in-house script.

This sequence is vector free and at least 200 bp in length. Funded
by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'
                                                                                                                                                                                                                                                                                                                                                        CK303615

SB02018A1G04.fl normalized Keck-Tagu Library SB02 Taeniopygia guttata cDNA clone SB02018A1G04.fl 5, mRNA sequence.
TGATTTCGCTCTTCAGTGTTCCTGTTATTTATGAGACATCAGGCCCAAATCGACCAT 604
                                                                                 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                                                       605 TACCTGGGACTTGTGAACAAGAACGTCAAAGATGCCATGGCAAAGATCCAAGCAAAGATC 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taeniopygia guttata
Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
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/note="Organ: brain; Vector: pBS II SK(+); Site_1:
EcoRI(5, side of insert); Site_2: Not (3, side of
insert); The library was constructed and normalized as
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
(1996), Genome Research (6): 791-806. An identiying tag
was added at the 3'during cDNA synthesis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 765)
Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,
Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="SB02018A1G04.f1"
/tissue_type="brain"
/dev_stagge="late embryo, post-hatch days 1, 10, 20, and allate pooled"
and allate (pooled)"
/lab_host="DH108"
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/mol_type="mRNA"
/db_xref="taxon:59729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: TAATACGACTCACTATAGGG(T7)
BACKWARD: ATTAACCCTCACTAAAG(T3)
Insert Length: 765 Std Brror: 0.00
Plate: SB02018A1 row: G column: 04
Seq primer: TAATACGACTCACTATAGGG (T7)
High quality sequence stop: 765.
Location/Qualifiers
                                                                                                                                                                                          ProGlyLeuLysArgLysAlaglu 189
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                               545
                                                                                    162
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KEYWORDS
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                                          Vector Trimming: Cross match from Washington University Genome Center PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script.

This sequence is vector free and at least 200 bp in length. Funded by PHS grant # RO1 NSO45264, 'Songbird Neurogenomics Initiative.' PCR PRIMERS
FOR PRIMERS
FORWARD: TAATACGACTGACTATAGGG(T7)
BACKWARD: ATTAACCACTATAGGG(T7)
BACKWARD: ATTAACCACTATAGGG(T7)
Insert Length: 736 Std Error: 0.00
Plate: SB02029Az row: B column: 02
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High quality sequence stop: 736.
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/mol_type="mRNA"

/do_xref="taxon:59729"

/clone="s880209282802.fl"

/tissue_type="brain"

/dew stage="late embryo, post-hatch days 1, 10, 20, 45, and dault [pooled]"

/lab host="DH10B"

/clone=lib="normalized Keck-Tagu Library SB02"

/clone=lib="normalized Keck-Tagu Library SB02"

/clone=lib="normalized Keck-Tagu Library SB02"

/clone=lib="normalized Keck-Tagu Library SB02"

/clone=lib="normalized Keck-Tagu Library SB02"

/clone=lib="normalized Keck-Tagu Library SB02"

/clone=library was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B.

(1996), Genome Research 6(9): 791-806. An identiying tag was added at the 3'during cDNA synthesis:
insertAAAAAAAAAAAAAAAAAAAAGGCGA."
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Base Calling/Quality Scores: PHRED from Washington University
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Genome Center:

Vector Trimming: Cross match from Washington University Genome Center PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script.

This sequence is vector free and at least 200 bp in length. Funded by PHS grant # RO1 NSO45264, 'Songbird Neurogenomics Initiative.' PCR PRIMETS

FOR PRIMETS

FORWARD: TAATACCACTATAAGG(77)

BACKWARD: ATTAACCACTATAAGG(77)

Insert Length: 793 Std Error: 0.00

Plate: SB02042A1 row: A column: 11

Seq primer: TAATACGACTACACTATAAGG (77)

High quality sequence stop: 793.

Location/Qualifiers
                                                                                                                                                                                                                   MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
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The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior
Unpublished (2004)
Contact: David F. Clayton
University of Illinois
Tel: 217 244 1618
Fax: 217 244 1648
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Bstrildinae; Taeniopygia.
[Dasses 1 to 793]
Clayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M.,
                                                                                                                                                               LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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BG109465 819 bp mRNA linear EST 30-JAN-2001 602280543F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4368011 5', mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 819)
11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 CAGAAGTCTGATGAGGGCCACCCCTTCAGGGCTTACCTGGACTCGGATGTGGCCGTGTCG
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Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                         LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
  852
1175
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                                                                                                                                                x CK304164 (1-852)
                                         Conservative:
Mismatches:
Indels:
                        Matches:
  Length:
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                                                                                                         Gaps:
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                                                                                                                                              US-09-830-972-29_COPY_990_1178 (1-189)
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  59e-98
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BG109465
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                                                                                                                                                                                                                                                                                             EST 01-MAR-2004
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The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior
Unpublished (2004)
Contact: David F. Clayton
University of Illinois
BIOT CLEL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 1648
                                                                                                                          628
                                         568
                                                                                 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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/clone_lib="normalized Keck-Tagu Library SB02"
/clone_lib="normalized Keck-Tagu Library SB02"
/note="forgan: brain; Vector: pBS II SK(+); Site= 1:
ECGR[(5' side of insert); Site=2: NotI (3' side_of
insert); The library was constructed and normalized as
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
(1996), Genome Research (6): 791-806. An identiying tag
was added at the 3'during cDNA synthesis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Passeriformes, Estrildidae,
Estrildinae, Taeniopygia.
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                                                                                                       LeulleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis
                     509 TIGATITICGCICTICAGIGITICCIGITATITIAIGAGAGACAICAGGCCCAAATCGACCAI
                                                                                                                                                                                                                                                                                852 bp mRNA linear EST 01-MAL SB02022B2C10.fl normalized Keck-Tagu Library SB02 Taeniopygia guttata cDNA clone SB02022B2C10.fl 5, mRNA sequence. CK304164 GI:44813738 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev stage="late embryo, post-hatch days 1, 10, 20, and adult (pooled)"
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Insert Length: 852 Std Error: 0.00
Plate: SB02022B2 row: C column: 10
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|db_xref="taxon:59729"
|clone="SB02022B2C10.f1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: TAATACGACTCACTATAGGG (T7)
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Taeniopygia guttata
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CK304164
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Alignment Scores:

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192 TIGGCCCTGCTITCTGTGACCAICAGCTTTAGGATATACAAGGAGTTATCCAGGCAATC 251
                                                                                  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                 (bases 1 to 685)
Alves, H.J., Jorge, B.C., Marchesin, M.L., Monteiro-Vitorello, C.B., Patricio, M., Ledur, M.C. and Coutinho, L.L.
Discovery of new genes expressed in the chicken breast muscle Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 LeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle
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                                                                                                                                                                                                  Contact: Helena J. Alves
Laboratory of Animal Biotennology, Dep. of Animal Production
ESALQ - University of Sao Paulo
Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4434
Fax: 55 19 3429 4285
Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br
PCR PRimers
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Mismatches:
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Matches:
        GGEZCB1022G02, mRNA sequence.
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                                    GI:50273989
                                                               Gallus gallus (chicken)
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                                                                                      CO503803 685 bp mRNA linear EST 13-JUL-2004 GGEZCB1022G02.g chicken breast muscle - CB1 Gallus gallus cDNA
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Matches:
Conservative:
Mismatches:
Indels:
                     12
http://image.llnl.gov
Plate: LLAM10021 row: f column:
High quality sequence stop: 647.
Location/Qualifiers
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/organism="Homo sapiens"
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us-09-830-972-29_copy_990_1178.rst

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CD511521
AGENCOURT 14353136 NIH MGC_187 Homo sapiens cDNA clone
IMAGE:30405928 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                              GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                               LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 GAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet
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                                                                                                                                                                                                                                                           PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Site_2: BsrG I; Created from CloneMiner cDNA Library Construction kit (catalog #18249-029)"
                                                                     960
180
3
                                                                                                                                                                      US-09-830-972-29_COPY_990_1178 (1-189) x CO581452 (1-960)
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Conservative:
Mismatches:
Indels:
Gaps:
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National Cancer Institute / NIH
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CD511521.1 GI:31443239
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILLUMIGEN MCQ 47216 Katze MMLV Macaca mulatta cDNA clone IBIUW:17799 5' similar to Bases 83 to 959 highly similar to human KTM4 (Hs.436349), mRNA sequence.
COS81452. GI:50412806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca. [1 (Dases 1 to 960)]

Katze, M.G. Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev stage="adult"
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                                                                                                TEGATTICGCTGTTCAGTGTTCCTGTTATTATGAGAGACATCAGGCCCAGATCGACAT
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BACKWARD: CACTATAGGGCGAATTGGGTA
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/strain="Indian"
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Macaca mulatta
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/clone="IBIUW:17799"
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263

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142

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/lab_host="DH10B (T1 phage-resistant)"

/clone=lib="NIH MGC 75"

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                                                                                                                                                                                                                                                                                             602501551F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614924 5', mRNA sequence.
BG427864.1 GI:13334370
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                                         162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet-AlaLysIleGlnAlaLysIl 181
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NIH-WGC http://mgc.nci.nih.gov/.

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov Ph.D.

Email: cgapbs-r@mail.nih.gov The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

thtp://mage.llnl.gov

Plate: LLCM137 row: f column: 13

High quality sequence stop: 712.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                             /Mol type="mRNA"
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Sfil (ggccgcctcggcc); 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-ATTCTAAAGGCCGAGGGCGCATG-dT (30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4 kb
(range 0.5-4.0 kb). 14/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA).
Note: this is a NIH_MGC Library."
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llnl.gov
Plate: NDCM193 row: n column: 17
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Conservative:
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Location/Qualifiers
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C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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1 (bases 1 to 820)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU364240 820 bp mRNA linear EST 28-NOV-2002
603585074F1 CSEQCHN72 Gallus gallus cDNA clone ChEST539d19 5', mRNA
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Mismatches:
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Gallus gallus
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 905)
NIH-MGC http://mgc.nci.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/Linl at:
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LLCM1331 row: g column: 07
High quality sequence stop: 708.
Location/Qualifiers
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/lab host="DH10B (T1 phage-resistant)"
/lab host="DH10B (T2 phage-resistant)"
/lone=lib="NH1 MGC 75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1:
Sfil (ggccgcctcggcc); Site 2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor sequence:
s-GACGGCCATATATGCCC3, and 3' adaptor sequence:
5'-GACGGCCATATATGCCC3, and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGGCGGCCGACATG-GT(30)BN-3' (where B = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG400408 905 bp mRNA linear EST 12-MAR-2001
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                                         266 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGAGATCCAAGCTATC
                                                                                                                326 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT
                                                                                                                                                                                                                                                                                                                      MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla
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                                                                                            GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGGATTGAAGCGCAAG 702
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BG400408.1 GI:13293856
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452

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/tissue type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (TI phage resistant)"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NHH BMAP_EXO"
/note="Organ: Brain"-Vector: pYX- Asc; Site_1: EcoR I;
/clone lib="NHH BMAP_EXO"
/note="Organ: Brain"-Vector: pYX- Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is ACCGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA322433 817 bp mRNA linear EST 09-JUL-2003
UI-M-FXO-cck-n-21-0-UI.rl NIH BMAP_FXO Mus musculus cDNA clone
IMAGE:6820918 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)
                                                                                                                     142 LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                  162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                                                                                                                                                                                                  636 TATTTGGGACTAGTGAACAAGAACGTCAAAGATGCGATGGCAAAGATCCAAGCAAAGATC 695
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NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                         576 TTGATTTCGCTGTTCAGTGTTCCTGTTATTTATGAGAGACATCAGGCCCAGATCGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                 182 Pro-GlyLeuLysArgLysAlaGlu 189
                                                                                                                                                                                                                                                                                                                                                                 696 cereggeergaagegeaaaacreag 720
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/clone="IMAGE:6820918"
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/ dev stage="adult"
/ lab_host="blubling"
/ dev stage="adult"
/ done lib="CSEQCHN72"
/ note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not!; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KA+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1966): 791, except that a significantly longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 TIGITICTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGGCTGACAGCTTACATTGCC 275
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                                                                                                                     Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002) 22335534
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Conservative:
Mismatches:
Indels:
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PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                     /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db xref="taxon:9031"
/clone="ChEST539d19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
                                                                                                 Contact: Simon Hubbard
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1. (basea I to 650;
1. (Anno.) Anno.

1. (Anno.) Anno.

2. (Circular rapid amplification of cDNA ends for high-throughput catenain genes Genomics 84 (1), 205-210 (2004)
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                                                                                                                                                                                                                                                                                                     281 TATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAA
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
                                                                                    US-09-830-972-29_COPY_990_1178 (1-189) x CA322433
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1 (bases 1 to 660)
Fu (5.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                      AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
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181 leProGlyLeu-LysArgLysAla 188
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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603397035F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5400584 5',
mRNA sequence.
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Email: gfu@incyte.com.
Location/Qualifiers
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Mus musculus
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/ organism="Mus musculus"
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Site 2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM12021 row, f column: 09
High quality sequence stop: 754.
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Unpublished (2000)

Cother, EsTs: inc7009.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, M. 2013
                                                                                                                                            BU949473 . 609 bp mRNA linear EST 21-OCT-2002 in67h09.yl HR85 islet Homo sapiens cDNA clone IMAGE:6127360 S' similar to TR:Q9X2X7 Q9X2X7 FOOCEN-M. [2] TR:O94962 ;, mRNA
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 609)

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Fax: 617-495-857
Fax: 617-49-8557
Fax: 617-49-8557
Figure 1 deeltonombiohop.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information cobtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 471.
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AUTHORS
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BE7131819 716 bp mRNA linear EST 15-SEP-2000 601569133F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGB:3843729 5',
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49
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/tissue type="choriocarcinoma"
/lab_hogt="BH10B (phage-resistant)"
/clone lib="NH1 MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site_1: Xho1;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor: GGCAGAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 716)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMS3 row: a column: 10
High quality sequence stop: 716.
                                                                                                                 SerPheArg11eTyrLysG1yVa111eG1nAla11eG1nLysSerAspG1uG1yHisPro
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/db_xref="taxon:9606"
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Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1364 row: j column: 21 http://mage.lln.gov High quality sequence stop: 716.
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Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Indels:
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                            Query Match
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VERSION
KEYWORDS
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DEFINITION
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AUTHORS
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JOURNAL
COMMENT
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/ Clone libe"nRNA"

/ Ab xref="taxon:966"

/ Alone="IMAGRA:4613876"

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/ Alone="IMAGRA:4613876"

/ Alone="IMAGRA:4613876"

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/ Adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGGCC-3' and 3' adaptor sequence: 5'-CACGGCC
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Indels:
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Matches:
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BU139629 1028 bp mRNA linear EST 25-NOV-2002
603134795F1 CSEQCHL24 Gallus gallus cDNA clone ChEST117m23 5', mRNA
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1 (bases 1 to 1028)

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                  GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLys 101
                                                                                                                                                                                                 121
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/lab host="DH10B"
/clone llab="CSBCCHL24"
/note="Organ: brain; Vector: pBluescript II KS(+); Site 1:
ECORI; Site 2: Not1; Modification of pBluescript II KS(+)
Examined percor to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
     TTGGCCCTGCTTTCTGTGACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCAATC 230
                                                                                                                                                                                                                                                                                                                                                                                       MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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                                                                                             GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                              GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
                                                                                                                                                                                                                                                                                                                                    351 GAGCTGAGACGCCTCTTCCTCGTTGATGACTTGGTTGATTCTCTGAAGTTTGCAGTGTTG
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University of Manchester Institute of Science and Technology
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/mol_type="mRNA"
/strain="White Leghorn, Hisex"
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Tel: 01612008930
Fax: 01612260409
Email: Simon.Hubbard@umist.ac.uk.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 CCNNNNCTGAAGCGCNNNACTGAG 614
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clone="ChEST117m23"
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Gallus gallus
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                                                                                                                                                                                                               B1394814 EST 06-AUG-2001 pgpln.pk009.15 Normalized Chicken Pituitary/Hypothalamus/Pineal Library Gallus gallus cDNA clone pgpln.pk009.15 5. similar to gil5902016 ref|NP 008939.1| reticulon 4; neuroendocrine specific protein C like (foocen) [Homo sapiens] gi|13637055 ref|XP 002439.3| neuroendocrine-specific protein C like (foocen) [Homo sapiens] gi|13637055 ref|XP 002439.3| pg|AAD27783.1|AF077050_1 (AF077050) neuroendocrii, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue at different ages. Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria, wetazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 646)
Porter, T.B. and Cogburn, L.A.
ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA library USDA/IFAPS Animal Genome Project.

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643 TTATCTAGGACTTGCAAATAAGAATGTTCACAGATGCTAATGGTAAAAATCCAAGCAAAA 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
/dev_stage="Embryonic (d12,d14,d19); post-hatch
(w1,w3,w5,w7,w9)"
/lab_host="E. Coll EMDH10B"
/clone_lib="Normalized Chicken
Pituitary/Hypothalamus/Pineal Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
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/strain="Commercial broiler chicken"
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Matches:
Conservative:
Mismatches:
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University of Delaware
Townsend Hall, Newark, DE 19717, USA
TTE: 302-831-1332
Fax: 302-831-2822
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                                                   181 leProGlyLeuLysArgLysAlaGlu 189
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/sex="Male and Female"
                                                                                     db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (chicken)
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                            RESULT 77
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(ggccattateggcc); Site_2: Sfil (ggccgctcggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a pooled samples of tissues from Skin, meninges, duramatter, pia matter and choroid plexus. and 3' adaptors were used in cloning as follows: 5' adaptors were used in cloning as follows: 5' adaptors sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CATGTAGGCCGACGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.77 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library"
                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
I column: 07
High quality sequence stops: 530.
Location/Qualifiers
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                                                                                                                                                                                                                     1. .735

/organism="Homo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/clone="INAGE:30321390"

/lab_host="hullob (TI phage-resistant)"

/lab_host="NHH MGC 186"

/note="Organ: Pooled-Skin; Vector: pDNR-LIB;
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Matches:
Conservative:
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Gaps:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425
end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NorI and EcoRI.
Ligate in double stranded adaptor containing BsgI and BamHI sites [15/ggccgcgtgcagccccggatccgaaaaaag]
                                                                                                                                                                                                                                                                                                                                                                                           40
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 735)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGENCOURT 13650322 NIH MGC_186 Homo sapiens cDNA clone INAGE:30321390 5', mRNA sequence.
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178
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Mismatches:
Indels:
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Matches:
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Homo sapiens
                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                  Alignment Scores:
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US-09-830-972-29_COPY_990_1178 (1-189) x CN791158 (1-677)
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/db_xref="reaxon:9031"
/clone="ChEST115a3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
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/organism="Gallus gallus"
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Tel: 01612008930
Fax: 0161236409
Email: Simon.Hubbard@umist.ac.uk.
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/dov_stage="Lactating, Neonatal"
/lab_host="DHIO TonA"
/lab_host="DHIO TonA"
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Not! Site_2: EcoR!; Normalized cow cDNA intestinal
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neonatal intestinal 45 Lactating, Proximal Duodenum,
Jejunum, Distal lleum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
                                                                                                                                                                                                                     EST 26-MAY-2004
                                899
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 161
                                                               181
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Baumann, K.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.
Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Contact: Richard G. Baumann
Bovine Functional Genomics Lab
                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                 aLeuIleSerLeuPheSer-ValProValIleTyrGluArgHisGlnAlaGlnIleAspH
                                                            161 isTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI
                                                                                                                                                                                                                     3 677 bp mRNA linear EST 26-1
BARC 8BOV Bos taurus cDNA clone 8BOV_41013 5', mRNA
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Email: solso48744
Email: rbaumann@anri barc usda.gov
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'mol_type="mRNA"
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'clone="8BOV 41013"
'sex="Female"
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Bos taurus
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BU138907 759 bp mRNA linear EST 25-NOV-2002
603133909F1 CSEQCHL24 Gallus gallus cDNA clone ChEST115a3 5', mRNA
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Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, B., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                 156 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 215
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Gallus gallus
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLygGlyValIleGlnAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                    62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT
                                                                                                                                   LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
(Martinsried/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp469C2337) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi.bin/products/ol.cgi?CloneID=DKFZp469C2337
Further information about the clone and the sequencing project is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pongo pygmaeus"
/mol type="mRNA"
/db xref="taxon:9600"
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/tissue_type="kidney"
/dev. stage="adult"
/lab_host="DHIOB"
/clone lib="469 (synonym: pkid1)"
/note="Vector: pSportl_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
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                        Pongo pygmaeus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pongo.
1 (bases 1 to 684)
Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A.,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 GTINTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
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      pygmaeus (orangutan)
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        Pongo
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/dev_stage="16 day embryo"
/lab host="DH10B"
/clone lib="CSEQCHL24"
/clone lib="CSEQCHL24"
/note="Organ: brain; Vector: pBluescript II KS(+); Site 1:
ECORI; Site 2: Not1; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3,
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing Bsgl and
BamHI sites [5'ggccgcgtgcagccccggatccgaaaaaaag]
[5'aattcttttttcggatccggatcagcgc]"
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603192073F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5263026 5',
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11 H-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tobhiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clore distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMM11663 row: b column: 19
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/tissue type="hippocampus"
/tis host="DH108"
/clone lil="WIH MGC 95"
/note="Organ: brain; Vector: pBluescriptR (modified
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Location/Qualifiers
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/db xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                               EST 16-OCT-2002
                                                                                                                        641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2825 row: p column: 09
High quality sequence stop: 160.
                                                          LeulleSerLeuPheSerValProVall1eTyrGluArgHisGlnAlaGlnIleAspHis 161
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   522 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACGCTACTGATTTTGGCT 581
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/note="Organ: Brain; Vector: pDNR-LIB; Site_1: SfiI
/note="Organ: Brain; Vector: pDNR-LIB; Site_1: SfiI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 813)
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                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                            mRNA linear ES:
musculus cDNA clone
                                                                                                                                                                            US-09-830-972-29_COPY_990_1178 (1-189) x BU848611 (1-813)
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AGENCOURT 10276498 NIH_MGC_144 Mus IMAGE:6596409 5', mRNA sequence.
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/mol_trope="manager-liber."
/db_xref="taxon.9606"
/db_xref="taxon.9606"
/db_xref="taxon.9606"
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/note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
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Nat. Biotechnol. 22 (6), 707-716 (
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
Garon Corporation Drive, Menlo Park
721: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 708 Std Error: 0.
Location/Qualifiers
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17000599934467 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (grcgag); Oligo-dT primed using primer 5.-TTTTTTTTTTTTVN-3. size_selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fi
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
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EST 10-APR-2001

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// do_type="mRNGE: 461669"
// do_tone='IMAGE: 461669"
// do_tone='IMAGE: 461669"
// do_tone='IMAGE: 461669"
// do_tone='IMAGE: 461679"
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// note='Organ: Kidney' Vector: pDNR-LIB (Clontech); Site_1:
// note='Organ: Kidney' Vector: pDNR-LIB (Glontech); Site_1:
// note='Organ: Kidney' Vector: pDNR-LIB (Glontech); Site_1:
// note='Organ: Kidney' Vector: pDNR-LIB (Glontech); Site_1:
// daptors were used in Cloning as follows: 5' adaptor
// sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
// ATTCTAGAGCCCATTATGGCC-3' and 3' adaptor sequence:
// or G and N = A, C, G, or T). Average insert size 1.65
// co G and N = A, C, G, or T). Average insert size 1.65
// co G and N = A, C, G, or T). Average insert size 1.65
// co G and N = A, C, G, or T). Average insert size 1.65
// corganish in the constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DC428512
602501030F1 NIH_MGC_75 Homo sapiens CDNA clone IMACE:4614679 5',
mRNA.sequence.
                                                                                                                                                                                                                                                                                                                          TyrLeuGlyLeuAlaAsnLysAsnValLysAspAla-MetAlaLys1leGlnAla--Lys 180
                                                                                                                                                                                                                          LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1366 row: I column: 08
High quality sequence stop: 730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 906)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                      478 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTTGAAGTTTGCAGTGTTG
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                            GlubeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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Homo sapiens
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/note="Organ: Ilyer; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGCGGCGGCATATGGCC-3' and 1' adaptor sequence:
5'-ATTCTAGAGGCGGCGGCGGCGATG-AT(30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                           Androyota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
En (bases 1 to 755)
I (bases 1 to 755)
NIH-MGC http://mgc.nci.nih.gov/.
I Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Location/Qualifiers
I.T.SS
Incorrection/Qualifiers
I.T.SS
Incorrection/Qualifiers
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III.C. T.SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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602587637F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4716393
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Homo sapiens
                            nRNA sequence.
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                                         ACCESSION
VERSION
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Mismatches:
Indels:
                                         /mol_type="mRNA"
/strain="White Leghorn, Hisex"
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                          organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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Location/Qualifiers
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gallus cDNA clone ChEST95f15 5', mRNA
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Gallus gallus
Gallus gallus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.
1 (Bases I to 915)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehenaive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                342
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                                                                                                    GITGITGACCICCIGIACIGGAGAGACALTAAGAAGACIGGAGIGGIGITITGGIGCCAGC 162
                                                                                                                                                                                                                                                                                                             GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
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                                                                                                                                                 163 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
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                                                                       ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                  LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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                                            x BG428512
 Indels:
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
               Gaps:
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603126259F1 CSEQCHL13 Gallus
                                            US-09-830-972-29_COPY_990_1178 (1-189)
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CR771272 644 bp mRNA linear EST 23-SEP-2004 DKFZp469F2235_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone DKFZp469F2235_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for
                                                                                     141
                                                                                                                            519
                                                                                                                                                                                            400 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 GITGITGACCICCICIACIGGAGAGACATIAAGAAGACIGGAGIGGIGITIIGGIGCCAGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryofta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
I (bases I to 64).
Pouetka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pongo pygmaeus mRNA (Poustka,A., Albert,R., Moosmayer,P., et al.)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469F2235
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                              580 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATG
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
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/mol type="maxwa"
/db_xrefe"-taxon:9544"
/db_xrefe"-taxon:9544"
/db_xrefe"-taxon:9544"
/db_xrefe"-taxon:9544"
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lone lib="NOI CGAP_BRIN7"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: NotI;
Site_2: ECoRV; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.2 kb. Constructed by Invitrogen.
Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
info@inmage.llnl.gov
Plate: LLAM11840 row: H column: 20
            BQB07975
NISC kk12d10.yl NCI CGAP Brn72 Macaca mulatta cDNA clone
IMAGE:5331139 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 TIGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTATC 279
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Matches:
Conservative:
Mismatches:
Indels:
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Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Macaca mulatta
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BQ807975.1 GI:22032184
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100.00%
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BI548612 815 bp mRNA linear EST 05-SEP-2001 603189563F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261007 5',
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                                                                                                                                                                                                               276 CTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGCC
                                                                                                                                                                                                                                                                             336 CCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGAGATCCAAGCTATCCAGAA
                                                                                                                                                                                                                                                                                                                                           396 ATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGA
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                                                                                                                                                              216 GACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTC
                                                                                                                                                                                                                                                                                                                                                                                           83 uLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 GGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGAT-TTGGCTCTCAT
                                                                                                                              4 AspleuleuTyrTrpArgAspileLysLysThrGlyValValPheGlyAlaSerLeuPhe
                                                                                                                                                                                            LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla
                                                                                                                                                                                                                                                           -LeuLeuSerValThr1]eSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLy
                                                                                                                                                                                                                                                                                                                           sSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGl
181
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                Conservative:
Mismatches:
   Matches:
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MDNA sequence.
EGS96431
EST
EST96431.1 GI:13961567
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Site_2: Salı, Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: James Cleaver, M.D.
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LiaM10697 row: o column: 08
    High quality sequence stop: 763.
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                            175 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGTGTAACAGCCTACATTGCC
                                                         235 TIGGCCCTGCTTTCTGTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                                                                                                                                                                               355 GAGGAGTIGNNICAGAAGTACAGTAATICTGCTCTTGGTCATGTGAACTGCACGATAAAG
                                                                                                                                                                                                                            GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
                                                                                                                                                                                                                                               GAATTCANGCGCNNCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG
                                                                                                                                                                                                                                                                                                                                                                             82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys
                                                                                                                                                                                                                                                                                                               ATGREGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACGCTACTGATTTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                         162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIle
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Pred. No.:
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AV702687 ADB Homo sapiens cDNA clone ADBBBB01 5', mRNA sequence. AV702687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCATTC 180
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                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 719)

                                                                                                                                                                                                                                                                                                                               Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
251 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                         Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z., and Han, Z. Homo sapiens CDNA ADB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATTAAGAAGACTGGAGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 PheArglleTyrLysGlyVallleGlnAlaileGlnLysSerAspGluGlyHisProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                               Fani: harzgechgc.sh.cn
This clone is available at CHGC in Shanghai
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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Homo sapiens
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                                                                  DEFINITION
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(grcgag); Oligo-dT primed using primer
5- TTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/MGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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Matches:
Conservative:
Mismatches:
                     column: 16
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                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 961)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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CSEQCHL15 Gallus gallus cDNA clone ChEST11g8 5', mRNA
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               ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
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Department of Biomolecular Sciences
University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gallus gallus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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                                                                                                                                                                                                                                                                                                                                                 mRNA linear EST 25-FEB-2004 musculus cDNA clone
                                                                                                                             151 IleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnVal 170
GATTTAGTTGATTCTCTGTAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 360
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 826)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NITH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Shioko Kimura/Atsushi Yamada, (NCI,CCR)
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencian by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM1156 row: a column: 13
High quality sequence stop: 680.

Location/Qualifiers
                                                                                                                                                                                                                                        481 AAAGATGCTATGGCTAANATCCAAGCAAAAATCCTTGGATTGAAGCGCANAGCTGAA 538
                                                                                                                                                                                                                   171 LysAspAlaMetAlaLysIleGlnAlaLysIlePro-GlyLeuLysArgLysAlaGlu 189
                                           LeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProVal
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AGENCOURT 18667576 NIH MGC_230 Mus IIMAGE:30848940 5', mRNA sequence.
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Pred. No.:

ORIGIN

Best Local

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

LOCUS

RESULT 94 CK791443

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I (Bases I to 665)

NIH-WGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CODM Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10691 row: h column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="minson" depress.
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Technologies. Note: this is a NCI_CGAP Library."
  602703292F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4800455
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
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                                                               BG698881.1 GI:13966613
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98.90%
98.90%
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Homo sapiens
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Query Match:
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Pred. No.:
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/dev_stage="adult"
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/lab_host="blublos"
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/clone lib="CSBCGHLIS"
/clone lib="CSBCGHLIS"
/clone lib="CSBCGHLIS"
/clone lib="CSBCGHLIS"
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[5'aattcttttttcggatccggagctgcacgc]"
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Conservative:
Mismatches:
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                     db_xref="taxon:9031"
clone="ChEST11g8"
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                                                             sex="Female"
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839.50
96.28%
93.09%
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DB:
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Query Match: 90.12% Indels: 2 DB: 7 Gaps: 0	-830-972-29_COPY_990_1178 (1-189)	Qy 3 ValAspLeuLeuTyrTrp-ArgAsplleLysThrGlyValValPheGlyAlaSerLe 22	Db 43 GTTGACCTCCTTTACTGGNCGAGACATTAAGAAGACAGGAGTGGTGTT-GGTGCCAGCTT 101	22 uPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLe	102 GTTCCTGCTGCTCTTTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTGCCTT	Qy 42 uAlaLeuLeuSerValThrIleSerPheArgileTyrLysGJyVallleGlnAlaileGl 62	162 GGCCCIGCIIICLGIGACCAICAGCIIIAGGAIAIACAGAGAGAGAIAIALCAGAGCAAICAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	73	82 uGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGl	282 AGAGCTGATTCAGAAATACAGCAGTGTTGTGCTTGGTCACATCAACGGCACAGTCAAGGA	Oy 102 uLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMe 122	Oy 122 tTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLleLeuAlaLe 142	Db 402 GIGGGIGIICACIIACGIIGCIGCIIGIIIAAIGGICIGACAIIACIGAIACIGGCIII 461	Qy 142 ulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHisTy 162	Db 462 GATTTCGCTGTTCGTGTTCCTGTTATTTATGAGAGACATCAGGCCCAGATCGACCATTA 521	162 rleuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePr	Db 522 TTTGGGACTAGTGAACAAGAACGTCAAAGATGCGATGGCAAAGATCCAAGCAAAGATCCC 581	Qy 182 oGlyLeuLysArgLysAlaGlu 189 Dh			n	S EST.	NISM Homo sapiens Eukarvota: Metazoa: Chordata:	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 676)	AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,	Lebkowski, J and Stanton, L.W. TITLE Transcriptome characterization elucidates signaling networks that	JOURNAL NAt. Biotechnol. 22 (6), 707-716 (2004)		230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658	Fax: 650 473 7760 Email: rbrandenbergeron.com Trant: roach: 676 etd From: 00	
		Db 542 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGAT	Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181		182 Pro	Db 661 CCT 663	CO505196 669 bp mRNA linear EST 13-JUI	N GGEZEB1026A09.g embryo breast muscle - EB1 Gallus gallus cD GGEZEB1026A09, mRNA sequence.	ACCESSION CO505196 VERSION CO505196.1 GI:50275382 KEYWORDS EST.	Gallus gallus (chicken) SM Gallus gallus		REFERENCE 1 (bases 1 to 669) AUTHORS Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B., Patricio, M. Indium M. and Continho, I. I.	TITLE Discovery of new genes expressed in the chicken breast muscle	COMMENT Contact: Helena J. Alves COMMENT Contact: Helena J. Alves Laboratory of Animal Biotecnology, Dep. of Animal Production	BSALO - University of Sao Paulo Av Padna Dias 11 Piracicaba SP, 13418-900, Brazil	Tel: 55 19 3429 4434 Fax: 55 19 3429 4285	Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br PCR PRimers	BACKWARD: T7. FEATURES Location/Qualifiers	BOULCE 1009 /organism="Gallus gallus" /mol type="mpNA"	/db_xref="f="mxxxx:9031" /clone="GGEZEB1026A09"	/tl88ue_rype="Dreast muscle" /dev_stage="embryos with 9 and 17 days old" /lah_host="nHs_alpha"	/	con library was constructed with the SuperScript Plasmid Sychem with Gateway Technology kit (Invitrogen), following	manufacture's protocols. Planning was purified using a modified alkaline lugis method. Semiencing reactions were	conducted using the DYEnamic Cycle Sequencing Kit for MegaBACE (Amersham biosciences) according to the	manufacturer's recommendations. Clones were sequenced by the 5' end with T7 primer. Sequencing reactions were	analyzed on MegaBACE1000 DNA Sequencer (Amersham biosciences). The quality and clustering of the ESTs were	analyzed using the Sottwares Fired/Labs. Unly Est sequences with Phred quality greater than 20 and at least 150 bn ware considered for chiefering "	ORIGIN	No.: 2.63e-93 Length:	SCOIE: 839.00 MACCHES: 1/5 Percent Similarity: 96.28% Conservative: 6 Best Local Similarity: 93.09% Mismatches: 6

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/lab_host="DH10B"
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/clone lib="CSEQCHLIS"
/clone lib="CSEQCHLIS"
/note="Organ: brain; Vector: pBluescript II KS(+); Site l:
EcoRI; Site 2: Not1; Modification of pBluescript II KS(∓)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624; Cut pBluescript II KS(+) with NotI and BcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggccgcgtgcagcccggatccgaaaaaaag]
[5'aattcttttttcggatccggagctgcacgc] "
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Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
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Matches:
Conservative:
Mismatches:
Indels:
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PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                           Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Compton Line 151"
                                                                                                                                                                              š
                                                                                                                                                                                                                                                                              organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                            /sex="Female"
/tissue_type="cerebrum"
                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9031"
/clone="ChEST12704"
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JOURNAL
MEDLINE
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                                        /mol type="manus" engines.
/mol type="manus" engines.
/db xref="taxon:9606"
/tissue type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEU"
/note="foligo dT primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic and mitogens."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 934)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal
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                                'organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          669 TATCTAGGACTTGCAAATAAAGAATGGTTAAAGATGCTATGGGCTAAAAATCCCAAGCAA 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 LeulleSerLeuPheSerValProvallleTyrGluArgHisGlnAlaGlnIleAspHis
                                                189 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
                                                                                                                                       249 CTATTCCTGCTGTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
                                                                                                                                                                                                                                 309 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 GAACTCAGGCGCCTCTTCTTAGTTGATTAGTTTAGTTGATTCTTGAAGTTTGCAGTGTTG
                         2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu
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                                                                                                           22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla
                                                                                                                                                                                                 42 LeuAlaLeuLeuSerValThrIleSerPheArglleTyrLysGlyValIleGlnAlaIle
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                                                                                                                                                                                                                                                                                        62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer
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Job time : 2580 secs
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Dasas 1 to 735)

S. NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llhi.gov

Plate: NDCM153 row: n column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /MOL type="mRNA"
/db Xref="taxon:9606"
/clone="IMAGE:3033314"
/lab host="DHIOB (T1 phage-resistant)"
/clone lib="NIH_MGC 184"
/clone lib="NIH_MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatgggc); Site_2: Sfil (ggccgctcggcc);
Library is oligo-dT primed_and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGCGCACATGAGGCGCACATGGGNS 13 olbn3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                          CBS56475
AGENCOURT_13665211 NIH MGC_184 Homo sapiens cDNA clone
AMAGE:30353314 5', mRNA sequence.
                                         LeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAlaGlnIleAspHis 161
                                                                                                                              162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
                                                                                     651
                                                                                                                                                                          652 TATTIGGGACTAGTGAACAAGAACGTCAAAGATGCGATGGCAAAGATCCAAGCAAAGATC 711
532 ATGTGGGTGTTCACTTACGTTGGTGCCTTGTTTAATGGTCTGACATTACTGATACTGGCT
                                                                                  592 TIGATITICSCIGITICAGIGITICCIGITATITATGAGAGACATCAGGCCCCGATCGACCAT
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Conservative:
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Indels:
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Pred. No.:
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                          RESULT 100
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AUTHORS
TITLE
JOURNAL
COMMENT
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completed: June 19, 2005, 10:16:59
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Similarity:

Best Local S Query Match:

Percent Similarity:

Sequence 6, Appli Sequence 6, Appli Sequence 24, Appl Sequence 72, Appl Sequence 8, Appli Sequence 4, Appli Sequence 24, Appli

Sequence 6, Appli Sequence 7, Appli Sequence 9, Appli Sequence 467, Appl Sequence 10, Appl Sequence 18, Appl Sequence 18, Appl

Sequence 164, App Sequence 431, App

Sequence 21, Appl

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

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1004 SVVDLLYWRDIKKTGVVFGASLFLLSSLTVFSIVSVTAXIALASVTISFRIXKGVIQA 1063
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               US-03-789-386-6
US-09-765-286-6
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US-09-9765-286-6
US-10-406-967-8
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Matches 189; Conservative
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Sequence 429, App
Sequence 9, Appli
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Sequence 1, Appli
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Sequence 23, Appl
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2960.058 Million cell updates/sec
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1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189
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| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-893-348-23
US-09-992-599A-6
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US-10-267-502-429
US-10-377-213-9
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence 21, Appl Sequence 20, Appl Sequence 11, Appl Sequence 11, Appl Sequence 7, Appli Sequence 6, Appli Sequence 430, Appl Sequence 430, Appli Sequence 1481, Appli Sequence 1881, Appli

Sequence 8, Appl:

Sequence 20, Sequence 26, Sequence

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931 931 931 931 931 931 931

Result No.

Sequence 432,

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1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
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TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REPERENCE: C077 CIP US
CURRENT APPLICATION NUMBER: US/09/972,599A
CURRENT FILING DATE: 2001-10-06
FRIOR PEDIATON NUMBER: PCT/US01/01041
PRIOR PELING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-12
PRIOR PELING DATE: 2000-09-29
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Pred. No. 1.1e-83;
                                                                                                                                                                                                                                                                                                                                   100.0%; Scor.
100.0%; Pred. No. 1...
''' 0; Mismatches
PRIOR APPLICATION NUMBER: US US/LING.
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: PCT/US98/14715
PRIOR APPLICATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
**CHART | 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09972599A; Patent No. US20020077295A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 189; Conservative
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SOFTWARE: Patentin Ver.
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US-09-972-599A-6
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Sequence 23, Application US/09893348
Patent No. US20020072493A1
Sequence 23, Application US/09893348
Patent No. US20020072493A1
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: BESERMAN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSUNEGO, Alon
APPLICANTON: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USF
FILE REFERENCE: EIS-SCHWARTZ=2A
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT FILING DATE: 2001-06-28
PRIOR FILING DATE: 1999-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Strittmatter, Stephen M.

TITLE OF INVENTION: No. US20020012965Alo Receptor-Mediated Blockade of Axonal Growth FILE OF INVENTION: No. US20020012965Alo Receptor-Mediated Blockade of Axonal Growth FILE OF INVENTION: 445-45073-408

CURRENT APPLICATION NUMBER: US 60/175,707

PRIOR APPLICATION NUMBER: US 60/207,366

PRIOR PILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: US 60/236,378

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.1
                                                                                                           1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANROVKDAMAKIQAK 1183
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       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063
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Best Local Similarity 100.0%; Pred. No. 1.1e-83;
Matches 189; Conservative 0; Mismatches 0;
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US-09-758-140-6
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; ORGANISM: Homo sapiens
US-10-327-213-9
                                      Query Match
Best Local Similarity
Matches 189; Conserv
 US-10-267-502-429
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1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123
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Fublication No. US20030073144A1
Fublication No. US20030073144A1
Fublication No. US20030073144A1
Fublication No. US20030073144A1
FAPPLICANT: Rabos, Michael D.
APPLICANT: Retain, David H.
FAPPLICANT: Persing, David H.
FAPPLICANT: Hepler, William T.
FILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 429, Application US/10267502; Publication No. US20040071700A1; GENERAL INFORMATION: APPLICANT: Kim, Jaeseob; APPLICANT: Galant, Ron TITLE OF INVENTION: Obesity Linked Genes; FILE REFERENCE: LSD-07416; CURRENT APPLICATION NUMBER: US/10/267,502; CURRENT PILING DATE: 2003-01-27; NUMBER OF SEQ ID NOS: 439
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1184 IPGLKRKAE 1192
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 1192
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Sequence 9, Application US/10327213
; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
    APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TILLE OF INVENTION: INTIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TILLE DEFERRENCE: CINY/003
; TILLE REFERENCE: CINY/003
; CURRENT PAPLICANTION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 9
; LENGTH: 1192
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100.0%; Score 931; DB 15; Length 1192; idarity 100.0%; Pred. No. 1.1e-83; Conservative 0; Mismatches 0; Indels 0;
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; Publication No. US20040132096A1
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APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: ASSAY
FILE REFERENCE: P80966 GCW
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Best Local Similarity 100.
Matches 189; Conservative
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APPLICANT: COHEN, ITUD. R.
APPLICANT: COHEN, ITUD. R.
APPLICANT: BESERMAN, Pierre
APPLICANT: BESERMAN, Pierre
APPLICANT: BESERMAN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
FILE REFERENCE: EIS-SCHWARTZ=2A
CURRENT FILING DATE: 1909-05-19
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
SOFTWARE: Patentin version 3.1
FROUTH FILING DATE: 1998-05-19
SOFTWARE: Patentin version 3.1
1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123
                                                                                                       121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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Publication No. US20040063131A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Janice
Goli, Surya K.
Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/09893348 Patent No. US20020072493A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: EISENBACH-SCHWARTZ,
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1184 IPGLKRKAE 1192
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Best Local Similarity
Matches 188; Conservat
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US-10-660-946-1
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APPLICANT: BESERMAN, PIETE
APPLICANT: BESERMAN, PIETE
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
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APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANTON: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTICENS AND THEIR USE
FILE REFERENCE: EIS-SCHWARTZ=2A
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: US/09/893,348
PRIOR PILING DATE: 1999-05-19
PRIOR PILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR FILING DATE: 1998-07-21
PRIOR PILING DATE: 1998-07-21
PRIOR PILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 23
TWENT BETTING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 23
TWENT BETTING DATE: DATE SEQ ID NOS: 29
TWENT PILING DATE: DATE SEQ ID NOS: 29
TWENT PILING DATE: DATE SEQ ID NOS: 29
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100.0%; Pred. No. 1.1e-83;
iive 0; Mismatches 0;
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; Pred. No. 1.1e-83;
0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/466,258 CURRENT FILING DATE: 2003-07-15 NUMBER OF SEQ ID NOS: 13 SOFTWARE: Patentin version 3.0
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Publication No. US20040253218A1
GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michal
                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 189; Conservative
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Matches 189; Conservative
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// ORGANISM: Homo sapiens
US-10-466-258-9
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ORGANISM: Homo sapiens
                                                                                                                                                  LENGTH: 1192
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US-10-810-653-23
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                                                                                                                      SEQ ID NO 9
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62 OKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
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Pred. No. 6.4e-84;
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FRIENT NO. US20020010324A1
GENERAL INFORMATION:
JAPPIICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANTON NOVBER: COMPOUNDS
FILE REPERBNCE: GP-30165-C1
CURRENT FILING DATE: 1099-07-19
FRIOR APPLICATION NUMBER: U.K. 9916898.1
FRIOR PILING DATE: 1999-07-19
FRIOR FILING DATE: 1999-07-22
FRIOR PILING DATE: 1999-07-22
NUMBER: OF SEQ ID NOS: 6
SEQ ID NO 6
SEQ ID NO 6
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION WUMBER: US/09/893,348
PRIOR FLING DATE: 2001-06-28
PRIOR PLING DATE: 1090-05-19
PRIOR PLING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR PLING DATE: 1998-12-22
PRIOR PLING DATE: 1998-12-22
PRIOR PLING DATE: 1998-12-22
PRIOR PLING DATE: 1998-12-22
PRIOR PLING DATE: 1998-12-22
PRIOR PLING DATE: 1998-12-21
PRIOR PLING DATE: 1998-12-21
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Similarity 100.0%;
38; Conservative 0
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SOFTWARE: Patentin versic
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-10-810-653-25
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US-09-789-386-6
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Matches 188;
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US-09-789-386-6
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APPLICANT: COHEN, Irun R.
APPLICANT: BESERMAN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOALDM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
FILE REFERENCE: EIS-SCHWARTZ=2A
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NAME: Billings, Lucy J.
REGISTATION UNDERF. 36,749
REFERENCE, DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
       ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/660,946
FILING DATE: 12-Sep-2003
PRIOR APPLICATION NUMBER: US/09/228,213A
APPLICATION NUMBER: US/09/228,213A
FILING DATE: <UNKNOWN-
APPLICATION NUMBER: OB/700,607
FILING DATE: <UNKNOWN-
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                   STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S.
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Publication No. US20040253218A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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Gaps

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Length 373;

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246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 305
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Pred. No. 6.4e-84;
                                                                                                                                                                                                                                                                                      Query Match 99.6%; Score 927; DB Best Local Similarity 100.0%; Pred. No. 6.4 Matches 188; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US98/14715
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: 11 124500
PRIOR FILING DATE: 1998-05-19
SOFTWARE: PALENT NOS: 29
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SOFTWARE: PALENT NOS: 29
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APPLICANT: COHEN, Irun R.
APPLICANT: COHEN, Irun R.
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APPLICANT: COHEN, Irun R.
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOALEM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
FILE REPERENCE: EIS-SCHWARTZ-2A
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT FILING DATE: 1990-106-28
PRIOR FILING DATE: 1990-12-22
PRIOR FILING DATE: 1990-12-22
                                                      246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 305
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US-09-765-205-6
US-09-765-205-6
Sequence 6, Application US/09765205
Fatent No. US20020034800A1
GENERAL INFORMATION:
APPLICANT: Cao, Li
TITLE REFERENCE: 1458.004/200130.449
FILE REFERENCE: 1458.004/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001-01.17
FRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 373
TYPE: PT
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Patent No. US20020072493A1
GENERAL INFORMATION:
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June 16, 2005, 12:31:51; Search time 27.2927 Seconds (without alignments) 2678.292 Million cell updates/sec
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931
1 SVVDLLYWRDIKKTGVVFGA......VKDAMAKIQAKIPGLKRKAE 189
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2	Description	Aay95012 Human sec	Abul1573 Human MDI	Aay71311 Human neu	Aay56967 Human MAG	Aab82349 Human NOG	Aau04591 Human Nog	Abg30938 Human Nog	Abp68600 Human pan	Abb81078 Human neu	Abr59667 Human Nog	Human	Ado26400 Human tru	Human	Adp67234 Human Nog	Adr13966 Human NOG	Aab64514 Human sec	Aaw53947 Human NSP	Aaw78313 Fragment	Aab12805 Human NSP	Aab82348 Human NOG	Abb81080 Human neu	Adp67236 Human Nog	Aay53624 A bone ma	Aay56969 Human MAG	Aab24242 Human Nog
SOUTHWATES	ID	AAY95012	ABU11573	AAY71311	AAY56967	AAB82349	AAU04591	ABG30938	ABP68600	ABB81078	ABR59667	AD008103	AD026400	ADP45551	ADP67234	ADR13966	AAB64514	AAW53947	AAW78313	AAB12805	AAB82348	ABB81080	ADP67236	AAY53624	AAY56969	AAB24242
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de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	7.66	99.6	99.6	99.6	9.66	99.6	9.66	99.6	99.6	9.66
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Aabb2250 Human NOG Aam47954 Human RTW Abp68601 Human Dan Abb6801 Human Dan Adi6704 Human neu Adi6704 Human neu Adi67503 Human neu Adi67502 Human RTW Adm9348 Human NOG Adk77502 Human RTW Adm9348 Human Pro Adk77504 Human RTW Adm93481 Human BCT Adt87504 Human Dan Adm771318 Human BCT Adt89537 Mus muscu Adm771318 Alternati Aay71384 Alternati Abb81074 Rat neuro Adc66399 Rat trunc	MENTS) NO:64.	mour; cardiovascular disorder; mune disease; diabetes; inflammation; ; HIV; allergy; arthritis; contraceptive.						Hall J, Rapiejko P;	ns and polynucleotides encoding them, disorders, autoimmune diseases and		n secreted proteins (AAY94981-Y95020), (AAA23423-A23462). The secreted proteins nat are thought to be only partially oteins. The proteins of the invention may
AABB2350 AAM47954 ABG30631 ABB686031 ABB686031 ABB680603 ADC67235 ADC67235 ADC67235 ADC67235 ADC67235 ADC67235 ADC67230 AAM33484 AAM331384 AAM321383 AAM31384 AAM71318 AAM71318 AAM71318 AAM71384 AAM71318	ALIGNMENTS		, SEQ ID	tum coimm iral; na; c						н,	ne proteins generative d	; English	P C E
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9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	95012 st	Y95012; -JUN-2000	ın secre	Human; secreted blood disorder; infection; funga neurodegenerativ	sapiens	015	-MAR-2000 -AUG-1999	-AUG-1998 -AUG-1998 -SEP-1998 -SEP-1998 -NOV-1998 -DEC-1998	PH-) ALPHAGENE	enzuela]	r secreted ful for ti	73;	vent NA s inv ed,
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29-MAR-2001; 2001US-0290068P. 16-MAY-2001; 2001US-029189P. 17-MAY-2001; 2001US-0291829P. 17-MAY-2001; 2001US-0291849P. 19-UTN-2001; 2001US-029948P. 20-UTN-2001; 2001US-029976P. 20-UTN-2001; 2001US-0390001P.

(INCY-) INCYTE GENOMICS INC.

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exhibit one or more activities selected from the following: cytokine activity; cell proliferation; differentiation; immune modulation; heamatopoiesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; anti-inflammatory activity; haemostatic and thrombolytic activity; anti-inflammatory activity; haemostatic and thrombolytic proteins may be administered to patients as vaccines, and the nucleotides of may be used as part of a gene therapy regime. Diseases or conditions that can be treated using the proteins or nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial; fungal and viral infections, especially HIV; culliple sclerosis; rheumatoid arthritis; pulmonary inflammation; culliples creations such as asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may additionally be useful as contraceptives. Nucleic acid as a curivity may additionally be useful as contraceptives. Nucleic acid as source of diagnostic primers and probes. The present sequence represents
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Best Local Similarity 100.
Matches 189; Conservative
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-inflammatory, immunosuppressive, osteopathic, cytostatic, neptrotropic activity. The polymerication antipsoriatic and hepatotropic activity. The polymucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are particularly useful for diagnosing, treating or preventing cell proliferative disorders (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma, anaemia, tymphoma, melanoma, myeloma or sarcoma, anaemia, crohn's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABU11450-ABU11455 described in the disclosure of the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                        New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis.
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Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
H, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME;
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100.0%; Pred. No. 5.2e-92;
iive 0; Mismatches 0;
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Dufour GE, Hillman JL,
Daugherty SC, Dam TC, I
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Matches 189; Conservative
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Best Local Similarity
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                                                                                                    Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer; disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yo proteins and nucleic acids useful for treating neoplastic disorders
the central nervous system and inducing regeneration of neurons.
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/note= "Region specifically described in claim 16"
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note= "Region specifically described in claim
                                                     Human neurite growth inhibitor Nogo.
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                       structural plasticity; screening
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growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromiscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; stroke; cytostatic; cerabroprotective; neuroprotective.
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Pred. No. 6.6e-92;
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                                                                                                                                                                                                           Similarity
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                                                                                                                                                      Sequence 1178 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200005364-A1.
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fatches 189;
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1124 IMWVFTYVGALFNGLFLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
          producing such polypeptides by recombinant techniques. The disclosed are methods for utilising NOGO-C polypeptides and polymucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and disagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein; cranial trauma; cerebral trauma; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasis demyelination; encephalowyelitis; multifocal leukoencephalopathy; panencephalitis; Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy; Pelizaeus-Merzbacher disease, Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; viral infection;
                                                                                                                                                                                                                                                                                                          1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                                                                                                                                       IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
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 and methods for
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|Jabel= Lumenal extracellular_domain
|note= "This sequence is specifically claimed"
                                                                                                                                                                                                                     Length 1192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Receptor binding inhibitory peptide.
sequence is specifically claimed"
1164. 1088
/label= Pep2
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claimed"
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provides NOGO-C polypeptides and polynucleotides,
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                                                                                                                                                                                                                     100.0%; Score 931; DB 4; 100.0%; Pred. No. 6.7e-92;
                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04591 standard; protein; 1192 AA
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'label= Pepl
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Matches 189; Conservative
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                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                      Sequence 1192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krabbe's disease.
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Best Local S
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              spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleoitde is also useful for chromosome localization and for tissue expression studies. The present sequence represents the human MAGI protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuroprotective; nootropic; neuroleptic; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
 including neuropathies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of human NOGO-A. NOGO-A is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel splice variant, NOGO-C (see AAB82348). It
                                                                                                                                                                                                                                                     1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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 antibodies are useful for treating diseases,
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                                                                                                                                                   Query Match
100.0%; Score 931; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.7e-92;
Matches 189; Conservative 0; Mismatches 0;
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                                                                                                                   Sequence 1192 AA;
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Human NogoA protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is the human Nogo protein, a 250kDa myelin-associated axon growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral trauma, spinal cord injury, stroke or a demyelinating disease selected from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sclerosis, monophasis demyelination, encephalomyelitis, multifocal leukcencephalopathy, panencephalitis, marchiafava-Bignami disease, portine myelinolysis, aderenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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/note= "Receptor binding inhibitory peptide. sequence is specifically claimed" 1095. .1119 /label= Pep5 /note= "Receptor binding inhibitory peptide. sequence is specifically claimed"
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Pred. No. 6.7e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 101-104; 109pp; English
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26-MAY-2000; 2000US-0207366P.
29-SEP-2000; 2000US-0236378P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disorders.
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Best Local Similarity 100.
Matches 189; Conservative
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ABG30938
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE BOLYpeptides, and determining if the test agent interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating acute neuronal injuries, such as spinal or head injury, stroke, terations in the proposition of peripheral nerve damage, and in neoplastic (e.g. glioblastomas), hyperproliferative or dysproliferative disorders (e.g. cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may be useful in treating Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polymucleotide encoding the EAGE polypeptide are useful in cereponsive to the modulation of Nogo or BACE polypeptides, and the polymucleotide encoding the treatment or prevention of disorders cymptoms or improving the condition of apatient wiffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polymucleotide may also be an essential component in assassy, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present amino acid sequence represents the human NogoA protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuronal injuries, neoplastic or dysproliferative disorders, comprises
providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoA; Nogo-associated disease; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
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100.0%; Pred. No. 6.7e-92;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 59-62; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blackstock WP, Hale RS, Prinjha R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2002; 2002WO-GB000228.
                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-2001; 2001GB-00001312
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N-PSDB; ABK90134.
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                                                                                                                                                                                                                                  Homo sapiens
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Matches 189;
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1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; noctropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.
                                                                                1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                   1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
                                                1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                          61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                       121 LAWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human neurotransmitter receptor protein Nogo-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurotransmitter receptor; human; receptor.
    Mismatches
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98WO-US014715.
98US-00218277.
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    Conservative
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21-JUL-1998;
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    189;
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    Matches
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1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jiang
                                                                                                                                                                                                                                                                                                                                                                                            Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
cytostatic; tumour.
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                                                                                                                                                                                                                                                                                                                                                       Human pancreatic cancer expressed protein SEQ ID NO 71.
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Pred. No. 6.7e-92;
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2001US-0291631P.
2001US-0305484P.
2001US-0313999P.
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2001US-0267568P.
2001US-0278651P.
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Best Local Similarity
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20-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, oberractive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobuli (1g)A- and 1gG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia atenangectasia, Friedreich's ataxia, amyloid polyneuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the human neurotransmitter receptor protein Nogo-A, an example of NS-specific
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              autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is disbetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disc hermiation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral neuropathies associated with various diseases, including but not limited
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100.0%; Pred. No. 6.7e-92;
ive 0; Mismatches 0;
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Best Local Similarity
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Matches 189;
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The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-109 of a 473 amino acid sequence (Pl., human Nogo receptor (NgR) NTLRCT domain), or residues 27-309 of Pl., than the first 39 consecutive, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive residues. The nucleic acid of the invention has neuroprotective activity. The polymocleocide may have a use in gene therapy. The nucleic acid is useful for decreasing inhibition of axonal growth by a central nervous system (Ns) neuron. The NgR coppendent signal transduction in the central nervous system meuron may be used in treating central nervous system disease, disorder or injury. Expression of an NgR protein may be associated with inhibition of axonal regeneration following cranial, cerebral or spinal cord injury. Expression of an NgR protein may be associated with inhibition of axonal regeneration following cranial, cerebral or spinal crauma, stroke or a demyelinating disease, such as multiple sclerosis, monophasic demyelination, encephalomyelitis, multifocal

C sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IOKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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antidiabetic.
                                                                       New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system neuron, or in treating central nervous system disease, disorder or injury, e.g. spinal cord injury.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 931; DB 6;
; Pred. No. 6.7e-92;
0; Mismatches 0;
                                                                                                                                                                    Disclosure; Page 131-135; 148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
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                   WPI; 2003-393433/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1192 AA;
                                     N-PSDB; ACC81048
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The present invention relates to an isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein from the rat and from the human. The truncated polypeptide is useful for identifying a compound having detectable affinity to a Nogo-A protein. The present sequence is a Nogo-A polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein, useful for identifying a compound having detectable affinity to a Nogo-A protein.
rat; human; Nogo-A; truncated; affinity; membrane-bound protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 6B; 80pp; English.
                                                                                                                                                                                                       31-OCT-2002; 2002WO-EP012210
                                                                                                                                                                                                                                                          31-OCT-2002; 2002WO-EP012210
                                                                                                                                                                                                                                                                                                          (PIER-) PIERIS PROTEOLAB AG.
                                                                                                                                                                                                                                                                                                                                                             Fiedler M;
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-376159/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1192 AA;
                                                                                                       WO2004039836-A1
                                                     Homo sapiens.
                                                                                                                                                       13-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                               Skerra A,
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                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene of relative to expression of the gene in an expression vector not exposed to the agent, traating a subject with the agent and identifying fat cell number or size in the subject with the agent comprises an antisense of igonucleotide. The subject comprises a mammal, preferably a human. The coligonucleotide are abject comprises an antisense configurable to the agent, detecting binding of the agent to the oppypeptide to a change in an activity of the polypeptide, treating a cubject with the agent and identifying fat cell number or size in the agent that changes the expression of a gene, and treating the subject comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the cubject is altered. The method is useful for identifying componings that influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents a human polypeptide used in the scope of the invention.
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                                                                                                                                                                                                                                                       Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
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                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; SEQ ID NO 429; 275pp; English.
                               09-OCT-2002; 2002US-00267502
                                                                             (LIFE-) LIFE SCI DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 189; Conservative
                                                                                                                                                                                  WPI; 2004-328526/30
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                                                                                                                               Galant R;
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                                                                                                                               Kim J,
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LMWVPTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
                                                                                                                                                                                                                                                                                                                                                                                                                 nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder.
                                                 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                         ö
 Length 1192;
                                                                                                                                                                                                                                                                                                                                                                                                    binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
                          Indels
100.0%; Score 931; DB 8;
100.0%; Pred. No. 6.7e-92;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                  ADP45551 standard; protein; 1192 AA
                                                                                                                                                                                                                                                                                                                                                                            Human NogoA protein SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                    (first entry)
             Best Local Similarity 100.
Matches 189; Conservative
                                                                                                                                                                                                                                   IPGLKRKAE 1192
                                                                                                                                                                                                         IPGLKRKAE 189
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                                                                                                                                                                                                                                                                                                                           ADP45551;
                                                                                                                                                                                                                                                                           RESULT 13
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1183

180

121 LMWVFTYVGALFNGLTLLIIALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK

ADO26400 standard; protein; 1192 AA.

RESULT 12

1184 iPGLKRKAE 1192 IPGLKRKAE 189

1124 181

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Human truncated Nogo-A protein.

(first entry)

29-JUL-2004

AD026400

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1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel composition comprising neurite outgrowth inhibitor (Nogo) and contactin-associated protein-1 (Caspr) or its mimetics or a substance capable of promoting interaction between Nogo and Caspr, in combination with a carrier. A composition of the invention has neuroprotective activity, and may have a use in gene therapy. The composition is useful for treating injury to or disease of the CNS, e.g. spinal cord injury, multiple sclerosis, epilepsy or stroke. The present sequence represents human Nogo-A.
                                                                                                                                                                                                                                                                                                                                                                New composition comprising Nogo and Caspr or a substance capable of promoting interaction between Nogo and Caspr useful for treating injury to or disease of the CNS, e.g., spinal cord injury, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; myelin-associated glycoprotein; MAG; neural growth; neural regeneration; apoptosis; amylotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease; Huntington's disease; multiple sclerosis; Creutzfeldt-Jacob disease; kuru; multiple system atrophy; Lou Gehrig's disease; kuru; progressive supranuclear palsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 931; DB 8;
; Pred. No. 6.7e-92;
0; Mismatches 0;
                                                                                                                                                                                                      (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD (FORR/) FORREST G R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 14; 202pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR13966 standard; protein; 1192 AA.
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                                                                                                                                    06-DEC-2002; 2002US-0431549P.
20-JUN-2003; 2003US-0480138P.
                                                                                            05-DEC-2003; 2003WO-GB005329
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                                                                                                                                                                                                                                                                                                                   WPI; 2004-468705/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                       epilepsy or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1192 AA;
    WO2004052389-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human NOGO-A.
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                                               24-JUN-2004
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                                                                                                                                                                                                                                                                           Xiao Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 1000nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the binding molecule and a carrier or diluent; and (5) treating the binding molecule and a carrier. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present exquence represents human NogoA, which is used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                              New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.
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                                                                                                                                                                                 Schwab ME,
                                                                                                                                                                                 Schnell L,
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 5; 121pp; English.
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                                                                                     (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
09-DEC-2003; 2003WO-EP013960
                                            10-DEC-2002; 2002GB-00028832
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ses 189; Conservative
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N-PSDB; ADP45550.
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Zurini M;
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The invention relates to a myelin-associated glycoprotein (MAG)

derivative comprising a mutation in or flanking MAG Ig-11ke domain 5

(Igd5), excluding the MAG derivative to regulate neutricon reduces or eliminates the ability of the derivative to regulate neurite outgrowth as compared to endogenous or soluble MAG without eliminating binding to neuronal surfaces. The inhibitors of MAG are useful for promoting neural degeneration associated with injuries, disorders, or treating neural degeneration associated with injuries, disorders, or diseases. The disorder, disease, or condition is associated with cappotrosis or results from a demyelinating disease and includes amylotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease, Huntington's disease, multiple sclerosis, alteral sclerosis (Lou Gehrig's disease), or progressive supranuclear palsy. The present sequence represents the amino acid sequence of human NOGO-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New myelin-associated glycoprotein (MAG) derivative comprises a mutation in or flanking MAG Ig-like domain 5 (Igd5), excluding the MAG derivative MAG (d1-3)-Fc, useful promoting neural growth and regeneration.
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Job time : 28.2927 secs
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(DOME/) DOMENICONI M.
(CAOZ/) CAO Z.
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(c) 1993 - 2005 Compugen Ltd.
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US-09-149-476-110
US-09-148-796A-16008
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Sequence 1, Application US/08700607

Sequence 1, Application US/08700607

Patent No. 5858708

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goli, Surya K.

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
US-09-543-681A-7510
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ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUTCATION INFORMATION:
TELECHONE: 415-85-055
TELEFAX: 415-85-055
TELEFAX: 415-85-055
TELEFAX: 419 amino acids
TWIND AMINORALION:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
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LIBRARY:
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STRANDEDNESS: sin
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63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 IDLLYWRDIKQTGIVFGSFLLILFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESCONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%; Score 682; DB 2;
68.4%; Pred. No. 3.8e-66;
tive 31; Mismatches 28;
                      E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: B6749
REFERENCE/DOCKET NUMBER: PF-0114 US
                                                                                                                                                                                                                                                                                                                                                                                             PF-0114 US
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
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Best Local Similarity 68.49
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
      CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
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                                                                 Palo Alto
                                                                                                           u.s.
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                                                              CITY: Palo
STATE: CA
COUNTRY: U.
ZIP: 94304
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COUNTRY: U.
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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US-08-700-607-6
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| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| PRIOR PELLING DATE: 2000-04-14-1755
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-30
| PRIOR FILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 9124
                                                                                           72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 133
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                                                                                                                                                                                 132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKVVKDAMAKIQAKI 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
                                                                 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
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APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
IIILE OF INTENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
99.6%; Score 927; DB 4;
Best Local Similarity 100.0%; Pred. No. 8e-93;
Matches 188; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/08700607; Patent No. 5858708; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             192 PGLKRKAE 199
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US-09-949-016-9124
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US-08-700-607-7
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Length 208;

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63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
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                                                                                                                                                                                                                                                                            3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ
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73.3%; Score 682; DB 4; Length 439; 68.4%; Pred. No. 1.1e-65; ive 31; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Gli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
RILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/08700607; Patent No. 5858708
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COUNTY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TOWNER: IBM Compatible
DOS
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Query Match
Best Local Similarity 68.4*
Matches 128; Conservative
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Matches 128; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                         183 GLKRKAE 189
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CLONE: 307307
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STATE: CA
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US-08-700-607-5
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| Sequence 9180, Application US/09949016
| Sequence 9180, Application US/09949016
| Patcent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VETER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| FILE REFERENCE: CL001307 |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR PELING DATE: 2000-10-20 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEQ ID NO 9180 |
| LENGTH: 439 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 WILTYVGALFNGITLILLMAVVSMFTLPVVYVKHQAQIDQYLGIVRTHINAVVAKIQAKIP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
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68.4%; Pred. No. 8e-66;
tive 31; Mismatches 28; Indels
                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 9F-0114 US
TELECOMUNICATION INFORMATION:
TELECHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 3.56 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 68.49
Matches 128; Conservative
  COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLKRKAE 189
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; ORGANISM: Human
US-09-949-016-9180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; CLONE: CLONE: US-08-700-607-6
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8 셤 ò 셤 ઠે 셤 ਨੇ 셤

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Sequence 8859, Application US/09949016
Sequence 8859, Application US/09949016
Sequence 8859, Application US/09949016
Sequence 8859, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Score 665; DB 2; Length 267; 67.2%; Pred. No. 3.8e-64; rive 33; Mismatches 27; Indels
                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTONNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELEPHONE: 415-855-0555
3174 Porter Drive
                                                                                                                                             E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPLOGY: linear TOPLOGY: LANGUAGE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 67.2
Matches 123; Conservative
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                          Palo Alto
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CLONE: 281046
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                                                                                              94304
                                                                                                                                                                       COMPUTER:
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STREET:
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Sequence 6998, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:

APPLICANT VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20
                                                                                                                      KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
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APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
ADDRESSE: ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6998
LENGTH: 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                               US-09-949-016-6998
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R APPLICATION NUMBER: 60/047,587
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,492
R FILING DATE: 1997-05-23
R PRPLICATION NUMBER: 60/047,598
R FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,601
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
                                                   FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,500
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-05-23
APPLICATION UNMBER: 60/047,612
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
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APPLICATION NUMBER: 60/043,669
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APPLICATION NUMBER: 60/056,889
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APPLICATION NUMBER: 60/056,878
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
                          APPLICATION NUMBER: 60/047,584
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/047,596
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FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,312
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APPLICATION NUMBER: 60/056,886
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APPLICATION NUMBER: 60/056,877
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APPLICATION NUMBER: 60/056,637
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                                                                                                                                                                                    Gaps
                                                                                                                                                                                    1;
                                                                                                                            Length 192;
                                                                                                                              67.4%; Score 627.5; DB 4; Length 61.1%; Pred. No. 2.9e-60; ive 38; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT PELLOATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER PILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,583
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,617
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/047,592
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; Sequence 563, Application US/09149476
: Patent No. 6420526
                                                                                                                            Query Match
Best Local Similarity 61.1
Matches 116; Conservative
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183 LPGIAKKKAE 192
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                        ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859
LENGTH: 192
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R APPLICATION NUMBER: 60,056,636
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60,056,874
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60,056,910
R APPLICATION NUMBER: 60,056,814
R APPLICATION NUMBER: 60,056,864
R PILING DATE: 1997-08-22
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R APPLICATION NUMBER: 60/047,585
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,586
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,590
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R APPLICATION NUMBER: 60/043,578

R FILING DATE: 1997-04-11

R PILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,576

R APPLICATION NUMBER: 60/047,501
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,880
R FILING DATE: 1997-08-22
A PAPLICATION NUMBER: 60/056,894
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/056,631
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,845
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,892
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,588
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614
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APPLICATION NUMBER: 60/056,632
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/047,595
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,589
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,670
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,875
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APPLICATION NUMBER: 60/057,761
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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                                                    BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIE
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61 AFHNYMNAAWVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAEL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45122, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILIS REFERENCE: FILE REFERENCE: 7126-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF EXQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 45132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 LIYWRDVKKSGIVFGAGLITLAAISSFSVISVFAYLSLLTLFGTVAFRIYKSVTQAVQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKS
                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                           Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.6%; Score 518; DB 4; Length 219; 51.4%; Pred. No. 2.8e-48;
                                                                                                                                                                                                                                                     34; Mismatches 31; Indels
                                                                                                                                                                                                           58.2%; Score 541.5; DB 4; 60.5%; Pred. No. 5.4e-51;
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             EARLIER APPLICATION NUMBER: 60/056,884
EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER PILING DATE: 1997-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Drosophila melanogaster
FILING DATE: 1997-09-05
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Best Local Similarity
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Matches 95; Conserv
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US-09-270-767-45132
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122 MWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
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                                                                                                                                                                                                                                                  Length 588;
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                                                                                                                                                                                                                                              50.9%; Score 473.5; DB 4; 47.3%; Pred. No. 7.8e-43; ative 37; Mismatches 56;
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7290
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APPLICATION NUMBER: 60/040,336
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APPLICATION NUMBER: 60/040,626
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APPLICATION NUMBER: 60/047,600
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APPLICATION NUMBER: 60/040,333
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EARLIER APPLICATION NUMBER: 60/038,621
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Patent No. 6420526
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                             TYPE: PRT
ORGANISM: Human
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                                                                                                                                      LENGTH: 588
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Batent No. 6812339
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IQKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Indels
                    APPLICANT: Hillman, Jennifer L.
TILLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CIT: Palo Alto
STATE: CA
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.0%; Score 512; DB 2; Best Local Similarity 52.4%; Pred. No. 1.4e-47; Matches 98; Conservative 35; Mismatches 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 FMWLMTYVGAVFNGITLLILAELLIXSVPIVYXKY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0114 US
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTERO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: THPINOB01
CLONE: 31870
                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
    Goli, Surya K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415-845-4166
                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 IPGLKRK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::|
207 TPWNROK 213
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    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-700-607-3
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Matches
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RELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612
RELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
RILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,601
RAPPLICATION NUMBER: 60/047,601
RAPPLICATION NUMBER: 60/043,580
RILING DATE: 1997-05-23
RAPPLICATION NUMBER: 60/043,580 RELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,500
RELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,587
RELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492 APPLICATION NUMBER: 60/048,974
PILING DATE: 1997-06-06
APPLICATION NUMBER: 60/056,886
PILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,877
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,592 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,581 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,584 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,503 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,598 FILING DATE: 1997-05-23 LING DATE: 1997-04-11 PLICATION NUMBER: 60/043,674 LING DATE: 1997-04-11 PPLICATION NUMBER: 60/043,669 LING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 ING DATE: 1997-08-22 LICATION NUMBER: 60/056,872 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,582 ILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 TLING DATE: 1997-04-11
PPPLICATION UNMBER: 60/043,311
TLING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,671 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,596 LICATION NUMBER: 60/043,313 APPLICATION NUMBER: 60/056,893 PPLICATION NUMBER: 60/056,662 TILING DATE: 1997-08-22 LING DATE: 1997-08-22 EARLIER SARLIER EARLIER EARLIER SARLIER SARLIER SARLIER SARLIER SARLIER PARLIER PARLIER ARLIER ARLIER SARLIER

R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,903
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,888
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,879
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,879
R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/057,761
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/047,595
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,599
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,588
R APPLICATION NUMBER: 60/047,588
R APPLICATION NUMBER: 60/047,588
R APPLICATION NUMBER: 60/047,588 APPLICATION NUMBER: 60/047,586
FILING DATE: 1997-65-23
APPLICATION NUMBER: 60/047,590
FILING DATE: 1997-65-23
APPLICATION NUMBER: 60/047,594
FILING DATE: 1997-65-23
FILING DATE: 1997-65-23
FILING DATE: 1997-65-23 R APPLICATION NUMBER: 60/056,631 R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,892 R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/047,593
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,614
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043,578
R PILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,664 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,874
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,632 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,862 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,887 LING DATE: 1997-08-22 PPLICATION NUMBER: 60/056,911 LING DATE: 1997-08-22 PPLICATION NUMBER: 60/043,670 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 CATION NUMBER: 60/056,875 LING DATE: 1997-08-22 1997-08-2 EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER SARLIER SARLIER

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Search completed: June 16, 2005, 12:33:40 Job time : 8.13706 secs/
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; Sequence 7861, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.;
; APPLICANT: Duclert, A.;
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; PILE REPERENCE: 59.US2.REG
; CURRENT PILING DATE: 2000-02-24
; PRIOR PPLICATION NUMBER: US 60/122,487
; PRIOR PLING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7861
; LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 NSALGHVNCTIKELRRIFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSVP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.4%; Score 246; DB 4; Length 114; Best Local Similarity 69.6%; Pred. No. 4.4e-19; Matches 48; Conservative 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.6%; Score 285; DB 4; Best Local Similarity 57.1%; Pred. No. 1.9e-23; Matches 52; Conservative 20; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 VIYERHOAQIDHYLGLANKNVKDAMAKIQAK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::||:::||||||:|:|
62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92
                  EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-06
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-05
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EARLIER FILING DATE: 1997-08-05
EARLIER FILING DATE: 1997-08-05
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER FILING DATE: 1997-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: -48..-1
OTHER INFORMATION: SCORE 4.6
OTHER INFORMATION: SEQ VFGSFLLLLFSLT/QF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: UNSURE
LOCATION: 22
OTHER INFORWATION: Xaa=Phe or Leu
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: UNSURE
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

June 16, 2005, 12:55:32 ; Search time 5.68322 Seconds Run on:

(without alignments) 3199.767 Million cell updates/sec

US-09-830-972-29_COPY_990_1178 931

1 SVVDLLYWRDIKKTGVVFGA......VKDAMAKIQAKIPGLKRKAE 189 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	rip
	682	73.3	208	. 7	I60904	neuroendocrine-spe
7	682	73.3	. 776	N	A46583	neuroendocrine-spe
e	665	71.4	267	~	A60021	tropomyosin-relate
4	335	36.0	2484	~	T26216	hypothetical prote
S	335	36.0	2607	7	T26215	
9	334	35.9	222	~	T26213	
7	191	20.5	255	7	E84899	
80	182		271	0	T13013	
Ø.	163	•	275	~	T05595	hypothetical prote
10	147	15.8	393	~	567763	ч
11	144.5	٦	242	~	B85016	hypothetical prote
12	131	٦	183	~	A84527	
13	127.5	7	295	~	S59439	mem
14	124	-	206	7	T01153	probable seed matu
15	109.5	11.8	264	~	T47948	
16	104.5	11.2	203	7	T47571	hypothetical prote
17	95		288	~	B90043	14
18	94.5	10.2	458	α,	A72258	hypothetical prote
19	93	10.0	160	~	C84422	hypothetical prote
20	92.5	٠	527	7	A84645	probable cytochrom
21	88.5	9.5	405	~	H71692	hypothetical prote
22	88	•	224	7	D71915	hydrogenase, cytoc
23	87.5	٠	296	7	S46018	probable membrane
24	85.5	9.5	442	7	C75057	hypothetical prote
25	ď.	9.5	823	~	H83724	
56	5	9.5	1065	7	E69795	Ψ
27		•	224	П	A64599	hydrogenase (EC 1.
28	82	9.1	459	~	G86264	n
29		9.1	468	~	O.	nicotinic acetylch

hypothetical prote	unknown protein, 7	hypothetical prote	NADH2 dehydrogenas	immunity protein,	conserved hypothet	hypothetical prote	secD protein - Str	hypothetical prote	transport ATP-bind	phospho-N-acetylmu	hypothetical prote	leukotoxin express	probable ABC trans	probable peroxisom	conserved hypothet
H90023	G96705	,H85095	C70414	F95232	96086Н	B69155	S52765	T33040	F64201	AE1700	H90587	T14886	T41622	T41400	G82873
~	~	~	~	N	~	N	~	~	N	~	N	~	~	0	N
'n	d	57	64	11.	280	663	570	955	689	124	69	86	322	937	537
105	15	4	4	v	•	•			٠,	,	m	un	~	•	
9.1 105				9.1							8.8	8.8	8.8	8.8	8.7
85 9.1 105	9.1	9.1	9.1		9.1			8.9		8.8	8.8	8.8	81.5 8.8 (8.8	81 8.7

ALIGNMENTS

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Cyacte: Armaylable Medutation 1970 and Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volume Volum
neuroendocrine-specific protein C - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22
```

ö Gaps ; 0 Length 208; 28; Indels 73.3%; Score 682; DB 2; 68.4%; Pred. No. 2.8e-55; iive 31; Mismatches 28. Query Match 73.3% Best Local Similarity 68.4% Matches 128; Conservative

KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122 22 IDLLYWRDIKQTGIVFGSFLLLFPSLTQFSVVSVVAYLALAAALSATISFRIYKSVLQAVQ 81 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ m 63 82 8 셤 셤 ò

WVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 182 123 ò

g

GAKRHAE 208 GLKRKAE 189 183 202 ò g

RESULT A46583

300000000000

neuroendocrine-specific protein, splice form A - human N;Contains: neuroendocrine-specific protein, splice form B C;Species: Homo sapiens (man) C;Daccess: Homo sapiens (man) C;Accession: A46583; 160903 R;Roebrock, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V B;Biol. Chem. 268, 13439-13447, 1993 A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe A;Reference number: A46583; MUID:93293865; PMID:7685762

```
A;Cross-references: UNIPROT:Q9U347; EMBL:278066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:Wt
A;Experimental source: clone W06A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein W06A7.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T5-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26215
R;Ainscough, R.
R;Ainscough, R.
R;Ainscough, R.
A;Accession: T26215
A;Reference number: Z20173
A;Reference number: Z20173
A;Reference number: Z20173
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2607 <WILL>
A;Residues: 1-2607 <WILL>
A;Residues: 1-2607 <WILL>
A;Residues: clone W06A7
A;Experimental source: clone W06A7
C;Genetics:
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A,Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
                                                  hypothetical protein W06A7.3c - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26216
R;Ainscough, R.
Bubmitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Sccession: T26216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recession: 1-2484 (MIL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2409 LWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2412 VLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAAGFRVFKKVEAQI
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A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 33.7%; Pred. No. 3.6e-22;
Matches 62; Conservative 46; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
36.0%; Score 335; DB 2;
Best Local Similarity 33.7%; Pred. No. 3.8e-22;
Matches 62; Conservative 46; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2469 PFLR 2472
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CippomyColes: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
Cipate: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
Cipates: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
Cipates: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
Riviersork, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
Airitle: Developmentally regulated cDNA expressed exclusively in neural tissue.
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A;Accession: A46583
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-776 «ROE1»
A;Cross-references: UNIPROT:Q16799; GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307
A;Accession: 160903
A;Accession: 160903
A;Accession: Logo: mRNA
A;Residues: 421-776 «ROE2»
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
C;Genetics: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
A;Cross-references: GB:L203968; OMIM:600865
A;Map position: 14q21-14q22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 267;
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hypothetical protein FBL21.10 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 13-Aug-1999 #text_change 09-Jul-2004 (Speciession: T13013 (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Specie
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R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999
A;Reference number: 215419
A;Accession: T05595
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A;Cross-references: UNIPROT:O9SUT9; EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.10
A;Experimental source: cultivar Columbia; BAC clone F8L21
                                                                                                                                                                         70 DVFLWRDKKLSGAVLGVATAIWVLFELVEYHLLSLLCHISILALG---GLFLWSNAHTLI 126
                                                                                                                                                                                                                                                                62 OKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
                                                                                                                                                                                                                                                                                                                            122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 181
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr_1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
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                                                                                       4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
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    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               122 MWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAM---
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    Indels
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A;Cross-references: UNIPROT:Q9SUR3; EMBL:AL035394
A;Experimental source: cultivar Columbia; BAC clone F9D16
    78;
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19.5%; Score 182; DB 2;
Best Local Similarity 26.1%; Pred. No. 3.1e-09;
Matches 47; Conservative 42; Mismatches 79;
    Mismatches
    40;
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A,Introns: 85/1; 145/2; 192/3; 216/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 AKIQAKIP--GLKRKAE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 EKVLSKIPIASĽKAKÁK 253
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: ATSP: F8L21.10
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A; Introns: 89/1; 1
A; Note: F9D16.100
    55;
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct 1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 126213
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Refatus: preliminary; translated from GB/EMBL/DDBJ
A;Refatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84899
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Buss, D.; Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A64420; MUID:20083487; PMID:10617197
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Best Local Similarity 33.2*
Matches 61; Conservative
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A;Introns: 27/1; 77/2; 201/2
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-255 <STO>
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PFLR 210
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A;Map position: 2
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Best Local Similarity
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A;Map position: 2
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RySchmidt, B.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.
Bubmitted to the Protein Sequence Database, July 1996
A; Reference number: S67756
A; Rocession: S67763
A; Rocession: S67763
A; Rocession: S67763
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A; Rocession: Aim Ricession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Rocession: Aim A; Roc
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R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85016
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                                                                                                                                                                                            91 DIFMWKNKKWSGGVLGGATAAWVVFELMEYHLLITLCHVMIVVLAVLF---LWSNATWFI 147
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                                                                                                                                                                                                                                                                                                                                                                 148 NKSPPKIP-----EVHIPEEPILQLASGLRIEINRGFSSLREIASGRDLKKFLIAIAG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                             122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA----KI 177
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                                                                                                                                                                                                                                                                                          62 OKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YDL204w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypotherical protein D1062
C.Species: Saccharomyces cerevisiae
C.Species: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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15.8%; Score 147; DB 2; Length 393;
Best Local Similarity 27.0%; Pred. No. 7.8e-06;
Matches 47; Conservative 34; Mismatches 51; Indels
   Length 275;
                                                                           82; Indels
; Score 163; DB 2;
; Pred. No. 1.7e-07;
42; Mismatches 82,
Query Match
Best Local Similarity 26.0%;
Matches 50; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 QAKIP--GLKRK 187
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9M145; GB:NC_001268; NID:g7267620; PIDN:CAB80932.1; GSPDB:C
GGenetics:
A;Gene: R14901230
A;Map position: 4
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A;Residues: 1-183 <STO>
A;Cross-references: UNIPROT:Q9SHU8; GB:AE002093; NID:g4662633; PIDN:AAD26905.1; GSPDB:G
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N,Alternate names: hypotherical protein YD9934.17c
C,Species: Saccharomyces cerevisiae
C,Species: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 144.5; DB 2,
; Pred. No. 7.5e-06;
47; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 15.5%;
1 Similarity 24.7%;
47; Conservative 4
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Best Local Similarity 24.0%
Matches 43; Conservative
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Length 206; Indels

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R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480
A;Accession: T47948
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AIQKSDEGHPFRAYLESEVA---ISEELVQKYSNSALGHVNCTI---KELRRLFLVDDLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 DSLKFA--VL-MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE002093; NID:g3152617; PIDN:AAC17096.1; GSPDB:GN00139 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                              2 VVDLLYWRDIKK--TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                     16 VEDIYLWRRKKLAFSTILUSTSTWILLSFYGFTTITIVSWIGIAVVSMIF---LWGSLLR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F2A19.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47948
                                                                                                      A,Gene: At2g23640; F26B6.29; F27L4.17
A,Map position: A.A.Introns: 14/1; 76/2; 147/1
C,Superfamily: Arabidopsis thaliana hypothetical protein F27L4.17
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A;Residues: 1-264 <DEH>
A;Cross-references: UNIPROT:Q9M312; EMBL:AL132962
A;Experimental source: cultivar Columbia; BAC clone F2A19
                                                                                                                                                                                                                                                                13.3%; Score 124; DB 2; I
24.4%; Pred. No. 0.00048;
tive 44; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 KGAYNTTHEKILEMKNK 193
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 24.4*
Matches 48; Conservative
                A; Residues: 1-206 <STO>
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A; Introns: 68/1; 1
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NyAlternate names: hypothetical protein F27L4.17
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01153; T02426; C84627
C;Accession: T01153; T02426; C84627
C;Accession: T01153
A;Redented to the EMBL Data Library, June 1998
A;Pescription: Arabidopsis thaliana chromosome II BAC F2686 genomic sequence.
A;Recession: T01153
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-206 cR0U>
A;Residues: 1-206 cR0U>
A;Residues: 1-206 cR0U>
A;Residues: 1-206 cR0U>
A;Residues: 1-206 cR0U>
A;Rebaidues: 1-206 cR0U>
A;Rebaidues: 1-206 cR0U>
A;Rebaidues: 1-206 cR0U>
A;Rebaidues: 1-206 cR0U>
A;Rebaidues: 1-206 cR0U>
A;Reperimental source: cultivar Columbia
B;Rounsley, S.D; Kaul, S.; Lin, X.; Retchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, May 1998
A;Rescription: Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence.
A;Reference number: Z14658
A;Recension: T02426
A;Ross-references: EMBL:Accond482; NID:3152602; PIDN:AAC17096.1; PID:3152617
A;Ressidues: 1-206 cR02>
A;Gross-references: EMBL:Acconday, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujui, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Fraser, C.M.; Venter, J. Film, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A; Tillo, C. A;
C;Accession: S59439
R;Murphy, L.; Harris, D.
Submitted to the EMBL Data Library, March 1995
S;Molecule to the EMBL Data Library, March 1995
A;Rolecule type: DNA
A;Residues: 1-295 <MUR>
A;Residues: 1-295 <MUR>
A;Residues: 1-295 <MUR>
A;Cross-references: UNIPROT:Q04947; EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YDR233c
A;Cross-references: SGD:S0002641
A;Map position: 4R
C;Reywords: transmembrane protein
C;Reywords: transmembrane #status predicted <TM1>
F;146-162/Domain: transmembrane #status predicted <TM2>
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A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Accession: C84627
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|LLLMRNPVQTGKYFGGSLLALLILKKVNLITFFLKVAYTILFTT------GSIEFV--
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181 ISKQKTQEFSQMACEKTKPYLDKVESKL 208
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A;Molecule type: DNA
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                                                                                                                                                                             Indels 57;
                                                                                                                 Length 264;
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                                                                                                          ch 11.8%; Score 109.5; DB 2; 1. Similarity 25.2%; Pred. No. 0.014; 55; Conservative 37; Mismatches 69;
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Job time : 6.68322 secs
A;Introns: 68/1; 128/2; 164/1; 210/1
A;Note: F2A19.160
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(TrEMBLrel. 27, Last annotation update)
(soform Ab) (RTN4 isoform D) (RTN4 isoform E)
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MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
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100.0%; Pred. No. 7.8e-71;
ive 0; Mismatches 0;
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GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
PF02453; Reticulon. 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 986 AA; 108449 MW; 0CDE8F6470364
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Q9BQ59
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Matches 189; Conservative
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Q8bhf5
Q99p72
Q99k11
Q9jk11
Q8k3g8
Q8k3g7
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06jrv9
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Q6im70
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Q7pcj7
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Q8k290
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06ify4
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                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           1612378 segs, 512079187 residues
                                                                                                                                                                   US-09-830-972-29_COPY_990_1178
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061PNO
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Q96B16
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Maximum Match 100%
Listing first 45 summaries
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Q6KSS8
Q7T224
Q9GM33
Q61FY5
Q6JFY2
Q6JRV2
Q6JRV0
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Q6JRV3
Q6JRV9
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OGJRV4
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
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Match Length DB
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Result

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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                         growth.
  917
                                                  918 LAMVETYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNYKDAMAKIQAK 977
             IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV
                                       LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK
Jin W.-L., Ju G.;
"Developmentally-regulated alternative splicing in a novel Nogo-A.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pituitary;
Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
Luo B., Hu R., Chen J.;
"Human neuroendocrine-specific protein C (NSP) homolog gene.";
                                                                                                                                                                                                                                                                                                                                                                                               Ö
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"A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity.";
Oncogene 19:5736-5746 (2000).
                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287; Putinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie Michalovich D., Simmons D.L., Walsh F.S.; "Inhibitor of neurite outgrowth in humans.";
                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 45, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Nouroendocrine-specific protein) (NSP) (Neuroendocrine specific protein) (NSP) (Neuroendocrine specific Protein) (NSP) (Neuroendocrine specific Protein) (NSP) (My043 protein).
Name=RIN4; Synonyms=ASY, KIAAO886, NOGO;
                                                                                                                                                                            RTN4 HUMAN STANDARD; PRT; 1192 AA.
Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9X293; Q9Y2Y7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE=Brain;
MEDLINE=21010696; PubMed=11126360; DOI=10.1038/8j.onc.1203948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20237542; PubMed=10773680;
Yang J., Yu L., Bi A.D., Zhao S.-Y.;
"Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14-->2p13 by radiation hybrid mapping.";
Cytogenet. Cell Genet. 88:101-102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the reticulon gene family in human."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation of a cell death-inducing gene."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
TISSUE=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2).
TISSUE=Fibroblast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 403:383-384(2000).
                                                                                       IPGLKRKAE 189
                                                                                                                IPGLKRKAE 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of a member
Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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TISSUESEROM N.A. (ISOFORMS 2 AND 3).

TISSUESERIAIN, Ovary, Pancreas, Placenta, and Skeletal muscle;

TISSUESERIAIN, Ovary, Pancreas, Placenta, and Skeletal muscle;

MEDINRE-228825; PubMed=12477932; Doi=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B. Buerow K.H., Schamfer C.R., Schuler G.D.,

A Altschul S.F., Zeeberg B. Buerow K.H., Schamfer C.R., Schuler G.D.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W. Sodergren E.J., Lu X., Gibbs R.A.,

Richards A.C., Grimwood J., Schwuchenko Y., Bouffard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Browner D.N., Maranan D.W., Marra M.A.,

Bromeration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE=20499367; PubMede-11042152; DOI=10.1101/gr.140200; Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.; Cloring and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohaza O.; Prediction of the coding sequences of unidentified human genes. XII The complete sequences of 100 new cDNA clones from brain which code
SEQUENCE FROM N.A. (ISOFORM 3).
Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                                                                                                                                                                                  human cDNA clones with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20129259; PubMed=10667797; DOI=10.1038/35000226; GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.; "Identification of the Nogo inhibitor of axon regeneration as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sha J.H., Zhou Z.M., Li J.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                               Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99156230; PubMed=10048485;
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TISSUE=Umbilical cord blood;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for large proteins in vitro.";
DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 10:1546-1560(2000)
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Nature 403:439-444(2000).
[15]
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                                                                                                                                                       Yu J., Han L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isoid=Q9NQC3-4; Sequence=VSP_005654; TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain and testis and weakly in heart and skeletal muscle. Isoform 2 is widely expressed excepted for the liver. Isoform 3 is expressed in brain, skeletal muscle and adipocytes. Isoform 4 is testis-specific.
                                                                                                                                                                                                      J. Neurosci. Res. 67:559-565 (2002).

-!- FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults. Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2. This is likely consecutive to their change in subcellular location, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.
-!- SUBGINIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
-!- SUBCELIOUAR LOCATION: Integral membrane protein. Endoplasmic reticulum reticulum. Anchored to the membrane of the endoplasmic reticulum
                              MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
Fournier A.E., Grandpre T., Strittmatter S.M.;
"Identification of a receptor mediating Nogo-66 inhibition of axonal
                                                                                                                                          MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134; Ng C.E.L., Tang B.L.; "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 931; DB 1; Length 1192; 100.0%; Pred. No. 9.4e-71; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 reticulon domain.
CAUTION: Ref.11 sequence differs from that shown due to
frameshifts in positions 1149 and 1156.
                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;
IsoId=Q9NQC3-1; Sequence=Displayed;
Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foocen-M;
IsoId=Q9NQC3-2; Sequence=VSP_005655;
Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                         through 2 putative transmembrane domains. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAA74909.2; ALT INIT.
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CAB99250.1;
BAB18927.1;
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AAG12176.1;
AAG12177.1;
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AAD31021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD31022.1;
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                                                                                              Nature 409:341-346(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB040463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC007109;
                                                                                                                                                                                            regeneration.";
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                                                                                regeneration."
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                  TISSUE=Brain;
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Best Local Similarity 100. Matches 189; Conservative

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An expleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Widdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Wokernan K.J., Malex J.A., Gunarare P.H.,
A Boak S.A., McEwan P.J., McKernan R.J., Malex J.A., Gunarare P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Palton B.K. Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Schwurz J., Myers R.M., Butcerfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
                                          1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063
                                                                                                                                                                                                             1124 IMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
                                                                                                                                                                                                                                                                                                                                LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
                                                                                                                                                              IOKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
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SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO16165; AAH16165.1; -.
EMBL; AY102278; AAM64247.1; -.
EMBL; AY102285; AAM64242.1; -.
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
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1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Reticulon 4, isoform D (RTW4 isoform B2).
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J. Mol. Biol. 325:299-323(2003).
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PGLKRKAE 189
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MEDLINE=22715887; PubMed=12832288;
Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
"A reticular rhapsody; phylogenic evolution and nomenclature of the RTN/Nogo gene family.";
FASEB J. 17:1238-1247(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-RTN4;
bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                   Length 392;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                    42274 MW; D7B2AA5E839E58AD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                               99.7%; Score 928; DB 2; Lk
99.5%; Pred. No. 5.5e-71;
tive 1; Mismatches 0;
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GO, GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
PF02453; Reticulon, 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 199 AA; 22395 MW; C60161DF3FB341
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
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Best Local Similarity 100.
Matches 188; Conservative
                                                                                                                                                                                                                                                                        Matches 188; Conservative
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                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                       392 AA;
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                                                                                                                                       SEQUENCE
                                                                                                                                                                                                          Query Match
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A WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broaks S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raber J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BEC010488; AAH71848.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
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PROSITE; PS50845; RETICULON; 1.
SEQUENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;
                                    Last sequence update)
Last annotation update)
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100.0%; Pred. No. 5.8e-71;
ive 0; Mismatches 0;
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Matches 188; Conservative
(TrEMBLrel.
                                    05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
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KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLM 122
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                                                                                                                                                                                                                                                                                    1 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ
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Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-22115887; PubMed=12832288;
MEDLINE-22115887; PubMed=12832288;
Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
"A reticular rhapsody: phylogenic evolution and nomenclature of the KTN/Nogo gene family.";
PASEB J. 17:1238-1247(2003)
-1- MISCELLANEOUS: The sequence shown here is derived from an EMBL; BROOL65: phylogopia party annotation (TPA) entry.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
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                                                                                                                                                               Score 919; DB 2; Length 187; Pred. No. 1.5e-70;
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                                                                                         NON TER 1 1 SEQUENCE 187 AA; 20967 MW; A17D87A143C4607C CRC64;
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PROSITE; PS50845; RETICULON; 1.
SEQUENCE · 199 AA; 22469 MW; 761A5FDB6C1DEC3C CRC64;
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Last sequence update)
Last annotation update)
    GO; GO:0005783; C:endoplasmic reticulum; IEA
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                        InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
                                                                                                                                                             Query Match
Best Local Similarity 99.5%;
Matches 186; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 GLKRKAE 189
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Matches 185; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9541;
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    SO FIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                           MEDLINE-22715887; PubMed=12832288;

Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;

A reticular rhapsody: phylogenic evolution and nomenclature of the TRIN/Nogo gene family.";

FASEB J. 17.1238-1247(2003).

-!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/Genbank/DDBJ third party annotation (TPA) entry.

GO, GO:0005783; C:endoplasmic reticulum; IEA.

InterPro; IPR003388; Reticulon.
                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;

A reticular Thapsody: phylogenic evolution and nomenclature of RTN/Nogo gene family.";

FASEB J. 17:1238-1247(2003).

-! MISCELLANGOUS: The sequence shown here is derived from an EMBL/Genbank/DbbJ third party annotation (TPA) entry.

EMBL; BK003966; DAA01973.1;
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Last annotation update)
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Last annotation update)
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                                                199
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                                                                                            Created)
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                                                                                       (TrEMBLrel. 27, TrEMBLrel. 27, TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, RTN4-Aw (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.5
Matches 187; Conservative
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                                                                                                                                                                                                      Sus scrofa (Pig).
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                                                                                       05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                   Name=RTN4;
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Q61G15;
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                                              061M70
RESULT 6
Q61M70
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Name=Rtn4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FVB/N; TISSUE=Mammary tumor. C3; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 578;
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                                                                                                                                                                                                                                                                                                                                                                                                                       578 AA; 63696 MW; 832670C171E4AC61 CRC64;
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Last annotation update)
                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.3%; Score 915; DB 2; 98.4%; Pred. No. 1e-69; ive 2; Mismatches 1;
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                                                                                                                                                                                                     Created)
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PROSITE; PS50845; RETICULON; 1.
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Matches 186; Conservative
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                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPGLKRKAE 189
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                                                       PGLKRKAE 199
                                                                                                                                                                                                                                                                Nogo-A (Fragment).
                PGLKRKAE
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                                                                                                                                                                                                                                                                                      Name=Nogo-A;
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SEQUENCE
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
R. Generation and initial analysis of more than 15,000 full-length human
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MEDLINE=22376840; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
OGertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2002) to the EMBL; BC032192; AAH32192.1; -. MGI, MGI, S15835; R.H4. GO, GO:0005783; C:endoplasmic reticulum; IEA. InterPro; IPR003388; Reticulon.
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Last annotation update)
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Pred. No. 1.2e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
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J. Mol. Biol. 325:299-323(2003).
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02453; Reticulon; 1. PROSITE; PS50845; RETICULON; 1.
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01-MAR-2003 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Best Local Similarity
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9

Gaps

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974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAXIALALLSVTISFRIXKGVIQA 1033
                                                                                                                                                                                                                                                                                                        1034 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1093
                                                                                                                                                                                                                                                                                                                                                               1094 IMMVPTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 1153
                                                                                                                                                                                                                                                                                     61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
                                                                                                                                                                                                                                                                                                                                               121 IMMVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=129/SvcJ7, and 129SvcJ7;

MEDINEE-22376540; PUMPGd=12488097; DOI=10.1016/S0022-2836(02)01179-8;

OGETIL T., Huber C., van der Putten H., Schwab M.E.;

"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                           1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NOBI_TaxID=10090;
                                                                                                                                                                                             ö
                                                                                                                                                              Length 1162;
                                                                                                                                                            98.3%; Score 915; DB 2; Length 11 98.4%; Pred. No. 2.1e-69; ive 2; Mismatches 1; Indels
            MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007399; P:neurogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PSS0845; RETICULON; 1.
SEQUENCE 1162 AA; 126612 MW; 855697FBEE11781F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvcJ7;
Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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PROSITE; PS50845; RETICULON; 1.
EMBL; AY102286; AAM73511.1; -.
                                                                                                                                                                            Best Local Similarity 98.4%;
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
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STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; Pubmed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                     Length 1046;
                                                                                                                                          MGD; MGI.1915835; REn4.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0001399; P:neurogenesis; IDA.
InterPro; IPR001388; Reticulon.
PFam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;
                                                                                                                                                                                                                                                                                                                                 1; Indels
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Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102284; AAM73506.1; -.
              Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                    Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102286; AAM73502.1; -.
EMBL; AY102286; AAM73507.1; -.
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Last annotation update)
                                                                                                                                                                                                                                                                                                  98.3%; Score 915; DB 2; 98.4%; Pred. No. 1.9e-69; ive 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003).
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Matches 186; Conservative
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01-MAR-2003 (TrEMBLrel. 23,
05-JUL-2004 (TrEMBLrel. 27,
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                                                        SEQUENCE FROM N.A. STRAIN=129SvcJ7;
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STRAIN=129/SvcJ7;
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Q8BGM9
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60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Q8BH78
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                                                                                                                                                                                                                                                        LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 366
                                                                                                                                                                   IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120
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SEQUENCE DF 170199 FROM N.A.

SEQUENCE DF 17199 FROM N.A.

CAZZAKI Y. FULTUDO M., KABUKAWA T., Adachi J., Bono H., Kondo S.,

CAZZAKI Y., FULTUDO M., KABUKAWA T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Golobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Baldarelli R., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Balae J., Satto D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

A Gasterland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,

Balae J., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawaji H., Marchioni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Perra B., Pons P.A.,

Nagashima T., Numata K., Okido T., Perra B., Pons P.A.,

Nagashima T., Reed D.J., Ring B.Z., Ringwal M.,

Sandelin A., Schneider C., Seepou M., Shimada K.,

Sandelin A., Schneider C., Seepou M., Shimada K.,

Nulming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Nulming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Nulming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Shiraki T., Waki K., Kawai D., Shibata R., Shinagawa I.,

Nalmicki A., Kawai L., Aizawa K., Arakawa T., Fikuda S.,

Nalmicki A., Nakhik K., Saaski K., Shibat K., Shinagawa R.,

Namishish A., Vanishish M., Saaski D., Shibata R.,

Namishish A., Shonicki K., Saaski D., Shibata R., Shinagawa R.,

Namishish A., Shaaski D., Shibata R., Shinagawa R.,

Namishish A., Shaaski D., Shibata R., Shinagawa R.,

Namishish A., Shaaski D., Shibata R., Shinagawa R.,

Namishish A., Shaaski D., Shibata R., Shinagawa R.,
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                                                                                                 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                  Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                   RIN4 MOUSE STANDARD; PRT; 199 AA.
099P72; O9CTE3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Retiqulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 40300 MW; 23D9EB19BE671AE6 CRC64;
                                                                   ij
                                 98.0%; Score 912; DB 2; 97.9%; Pred. No. 1.2e-69;
                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=3T3-L1; TISSUE=Adipocyte;
Coulson A.C., Craggs P.D., Morris N.J.;
"Mouse vp20/RTN4C cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 170-199 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Rtn4; Synonyms=NOGO;
Mus musculus (Mouse).
                                                                  Conservative
                                                                                                                                                                                                                                                                                                     IPGLKRKAE 189
                                                                                                                                                                                                                                                                                                                                      IPGLKRKAE 375
 375 AA;
                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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"Analysis of
                                                                Matches 185;
                                                                                                                                                                                                                                                                                                     181
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SEQUENCE
                                  Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
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Nature 420:563-573(2002).
-!- FUNCTION: Potent neurite outgrowth inhibitor which may also helblock the regeneration of the nervous central system in adults
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULÂR LOCATION: Integral membrane protein. Anchored to membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                    similarity).
-!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
Alternative splicing; Endoplasmic reticulum; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07BE5D580059ED9C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms may be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lumenal (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 911; DB 1;
Pred. No. 7.8e-70;
                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 reticulon domain.
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                                                                                                                                                                                                                                                                                                                                                            IsoId=Q99P72-1; Sequence=Displayed;
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01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22466 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF326337; AAK08076.1; -.
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98.4%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
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                                                                                                                                                                 Mus musculus (Mouse).
Wararyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/SvcJ7;
Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129SvcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102286; AAM73503.1; -.
EMBL; AY102286; AAM73508.1; -.
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PROSITE; PS50845; RETICULON; 1.
SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;
01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001255; P:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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